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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 142.194 Seconds  
(without alignments)  
49.440 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIVHSGNTYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	16	ADJ76836	Adj76836 CDR seque
2	81	100.0	16	ADZ67006	Adz67006 Murine in
3	81	100.0	112	ADJ76888	Adj76888 Anti-IGF-
4	81	100.0	112	ADJ76899	Adj76899 Anti-IGF-
5	81	100.0	112	ADJ76895	Adj76895 Anti-IGF-
6	81	100.0	112	ADZ67058	Adz67058 Murine im
7	81	100.0	112	ADZ67069	Adz67069 Human ant
8	81	100.0	112	ADZ67065	Adz67065 Human ant
9	81	100.0	114	AE821358	Aeb21358 Mouse ant
10	81	100.0	114	AE831116	Aeb31116 Antibody
11	81	100.0	122	ADJ76883	Adj76883 Anti-IGF-
12	81	100.0	122	ADZ67053	Adz67053 Murine im
13	81	100.0	131	ADJ76901	Adj76901 Anti-IGF-
14	81	100.0	131	ADJ76897	Adj76897 Anti-IGF-
15	81	100.0	131	ADZ67071	Adz67071 Human ant
16	81	100.0	131	ADZ67067	Adz67067 Human ant
17	79	97.5	238	AAW14937	Aaw14937 Murine an
18	79	97.5	238	AAW14942	Aaw14942 3F4 Human
19	79	97.5	251	AAW53587	Aay53587 Anti-HPV1
20	78	96.3	16	AAW70451	Aar70451 VL sequen
21	78	96.3	16	ABP52343	Abp52343 Fv region
22	78	96.3	16	ADC03151	Adc03151 Colon spe
23	78	96.3	16	ADD94147	Add94147 Mouse HUI
24	78	96.3	16	ADH61992	Adh61992 Mouse ant

Adl27487 CDR from  
Adm78123 Human SJB  
Adm78129 Human SJB  
Adm78081 Human SJB  
Adp84865 Complemen  
Adri9270 Glycosyla  
Adm87339 Humanised  
Aar27009 Hypercalc  
Aae06963 Mouse ger  
Aae06965 Mouse ger  
Adhl7816 Antibody  
Adq89248 Mouse imm  
Adq89250 Mouse imm  
Adw11447 House mou  
Aeb09521 Murine ge  
Aeb09523 Murine ge  
Abg74916 Murine NM  
Abp52310 Fv region  
Abg72733 Mouse U4  
Adc03138 Colon spe  
Aar32239 Humanised

#### ALIGNMENTS

RESULT 1  
ADJ76836  
ID ADJ76836 standard; peptide; 16 AA.  
XX AC ADJ76836;  
XX AC ADJ76836;  
DT 06-MAY-2004 (first entry)  
XX DE CDR sequence for anti-IGF-1R antibody.  
XX KW cytotstatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX OS Mus musculus.  
XX DN WO2003059951-A2.  
XX PD 24-JUL-2003.  
XX PF 20-JAN-2003; 2003WO-FR000178.  
XX PR 18-JAN-2002; 2002FR-00000653.  
PR 18-JAN-2002; 2002FR-00000654.  
XX PR 07-MAY-2002; 2002FR-00005753.  
PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX FI Goetsch L, Corvaia N, Leger O;  
XX DR WPI; 2003-569653/53.  
XX DR N-PSDB; ADJ76835.  
PT New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.  
XX PS Claim 1; SEQ ID NO 2; 164pp; French.  
XX CC The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC IR) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 81; DB 7; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-07; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0;  
 QY 1 RSSQSIHVSNGNTYLQ 16  
 Db 1 RSSQSIHVSNGNTYLQ 16  
 RESULT 2  
 ADZ67006  
 ID ADZ67006 standard; peptide; 16 AA.  
 AC ADZ67006;  
 XX  
 DT 30-JUN-2005 (first entry)  
 DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:2.  
 DE Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasia; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2005084906-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 PF 16-DEC-2003; 2003US-00735916.  
 XX  
 PR 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 PR 20-JAN-2003; 2003WO-FR000178.  
 PR 11-JUL-2003; 2003FR-00008538.  
 XX  
 PA (GOET/) GOETSCH L.  
 PA (CORV/) CORVAIA N.  
 PA (LEGE/) LEGER O.  
 PA (DUEL/) DUFLOS A.  
 PA (HAEU/) HAEUW J.  
 PA (BECK/) BECK A.  
 XX  
 PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 DR WPI; 2005-321968/33.  
 DR N-PSDB; ADZ67005.  
 XX  
 PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX  
 PS Claim 1; SEQ ID NO 2; 125pp; English.  
 PS  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 81; DB 9; Length 16;

Best Local Similarity 100.0%; Pred. No. 4.8e-07; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0;

QY 1 RSSQSIHVSNGNTYLQ 16

Db 1 RSSQSIHVSNGNTYLQ 16

RESULT 3

ADJ76888

ID ADJ76888 standard; protein; 112 AA.

XX

AC ADJ76888;

XX

DT 06-MAY-2004 (first entry)

XX

DE Anti-IGF-IR related protein #5.

XX

KW cytostatic; antipsoriatic; antibody;

KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;

KW or epidermal growth factor receptor; EGFR; signal transduction pathway;

KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;

XX CDR.

XX

OS Mus musculus.

XX

PN WO2003059951-A2.

XX

PD 24-JUL-2003.

XX

PF 20-JAN-2003; 2003WO-FR000178.

XX

PR 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

```

XX PI Goetsch L, Corvaia N, Leger O;
XX DR WPI; 2003-569653/53.
XX PT New antibodies that bind to human insulin-like growth factor receptor,
XX PT useful for treatment, prevention and diagnosis of cancers.
XX PS Disclosure; SEQ ID NO 54; 164pp; French.
XX CC The invention relates to an isolated antibody (Ab), and its functional
XX CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
XX CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
XX CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
XX CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
XX CC treat diseases associated with overexpression and/or abnormal activity of
XX CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
XX CC hyperactivity of signal transduction pathways mediated by interaction of
XX CC these receptors with their ligands. Especially they inhibit
XX CC transformation of normal cells to tumor cells, inhibit growth and/or
XX CC proliferation of tumor cells, so are useful against cancers of the
XX CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
XX CC also for treating psoriasis. Ab are also used to diagnose diseases caused
XX CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
XX CC protein sequence used to generate the Ab of the invention.
XX SQ Sequence 112 AA;

Query Match 100.0%; Score 81; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 24 RSSQSIVHSNGNTYLQ 39

RESULT 4
ID ADJ76899 standard; protein; 112 AA.
XX AC ADJ76899;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-IGF-1R related protein #14.
XX KW cytosolic; antipsoriatic; antibody;
XX KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
XX KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
XX KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
XX KW CDR.
XX OS Homo sapiens.
XX PN WO2003059951-A2.
XX XX 24-JUL-2003.
XX PF 20-JAN-2003; 2003WO-FR000178.
XX PR 18-JAN-2002; 2002FR-00000653.
XX PR 18-JAN-2002; 2002FR-00000654.
XX PR 07-MAY-2002; 2002FR-000005753.
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.
XX PI Goetsch L, Corvaia N, Leger O;
XX DR WPI; 2003-569653/53.
XX PT New antibodies that bind to human insulin-like growth factor receptor,
XX PT useful for treatment, prevention and diagnosis of cancers.

Query Match 100.0%; Score 81; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 24 RSSQSIVHSNGNTYLQ 39

RESULT 5
ID ADJ76899 standard; protein; 112 AA.
XX AC ADJ76899;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-IGF-1R related protein #12.
XX KW cytosolic; antipsoriatic; antibody;
XX KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
XX KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
XX KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
XX KW CDR.
XX OS Homo sapiens.
XX PN WO2003059951-A2.
XX XX 24-JUL-2003.
XX PF 20-JAN-2003; 2003WO-FR000178.
XX PR 18-JAN-2002; 2002FR-00000653.
XX PR 18-JAN-2002; 2002FR-00000654.
XX PR 07-MAY-2002; 2002FR-000005753.
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.
XX PI Goetsch L, Corvaia N, Leger O;
XX DR WPI; 2003-569653/53.
XX PT New antibodies that bind to human insulin-like growth factor receptor,
XX PT useful for treatment, prevention and diagnosis of cancers.

```

CC kinase activity of IGF-IR. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 112 AA;

Query Match 100.0%; Score 81; DB 7; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16  
 |||||  
 Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 6  
 AD267058  
 ID AD267058 standard; protein; 112 AA.

AC AD267058;  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:54.  
 XX  
 KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW immunoglobulin; light chain variable region.  
 XX  
 OS Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFLOS A.

PA (HAEU/) HAEUW J.

PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

PT antibody or its functional fragment, being capable of binding human IGF-

PT IR and specifically inhibiting tyrosine kinase activity of receptor,

PT useful for treating cancer.

XX

XX Example 12; SEQ ID NO 54; 125pp; English.

PS

XX

CC The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (AD267006 and AD267014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX Sequence 112 AA;

Query Match 100.0%; Score 81; DB 9; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16

Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 7

AD267069

ID AD267069 standard; protein; 112 AA.

AC AD267069;

DT 30-JUN-2005 (first entry)

XX

DE Human antibody 7C10 2 light chain variable region SEQ ID NO:65.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;

KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;

KW musculoskeletal disease; respiratory disease; lung tumor;

KW endocrine disease; gynecology and obstetrics; breast tumor;

KW endometrial carcinoma; gastrointestinal disease; colon tumor;

KW antipsoriatic; psoriasis; dermatological disease; immune disorder;

KW light chain variable region.

XX

OS Homo sapiens.

XX US2005084906-A1.

PN 21-APR-2005.

PD

XX 16-DEC-2003; 2003US-00735916.

PF

XX





CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX  
 SQ Sequence 112 AA;

Query Match 100.0%; Score 81; DB 9; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 56-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;

QY 1 RSSQSIHVSNGNTYLQ 16  
 |||||  
 DB 24 RSSQSIHVSNGNTYLQ 39

RESULT 9  
 AEB21358  
 ID AEB21358 standard; protein; 114 AA.

XX AEB21358;

DT 22-SEP-2005 (first entry)

XX Mouse anti-IL-13 antibody 227-26 light chain variable region (VK).

XX Interleukin-13; IL-13; antibody engineering; humanized antibody;  
 KW Antiasthmatic; Antiinflammatory; Dermatological; Antiallergic;  
 KW Respiratory-Gen.; Antitumor; Gastrointestinal-Gen.; Ophthalmological;  
 KW Osteopathic; Virucide; asthma; allergic rhinitis; atopic dermatitis;  
 KW allergic conjunctivitis; eczema; urticaria; allergy;  
 KW chronic obstructive pulmonary disease; ulcerative colitis;  
 KW respiratory syncytial virus infection; uveitis; scleroderma;  
 KW osteoporosis; monoclonal antibody; light chain variable region.

XX Mus sp.

XX WO2005062967-A2.

XX 14-JUL-2005.

XX 23-DEC-2004; 2004WO-US043501.

XX 23-DEC-2003; 2003US-0532130P.

XX (TANO-) TANOX INC.

XX Fung SC, Moyle M, Lu M, Yan C, Singh S, Huang D;

XX WPI; 2005-506603/51.

XX New antibody or its antigen-binding fragment that binds specifically and  
 PT with high affinity to glycosylated and non-glycosylated human interleukin  
 PT -13 (IL-13), useful for treating IL-13-mediated disorders, such as asthma  
 PT and eczema.

XX Claim 10; SEQ ID NO 7; 129pp; English.

CC The invention relates to an antibody or its antigen-binding fragment that  
 CC binds specifically and with high affinity to glycosylated and non-  
 CC glycosylated human interleukin-13 (IL-13), does not bind mouse IL-13, and  
 CC neutralizes human IL-13 activity at an approximate molar ratio of 1:2  
 CC (Mab:IL13). Also included are an antibody that binds to the same epitope  
 CC as the antibody cited above, an antibody comprising antigen binding  
 CC regions derived from the light and heavy chain variable regions of the  
 CC novel antibody, a hybridoma cell line that produces a monoclonal antibody  
 CC (selected from 228B/C-1, 228A-4, 227-26, and 227-43 and designated with  
 CC the ATCC deposit number PTA-5657, PTA-5656, PTA-5654, and PTA-5655,  
 CC respectively), a cell line comprising a nucleic acid encoding the  
 CC antibody, a vector comprising the nucleic acid encoding the antibody, a  
 CC composition (comprising the antibody and a physiologically acceptable  
 CC carrier, diluent, excipient, or stabilizer), a variable light chain  
 CC region (comprising an amino acid sequence having the formula: FRL1-CORL1-  
 CC FRL2-CORL2-FRL3-CORL3-FRL4) a variable heavy chain region (comprising an  
 CC amino acid sequence having the formula: FRH1-CORH1-FRH2-CORH2-FRH3-CORH3-  
 CC FRH4), an antibody (or its antigen binding fragment, comprising the  
 CC variable light or heavy chain region, where the antibody binds  
 CC specifically to IL-13), treating a subject suffering from asthmatic  
 CC symptoms (comprising administering an antibody to reduce the asthmatic  
 CC symptoms), an inhalation device that delivers the antibody to a patient,  
 CC detecting interleukin-13 protein in a sample, diagnosing overexpression  
 CC of IL-13 in a subject, producing the antibody, a recombinant antibody  
 CC molecule (or an IL-13-binding fragment, comprising at least one antibody  
 CC heavy chain, or an IL-13-binding fragment, comprising non-human CDRs at  
 CC positions 31-35 (CDR1), 50-65 (CDR2) and 95-102 (CDR3) (Kabat numbering)  
 CC from a mouse anti-IL-13 antibody, where positions 27-30 have the amino  
 CC acid Gly 26, Phe 27, Ser 28, Leu 29, Asn 30), and at least one antibody  
 CC light chain (or an IL-13-binding fragment, comprising non-human CDRs at  
 CC positions 24-34 (CDR1), 50-56 (CDR2) and 89-97 (CDR3) from a mouse anti-  
 CC IL13 antibody and framework regions from a monoclonal antibody), a vector  
 CC comprising the DNA sequence, a host cell comprising the vector,  
 CC inhibiting IGE antibody production in a patient, treating an IL-13-  
 CC mediated disorder in a patient, reducing the severity of asthma in a  
 CC mammal, and an IL-13 epitope peptide appearing as AEB21369 or AEB21370.  
 CC The antibody and methods are useful for treating IL-13-mediated  
 CC disorders, such as allergic asthma, non-allergic (intrinsic) asthma,  
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis, eczema,  
 CC urticaria, food allergies, chronic obstructive pulmonary disease,  
 CC ulcerative colitis, RSV infection, uveitis, scleroderma, or osteoporosis.  
 CC The present sequence represents a the light chain variable region of a  
 CC mouse anti-IL-13 monoclonal antibody.

Sequence 114 AA;

Query Match 100.0%; Score 81; DB 9; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;

QY 1 RSSQSIHVSNGNTYLQ 16  
 |||||  
 DB 24 RSSQSIHVSNGNTYLQ 39

RESULT 10  
 AEB31116

ID AEB31116 standard; protein; 114 AA.

AC AEB31116;

DT 22-SEP-2005 (first entry)

DE Antibody 227-26/227-26.1 variable light chain.

XX cytostatic; antibody therapy; neoplasm; interleukin 13; IL-13; cancer;  
 KW diagnosis; tumor; humanized antibody; cell proliferation;  
 KW Hodgkin disease; cytotoxin; chemotherapy; lymphoma; skin tumor;  
 KW stomach tumor; colon tumor; breast tumor; pancreatic tumor; liver tumor;  
 KW prostate tumor; lung tumor; head and neck tumor; renal tumor;  
 KW squamous cell carcinoma; brain tumor; Kaposi's carcinoma; solid tumor;  
 KW monoclonal antibody; 227-26; 227-26-1, light chain variable region.

OS Mus sp.  
XX Synthetic.  
XX WO2005062972-A2.  
XX 14-JUL-2005.  
XX 23-DEC-2004; 2004WO-US043541.  
XX 23-DEC-2003; 2003US-0532130P.  
XX (TANO-) TANOX INC.  
XX Pung SC, Moyle M;  
XX WPI; 2005-506604/51.  
XX Treating a neoplasm, e.g. Hodgkin's disease, that expresses and/or binds  
PT interleukin-13 (IL-13) comprises administering an anti-IL-13 antibody or  
PT its binding fragment that binds to both glycosylated and non-glycosylated  
PT human IL-13.  
XX Claim 13; SEQ ID NO 7; 98pp; English.  
XX This invention describes a novel method for treating a neoplasm that  
CC expresses and/or binds interleukin-13 (IL-13). The method comprises  
CC administering an anti-IL-13 antibody or its binding fragment that binds  
CC specifically and with high affinity to both glycosylated and non-  
CC glycosylated human IL-13, and neutralizes human IL-13 activity at an  
CC approximate molar ratio of 1:2 (MAB:IL-13). The method also describes 1)  
CC a method for treating Hodgkin's disease comprising administering a  
CC humanized or chimeric antibody or binding fragment to a patient; 2)  
CC inhibiting IL-13 dependent proliferation of neoplastic cells in a mammal  
CC comprising administering the antibody, or a binding fragment that  
CC inhibits the biological activity of IL-13 and 3) diagnosing a cancer or  
CC tumor overexpressing IL-13 comprising the use of the anti-IL-13 antibody  
CC to detect overexpression of IL-13 in the biological sample taken from a  
CC patient suspected of having the cancer or tumor. The antibodies used in  
CC the method of the invention are 228B/C produced by the hybridoma  
CC designated PTA-5657, 228A-4 and produced by the hybridoma designated PTA-  
CC 5656; 227-26, produced by the hybridoma designated PTA-5654; or 227-43  
CC produced by the hybridoma designated PTA-5655. The antibody is a human  
CC antibody, a chimeric antibody, a single domain antibody or a humanized  
CC antibody. The antibody is a fragment, such as Fv, Fab, and F(ab')<sub>2</sub>  
CC fragments, single-chain antibodies such as scFv, and various chain  
CC combinations. The antibody further comprises a physiologically acceptable  
CC carrier, diluent, excipient, or stabilizer. The antibody mediates killing  
CC by antibody dependent cell-mediated cytotoxicity and/or complement  
CC mediated cytotoxicity. The antibody comprises at least a variable, light  
CC chain region comprising an amino acid sequence having the formula: FRU1-  
CC CDRU1-FRU2-CDRL2-FRU3-CDRL3-FRU4. The antibody comprises at least a  
CC variable light or heavy chain region. The variable light or heavy chain  
CC region further comprises a constant region. The constant region is from  
CC an IgG antibody. The IgG antibody is an IgG1, IgG2, IgG3 or an IgG4  
CC antibody. The antibody further comprises the heavy chain. The antibody is  
CC associated with a cytotoxic agent, such as a radioisotope or a  
CC chemotherapeutic agent. The methods and antibodies are useful for  
CC treating neoplasms such as Hodgkin's lymphoma, skin cancer, stomach  
CC cancer, colon cancer, breast cancer, pancreatic cancer, liver cancer,  
CC prostate cancer, lung cancer, head-and-neck cancer, renal cell cancer,  
CC squamous cell carcinoma, AIDS-associated Kaposi's carcinoma and brain  
CC cancer. This sequence represents the humanized mouse monoclonal antibody  
CC 227-26 and 227-26-1 variable light chain.  
XX Sequence 114 AA;  
SQ  
Query Match 100.0%; Score 81; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RSSQSIVHSNGNTYLIQ 16  
DB 24 RSSQSIVHSNGNTYLIQ 39

RESULT 11  
ADJ76883  
ID ADJ76883 standard; protein; 122 AA.  
XX  
XX ADJ76883;  
XX  
XX 06-MAY-2004 (first entry)  
DT  
DE  
DE Anti-IGF-1R related protein #3.  
XX  
XX cytostatic; antiproliferative; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX  
XX Mus musculus.  
OS  
XX  
XX WO2003059951-A2.  
PN  
XX  
XX 24-JUL-2003.  
PD  
XX  
XX 20-JAN-2003; 2003WO-FR000178.  
PF  
XX  
XX 18-JAN-2002; 2002FR-00000653.  
PR  
XX 18-JAN-2002; 2002FR-00000654.  
PR  
XX 07-MAY-2002; 2002FR-00005753.  
PR  
XX (FABR ) PABRE MEDICAMENT SA PIERRE.  
PA  
XX  
XX Goetsch L, Corvaia N, Leger O;  
PI  
XX WPI; 2003-569653/53.  
XX  
XX New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.  
XX  
XX Disclosure; SEQ ID NO 49; 164pp; French.  
PS  
XX The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
CC hyperactivity of signal transduction pathways mediated by interaction of  
CC these receptors with their ligands. Especially they inhibit  
CC transformation of normal cells to tumor cells, inhibit growth and/or  
CC proliferation of tumor cells, so are useful against cancers of the  
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
CC protein sequence used to generate the Ab of the invention.  
XX  
XX Sequence 122 AA;  
SQ  
Query Match 100.0%; Score 81; DB 7; Length 122;  
Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RSSQSIVHSNGNTYLIQ 16  
DB 34 RSSQSIVHSNGNTYLIQ 49

RESULT 12  
ADZ67053  
ID ADZ67053 standard; protein; 122 AA.  
XX  
XX ADZ67053;  
AC

XX 30-JUN-2005 (first entry)

DE Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:49.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;

KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;

KW musculoskeletal disease; respiratory disease; lung tumor;

KW endocrine disease; gynecology and obstetrics; breast tumor;

KW endometroid carcinoma; gastrointestinal disease; colon tumor;

KW antipsoriatic; psoriasis; dermatological disease; immune disorder;

XX immunoglobulin, light chain variable region.

OS Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..10

FT /note= "leader peptide"

FT Region 34..49

FT /note= "CDR1"

FT Region 65..71

FT /note= "CDR2"

FT Region 104..111

FT /note= "CDR3"

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFLOS A.

PA (HAEU/) HAEUW J.

PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI: 2005-321968/33.

DR N-PSDB; AD267052.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.

XX Example 8; SEQ ID NO 49; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (AD267006 and AD267014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-

CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.

XX Sequence 122 AA;

Query Match 100.0%; Score 81; DB 9; Length 122;  
Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVSNGNTYLQ 16  
| | | | | | | | | | | | | | | |  
Db 34 RSSQSIHVSNGNTYLQ 49

RESULT 13

ADJ76901

ID ADJ76901 standard; protein; 131 AA.

AC ADJ76901;

DT 06-MAY-2004 (first entry)

DE Anti-IGF-IR related protein #15.

XX cytostatic; antipsoriatic; antibody;

XX insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;

XX or epidermal growth factor receptor; EGFR; signal transduction pathway;

XX ligand; tumor; cancer; osteosarcoma; complementarity determining region;

XX CDR.

OS Homo sapiens.

XX WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

PR 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

PI Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 67; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 131 AA;

Query Match 100.0%; Score 81; DB 7; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVSNGNTYLQ 16  
 DB 43 RSSQSIHVSNGNTYLQ 58  
 |||||  
 |||||

RESULT 14  
 ADJ76897  
 ID ADJ76897 standard; protein; 131 AA.

AC ADJ76897;

XX 06-MAY-2004 (first entry)

XX Anti-IGF-1R related protein #13.

XX cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX Homo sapiens.

XX WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,

XX useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 63; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the

CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 131 AA;

Query Match 100.0%; Score 81; DB 7; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVSNGNTYLQ 16  
 DB 43 RSSQSIHVSNGNTYLQ 58  
 |||||  
 |||||

RESULT 15  
 ADZ67071  
 ID ADZ67071 standard; protein; 131 AA.

XX AC ADZ67071;

XX 30-JUN-2005 (first entry)

XX Human antibody 7C10 2 light chain variable region SEQ ID NO:67.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW light chain variable region.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Peptide 1..19  
 /note= "leader peptide"

FT Region 43..58  
 /note= "CDR1"

FT Region 74..80  
 /note= "CDR2"

FT Region 113..121  
 /note= "CDR3"

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUEF/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX N-PSDB; ADZ67070.

Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 antibody or its functional fragment, being capable of binding human IGF-  
 IR and specifically inhibiting tyrosine kinase activity of receptor,

PT useful for treating cancer.  
XX  
PS  
XX Example 12; SEQ ID NO 67; 125pp; English.  
CC  
CC The invention relates to a novel isolated anti-insulin-like growth factor  
CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
CC capable of binding to human IGF-IR and, if necessary, capable of  
CC specifically inhibiting tyrosine kinase activity of the receptor,  
CC comprising a light or heavy chain having at least one complementary  
CC determining region (CDR) consisting of one of two fully defined 16 amino  
CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
CC the preparation of a medicament intended for the prevention or treatment  
CC of an illness connected with an overexpression and/or an abnormal  
CC activation of the IGF-IR and/or EGFR, and/or connected with a  
CC hyperactivation of the transduction pathway of the signal mediated by the  
CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
CC the administration of the medicament does not induce or only slightly  
CC induces secondary effects connected with inhibition of the insulin  
CC receptor. The antibody is useful for preparation of a medicament intended  
CC to inhibit the transformation of normal cells into cells with tumoral  
CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
CC useful for preparation of a medicament intended to inhibit the growth  
CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
CC medicament intended for prevention or for the treatment of cancer, where  
CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
CC preparation of a medicament intended for the prevention or for the  
CC treatment of psoriasis. (I) is useful in preparation of a medicament  
CC intended for the specific targeting of a biologically active compound to  
CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
CC is useful for in vitro diagnosis of illnesses induced by an  
CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
CC starting from a biological sample in which the abnormal presence, of IGF-  
CC IR and/or EGFR receptor is suspected, which involves contacting the  
CC biological sample with (I), which is optionally labeled. The present  
XX sequence is used in the exemplification of the invention.  
SQ Sequence 131 AA;

Query Match 100.0%; Score 81; DB 9; Length 131;  
Best Local Similarity 100.0%; Pred. No. 6.1e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RSSQSIVHSGNTYIQ 16  
Db 43 RSSQSIVHSGNTYIQ 58

Search completed: December 30, 2005, 13:23:55  
Job time : 144.194 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 22.7097 Seconds  
(without alignments)  
67.789 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIVHSGNTYLIQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	97.5	130	2 C29380	Ig kappa chain pre
2	79	97.5	131	2 D29380	Ig kappa chain pre
3	78	96.3	46	2 S07456	Ig kappa chain v r
4	78	96.3	91	2 S25463	Ig kappa chain v r
5	78	96.3	93	2 S24502	Ig kappa chain v r
6	78	96.3	99	2 S24504	Ig kappa chain v r
7	78	96.3	99	2 S24501	Ig kappa chain v r
8	78	96.3	101	2 S11126	Ig kappa chain v r
9	78	96.3	102	2 S14590	Ig kappa chain v r
10	78	96.3	103	2 PH1042	Ig light chain v r
11	78	96.3	103	2 PH1043	Ig light chain v r
12	78	96.3	110	2 S26335	Ig kappa chain v r
13	78	96.3	112	2 P27887	Ig kappa chain v r
14	78	96.3	112	2 A31807	Ig kappa chain v r
15	78	96.3	113	2 P10203	anti-DNA autoantib
16	78	96.3	113	2 S24538	Ig kappa chain v r
17	78	96.3	118	2 S24536	Ig kappa chain v r
18	78	96.3	118	2 S24503	Ig kappa chain v r
19	78	96.3	118	2 S24531	Ig kappa chain v r
20	78	96.3	118	2 S24535	Ig kappa chain v r
21	78	96.3	118	2 S24535	Ig kappa chain v r
22	78	96.3	118	2 S24500	Ig kappa chain v r
23	78	96.3	118	2 S24508	Ig kappa chain v r
24	78	96.3	118	2 S24506	Ig kappa chain v r
25	78	96.3	118	2 S24532	Ig kappa chain v r
26	78	96.3	118	2 S24507	Ig kappa chain v r
27	78	96.3	118	2 S24537	Ig kappa chain v r
28	78	96.3	118	2 S24539	Ig kappa chain v r
29	78	96.3	119	2 A45032	Ig kappa chain v r

30	78	96.3	131	2 B39276	Ig light chain pre
31	78	96.3	219	2 S52028	Ig kappa chain - m
32	75	93.8	46	2 S07455	Ig kappa chain v r
33	75	92.6	112	2 B31485	Ig kappa chain v r
34	75	92.6	118	2 S24509	Ig kappa chain v r
35	75	92.6	131	2 D34904	Ig kappa chain pre
36	75	92.6	219	2 PC4203	Ig kappa chain (mo
37	74	91.4	93	2 PH1039	Ig light chain v r
38	74	91.4	100	2 A28833	Ig heavy chain v r
39	74	91.4	100	2 S26334	Ig light chain v r
40	74	91.4	103	2 PH1040	Ig light chain v r
41	74	91.4	103	2 PH1031	Ig light chain v r
42	74	91.4	103	2 PH1038	Ig light chain v r
43	74	91.4	103	2 PH1030	Ig light chain v r
44	74	91.4	103	2 PH1037	Ig light chain v r
45	74	91.4	107	2 D32530	Ig kappa chain v r

ALIGNMENTS

RESULT 1

C29380

Ig kappa chain precursor V region (BC-1004) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 21-Jul-2000

C;Accession: C29380

R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.

J. Biol. Chem. 262, 13579-13583, 1987

A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable

A;Reference number: A92612; MUID:88007582; PMID:3115981

A;Accession: C29380

A;Molecule type: mRNA

A;Residues: 1-130 <CHE>

A;Cross-references: UNIPARC:UPI000011677D; GB:M17162; GB:J02815; NID:g196899; PIDN:AAA38

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-113/Domain: immunoglobulin homology <IMM>

Query Match 97.5%; Score 79; DB 2; Length 130;

Best Local Similarity 93.8%; Pred. No. 3.4e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNTYLIQ 16

Db 42 RSSQSLVHSGNTYLIQ 57

RESULT 2

D29380

Ig kappa chain precursor V region (B003 46/2D7) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004

C;Accession: D29380

R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.

J. Biol. Chem. 262, 13579-13583, 1987

A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable

A;Reference number: A92612; MUID:88007582; PMID:3115981

A;Accession: D29380

A;Molecule type: mRNA

A;Residues: 1-131 <CHE>

A;Cross-references: UNIPROT:Q8VC16; UNIPARC:UPI000017678A

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-113/Domain: immunoglobulin homology <IMM>

Query Match 97.5%; Score 79; DB 2; Length 131;

Best Local Similarity 93.8%; Pred. No. 3.5e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNTYLIQ 16

Db 42 RSSQSLVHSGNTYLIQ 57

```
RESULT 3
S07456
IG kappa chain V region (hybridoma G8 Ad 3.8) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-May-1997
C:Accession: S07456
R:Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A:Reference number: S07453; MUID:83058021; PMID:6815271
A:Accession: S07456
A:Molecule type: protein
A:Residues: 1-46 <ROC>
A:Cross-references: UNIPARC:UPI0000176D8D
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      96.3%; Score 78; DB 2; Length 46;
Best Local Similarity 93.8%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLE 39

RESULT 4
S25463
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S25463
R:Noneatier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A:Description: Structure and binding properties of monoclonal antibodies to core histone
A:Reference number: S25174
A:Accession: S25463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <MON>
A:Cross-references: UNIPARC:UPI00001160C6; EMBL:X67624; NID:952189; PIDN:CAA47882.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      96.3%; Score 78; DB 2; Length 91;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLE 39

RESULT 5
S24502
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24502
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24502
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <KAA>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B20; EMBL:X66639
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-89/Domain: immunoglobulin homology <IMM>

Query Match      96.3%; Score 78; DB 2; Length 91;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLE 39

RESULT 6
S24504
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24504
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24504
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <KAA>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B19; EMBL:X66641
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      96.3%; Score 78; DB 2; Length 99;
Best Local Similarity 93.8%; Pred. No. 3.8e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLE 39

RESULT 7
S24501
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24501
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24501
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <KAA>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B17; EMBL:X66638
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      96.3%; Score 78; DB 2; Length 99;
Best Local Similarity 93.8%; Pred. No. 3.8e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLE 39

RESULT 8
S11126
IG kappa chain V region (clone NQ2-45.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 23-Aug-1997
C:Accession: S11126
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
```

```
Query Match      96.3%; Score 78; DB 2; Length 93;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      18 RSSQSIVHSNGNTYLE 33

RESULT 6
S24504
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24504
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24504
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <KAA>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B19; EMBL:X66641
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      96.3%; Score 78; DB 2; Length 99;
Best Local Similarity 93.8%; Pred. No. 3.8e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLE 39

RESULT 7
S24501
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24501
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24501
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <KAA>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B17; EMBL:X66638
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      96.3%; Score 78; DB 2; Length 99;
Best Local Similarity 93.8%; Pred. No. 3.8e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLE 39

RESULT 8
S11126
IG kappa chain V region (clone NQ2-45.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 23-Aug-1997
C:Accession: S11126
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
```



A;Accession: S11126  
A;Molecule type: mRNA  
A;Residues: 1-101 <NAT>  
A;Cross-references: UNIPARC:UPI0000176E8F  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match           96.3%; Score 78; DB 2; Length 101;  
Best Local Similarity 93.8%; Pred. No. 3.9e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNTYLQ 16  
| | | | | | | | | |  
Db 24 RSSQSIVHSGNTYLE 39

RESULT 9  
S14590  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S14590; S14589  
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.  
submitted to the EMBL Data Library, March 1991  
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH C  
A;Reference number: S14484  
A;Accession: S14590  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-102 <CHE>  
A;Cross-references: UNIPARC:UPI0000115F40; EMBL:X58662; MID:g52927; PIDN:CMA41519.1; PTD:  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
P:16-95/Domain: immunoglobulin homology <IMW>

```

Query Match          96.3%; Score 78; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. No. 3.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSGNTYIQ 16
      |||||
DB      24 RSSQSIVHSGNTYLE 39

RESULT 10
PHI042
Ig light chain V region (clone 202.s38) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PHI042
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PHI042
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-103 <TIL>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176AA4
A:Experimental source: B cell, strain [NZB x NZM]F1
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: immunoglobulin
P:16-95/Domain: immunoglobulin homology <IMM>

```

```

Query Match          96.3%;   Score 78;   DB 2;   Length 103;
Best Local Similarity 93.8%;   Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  RSSQSIHVSNGNTYLIQ 16
        |||||
Db      24  RSSQSIHVSNGNTYLE 39
        |||||

RESULT 11

```

PH1043  
Ig light chain V region (clone 1l1.68) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993#sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: PH1043  
F:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971, MUID:92381444; PMID:1512540  
A:Accession: PH1043  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-103 <fil>  
A:Cross-references: UNIPROT:Q9M37; UNIPARC:UPI0000176AA5  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin v region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

```

Query Match      96.3%; Score 78; DB 2; Length 103;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNTYLQ 16
   |||||
DB 24 RSSQSIVHSGNTYLE 39

```

RESULT 12

S26335  
Ig kappa chain V region - mouse  
S26335  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26335  
R:Stark, S.B.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e  
A:Reference number: S26309; MUID:91341421; PMID:1908510  
A:Accession: S26335  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-110 <STA>  
A:Cross-references: UNIPARC:UPI0000115F78; EMBL:X51983; NID:G52314; PIDN:CAA41893.1; PIR  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
P:16-95/Domain: immunoglobulin homology <IMM>

Query Match	96.3%	Score 78;	DB 2;	Length 110;
Best Local Similarity	93.8%	Pred. No.	4.2e-06;	
Matches 15;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 RSSQSIVHSGNGNTYLQ	16		
DG	24 RSSQSIVHSGNGNTYLE	39		

RESULT 13  
F27887  
Ig kappa chain V region (HIC5-4D1) - mouse  
C.Species: Mus musculus (house mouse)  
C.Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C.Accession: F27887  
R.Catlon, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A.Title: Structural and functional implications of a restricted antibody response to a d  
A.Reference number: A91043; MUID:86300658; PMID:2427335

A;Residues: 1-112 <CAT>  
A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176A19  
A;Experimental source: Strain Balb/c  
A;Note: This sequence was determined from the germline gene  
A;Comment: This chain was isolated from a hybridoma protein that binds influenza virus

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 96.3%; Score 78; DB 2; Length 112;  
Best Local Similarity 93.8%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHNSNGNTYLQ 16  
|||  
Db 24 RSSQSIVHNSNGNTYLE 39

## RESULT 14

A31807  
IG kappa chain V region (PAC1) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Jul-1989 #sequence\_revision 20-Jul-1989 #text\_change 09-Jul-2004  
C;Accession: A31807  
R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt  
J. Biol. Chem. 264, 259-265, 1989  
A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a sequ  
A;Reference number: A31807; MUID:89079661; PMID:2909518  
A;Accession: A31807  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <TAU>  
A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI00001424F9  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 96.3%; Score 78; DB 2; Length 112;  
Best Local Similarity 93.8%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHNSNGNTYLQ 16  
|||  
Db 24 RSSQSIVHNSNGNTYLE 39

## RESULT 15

PL0203  
anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: PL0203  
R;Smith, R.G.; Voss Jr., E.W.  
Mol. Immunol. 27, 463-470, 1990  
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N  
A;Reference number: PL0198; MUID:90309768; PMID:2114528  
A;Accession: PL0203  
A;Molecule type: mRNA  
A;Residues: 1-113 <SMI>  
A;Cross-references: UNIPARC:UPI0000113786; GB:X53643; NID:G50196; PIDN:CAA37694.1; PID:G  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-95/Domain: immunoglobulin homology <IMM>  
F;24-39/Region: complementarity-determining 1  
F;55-61/Region: complementarity-determining 2  
F;94-102/Region: complementarity-determining 3  
F;101-113/Region: D region

Query Match 96.3%; Score 78; DB 2; Length 113;  
Best Local Similarity 93.8%; Pred. No. 4.4e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHNSNGNTYLQ 16  
|||  
Db 24 RSSQSIVHNSNGNTYLE 39

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 144 Seconds  
(without alignments)  
78.392 Million cell updates/sec

Title: US-10-735-916A-2  
Perfect score: 81  
Sequence: 1 RSSQSIHNGNTVLQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	91.4	113	1 KV2G_MOUSE	P01631 mus musculus
2	74	91.4	115	2 QSF2IO_MOUSE	Q5f2i0 mus musculus
3	72	88.9	248	2 Q5ZQ7_MOUSE	Q5zq7 mus sp. b3(
4	71	87.7	219	2 Q5ZCO_MOUSE	Q5zco mus musculus
5	68	84.0	239	2 Q6P491_HUMAN	Q6p491 homo sapien
6	67	82.7	113	1 KV2F_MOUSE	P01630 mus musculus
7	63	77.8	86	2 Q7Z3V5_HUMAN	Q7z3v5 homo sapien
8	63	77.8	133	1 KV2F_HUMAN	P06310 homo sapien
9	62	76.5	239	2 Q5E08_MOUSE	Q5e08 mus musculus
10	61	75.3	112	2 Q5LEM8_MOUSE	Q5lem8 mus musculus
11	60	74.1	239	2 Q8TCD0_HUMAN	Q8tcd0 homo sapien
12	58	71.6	112	2 Q53VP8_MOUSE	Q53vp8 mus musculus
13	58	71.6	113	1 KV2B_MOUSE	P03976 mus musculus
14	58	71.6	114	2 Q9UL80_HUMAN	Q9ul80 homo sapien
15	58	71.6	117	1 KV2B_HUMAN	P06309 homo sapien
16	57	70.4	113	1 KV2B_HUMAN	P01615 homo sapien
17	56	69.1	234	2 Q5XKG4_MOUSE	Q5xkg4 mus musculus
18	54	66.7	240	2 Q6PIH6_HUMAN	Q6pih6 homo sapien
19	53	65.4	239	2 Q8NEK0_HUMAN	Q8nek0 homo sapien
20	52	64.2	113	1 KV2D_HUMAN	P01617 homo sapien
21	49	60.5	202	2 Q86IX8_DICDI	Q86ix8 dictyosteli
22	46.5	57.4	115	1 KV2A_HUMAN	P01614 homo sapien
23	46	56.8	112	1 KV2A_MOUSE	P01626 mus musculus
24	46	56.8	113	1 KV2C_MOUSE	P01628 mus musculus
25	46	56.8	120	1 KV2B_MOUSE	P01627 mus musculus
26	46	56.8	172	2 Q8PR28_XANAC	Q8pr28 xanthomonas
27	46	56.8	2738	2 Q5EN26_DEBHA	Q5en26 debaryomyce
28	45	55.6	393	2 Q4PDR3_USTMA	Q4pdr3 ustilago ma
29	45	55.6	771	2 Q5AVM5_DICDI	Q5avm5 dictyosteli
30	45	55.6	1976	2 Q7NAT4_MYCGA	Q7nat4 mycoplasma
31	44	54.3	302	2 Q7Y106_9LAMI	Q7y106 antirrhinum

32	44	54.3	448	2	Q8A7N7_BACTN	Q8a7n7 bacteroides
33	44	54.3	480	2	Q9LRN2_ARATH	Q9lrn2 arabidopsis
34	44	54.3	2399	2	Q9ZKS9_HELPJ	Q9zks9 helicobacte
35	44	54.3	2529	2	Q25579_HELPJ	Q25579 helicobacte
36	43.5	53.7	647	2	Q68S95_CHDEL	Q68s95 chlorella e
37	43	53.1	118	2	Q08922_MOUSE	Q08922 mus muscula
38	43	53.1	283	2	Q8EHQ2_SHEON	Q8ehq2 shewanella
39	43	53.1	318	2	Q6V4Z7_SCHMA	Q6v4z7 schistosoma
40	43	53.1	327	2	Q26703_TRYBR	Q26703 trypanosoma
41	43	53.1	438	2	Q4W58_ASPEU	Q4w58 aspergillus
42	43	53.1	873	2	Q9SV81_DROME	Q9sv81 drosophila
43	43	53.1	882	2	Q7YU02_DROME	Q7yu02 drosophila
44	43	53.1	1409	2	Q4QGZ6_LEIMA	Q4qgz6 leishmania
45	43	53.1	1643	2	Q9G244_PLAF7	Q9g244 plasmodium

ALIGNMENTS

RESULT 1

KV2G\_MOUSE  
ID KV2G\_MOUSE STANDARD; PRT; 113 AA.  
AC P01631;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-II region 26-10.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=83178921; PubMed=6404298;  
RA Novotny J., Margolies M.N.;  
RT "Amino acid sequence of the light chain variable region from a mouse  
anti-digoxin hybridoma antibody."  
RL Biochemistry 22:1153-1158(1983).  
CC -1- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma  
protein that binds digoxin.

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use as long as its content is in no way modified and this statement is not  
removed.  
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PIR: A01914; KWS26.  
HSSP: Q99W37, 1191.  
ENSEMBL: ENSMUSG00000055315; Mus musculus.  
InterPro: IPR007110; Ig-like.  
InterPro: IPR003596; Ig\_v.  
SMART: SM00406; IGV; 1.  
PROSITE: PS50835; IG\_LIKE; 1.  
Direct protein sequencing; Hybridoma; Immunoglobulin domain;  
Immunoglobulin v region; Monoclonal antibody.  
REGION 1 23  
REGION 24 39  
REGION 40 54  
Complementarity-determining-1.  
REGION 55 61  
Complementarity-determining-2.  
REGION 62 93  
Complementarity-determining-3.  
REGION 94 102  
Complementarity-determining-4.  
REGION 103 112  
By similarity.  
REGION 113 113  
NON\_TER 113 113  
SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 91.4%; Score 74; DB 1; Length 113;  
Best Local Similarity 93.3%; Pred. No. 5.2e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHNGNTYL 15  
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 Db 24 RSSQSLVHNGNTYL 38

## RESULT 2

QSP210 MOUSE  
 ID Q5F210 MOUSE PRELIMINARY; PRT; 115 AA.  
 AC Q5F210;  
 DT 10-MAY-2005 (T-EMBLrel. 30, Created)  
 DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)  
 DE Kappa light chain variable region (Fragment).  
 GN Name=IgG1 anti-Ts1 VL;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Erlandsson A.; Holm P.; Ullen A.; Stigbrand T.; Sundstrom B.E.;  
 RT "Studies of the interactions between the anticytokeratin 8 monoclonal  
 antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.";  
 RL J. Mol. Recognit. 16:157-163 (2003).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Erlandsson A.;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; AJ884575; CA156337.1; -; mRNA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 115 115  
 SQ SEQUENCE 115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;

Query Match 91.4%; Score 74; DB 2; Length 115;  
 Best Local Similarity 93.3%; Pred. No. 5.3e-05;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHNGNTYL 15  
 |||||:|||||||  
 Db 24 RSSQSLVHNGNTYL 38

## RESULT 3

Q65ZQ7\_9MURI  
 ID Q65ZQ7\_9MURI PRELIMINARY; PRT; 248 AA.  
 AC Q65ZQ7;  
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
 DE B3(Fv)-PE40 (Fragment).  
 GN Name=B3(Fv)-PE40;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Brinkmann U.; Fai L.H.; FitzGerald D.J.; Willingham M.; Pastan I.;  
 RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete  
 regression of a human carcinoma in mice."  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).  
 DR ENBL; S57990; BAB19971.2; -; mRNA.  
 DR SNR; Q65ZQ7; 4-247.

DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; IPR003596; IG\_V.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 2.  
 DR PROSITE; PSS0835; IG\_LIKE; 2.  
 FT NON\_TER 248 248  
 SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 88.9%; Score 72; DB 2; Length 248;  
 Best Local Similarity 87.5%; Pred. No. 0.0003;  
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIHVHNGNTYLQ 16  
 |||||:|||||||  
 Db 159 RSSQIIVHNGNTYLE 174

## RESULT 4

Q65ZC0 MOUSE  
 ID Q65ZC0 MOUSE PRELIMINARY; PRT; 219 AA.  
 AC Q65ZC0;  
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
 DE Kappa light chain C-region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Balb/c; TISSUE=Spleen;  
 RX MEDLINE=96319505; PubMed=8768802;  
 RA Kipp B.; Schlaak M.; Becker W.M.;  
 RT "Cloning and expression of a recombinant mouse Fab-fragment  
 recognizing a defined linear epitope of Chironomus thummi major  
 allergen Chi t I.";  
 RL Int. Arch. Allergy Immunol. 110:348-353 (1996).  
 DR ENBL; Z37459; CA385724.1; -; mRNA.  
 DR SMR; Q65ZC0; 1-219.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 2.  
 DR PROSITE; PSS0290; IG\_MHC; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 219 219  
 SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

## Query Match

87.7%; Score 71; DB 2; Length 219;

Best Local Similarity 86.7%; Pred. No. 0.00039;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHNGNTYL 15  
 |||||:|||||||  
 Db 24 RSSQSLVHNGNTYL 38

## RESULT 5

Q6P491 HUMAN  
 ID Q6P491 HUMAN PRELIMINARY; PRT; 239 AA.  
 AC Q6P491;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

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DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RA Strausberg R.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063599; AAH63599.1; -, mRNA.
DR HSP; P01837; 1KCU.
DR SMR; Q6P491; 21-237.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; Ig-2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE. 239 AA; 26245 MW; CD7313DDPFD358B3 CRC64;

Query Match 84.0%; Score 68; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 0.0015;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSVHNSNGNTYL 15
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DB 44 RSSESLHNSNGNTYL 58

RESULT 6
KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01913; KWS7S.
CC HSP; Q99M37; 1191.
CC SMR; P01630; 1-113.
CC Ensembl; ENSMUSG00000061260; Mus musculus.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG_LIKE; 1.
CC Direct protein sequencing; Hybridoma; Immunoglobulin domain;
CC Immunoglobulin V region; Monoclonal antibody.
CC REGION 1 23 Framework-1.
CC REGION 24 39 Complementarity-determining-1.
CC REGION 40 54 Framework-2.
CC REGION 55 61 Complementarity-determining-2.
CC REGION 62 93 Framework-3.
CC REGION 94 102 Complementarity-determining-3.
CC REGION 103 112 Framework-4.
CC DISULFID 23 93 By similarity.
CC NON TER 113 113
CC SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 82.7%; Score 67; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.00092;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSVHNSNGNTYL 15
| | | | |
DB 24 RSSKSLHNSNGNTYL 38

RESULT 7
Q7Z3Y5 HUMAN PRELIMINARY; PRT; 86 AA.
AC Q7Z3Y5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rearranged VKA17 V gene segment (Fragment).
GN Name=VKAL17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hodgkin lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA Hanemann M.L., Brauning A.
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564426; CAD92033.1; -, Genomic DNA.
DR HSP; P01625; 1EEQ.
DR SMR; Q7Z3Y5; 1-80.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 86
FT SEQUENCE 86 AA; 9764 MW; D198FC04FE0C78FD CRC64;
SQ
Query Match 77.8%; Score 63; DB 2; Length 86;
Best Local Similarity 80.0%; Pred. No. 0.0034;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RSSQSVHSGNGNTYL 15
Db 3 RSSQSLVYSDGNTYL 17
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Qy 1 RSSQSIVHSNGNTYL 15
Db 44 KSSQSLHSHNGNTYL 58

RESULT 10
O6LEMB_MOUSE PRELIMINARY; PRT; 112 AA.
AC O6LEMB;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22267451; PubMed=12379368; DOI=10.1016/S0022-1759(02)00242-9;
RA Hikumi E., Mitsuda Y., Ohara K., Uda T.;
RT "Targeted destruction of the HIV-1 coat protein gp41 by a catalytic
antibody light chain.";
RL J. Immunol. Methods 269:283-298(2002).
DR EMBL; D85104; BAD00151.1; -; mRNA.
DR HSSP; P01820; 1A70.
DR SMR; O6LEMB; 1-112.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein.
FT NON_TER 112 112
FT TER 112 112
SQ SEQUENCE 112 AA; 12443 MW; BAD3E14B90BCF122 CRC64;

Query Match 75.3%; Score 61; DB 2; Length 112;
Best Local Similarity 73.3%; Pred. No. 0.011;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYL 15
Db 24 RSSKSLYSNGNTYL 38

RESULT 11
Q8TCD0_HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1598223;
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus
nephritis-associated idiotype.";
RL Nucleic Acids Res. 20:2601-0(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1551402;
RA Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,
RA Thiele R., Zocher I., Zachau H.G.;
RT "The human immunoglobulin kappa locus. Characterization of the
duplicated A regions.";
RL Eur. J. Immunol. 22:1023-1029(1992).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8258341;
RA Klein R., Jaenichen R., Zachau H.G.;
RT "Expressed human immunoglobulin kappa genes and their hypermutation.";
RL Eur. J. Immunol. 23:3248-3262(1993).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; BC022362; AAH22362.1; -; mRNA.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 1I72.
DR SMR; Q8TCD0; 21-237.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 239 AA; 26235 MW; FAGEDC3A3B03871D CRC64;

Query Match 74.1%; Score 60; DB 2; Length 239;
Best Local Similarity 73.3%; Pred. No. 0.039;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYL 15
Db 44 RSTQSLVSDGNTYL 58

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RESULT 12
Q53VP8 MOUSE
ID Q53VP8_MOUSE PRELIMINARY; PRT; 112 AA.
AC Q53VP8_MOUSE
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Kappa chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigenic encoded Ab2 (anti-idiotypic)
RT antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 108-109.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03386; CAA27113.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12266 MW; C844B7881A9C18A CRC64;

Query Match 71.6%; Score 58; DB 2; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.036;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVSNGFTYLE 39

RESULT 13
KV2E_MOUSE
ID KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Aebersold R., Herbet H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -!- FUNCTION: Anti-streptococcal group A carbohydrate antibody.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01912; KWS17.
DR HSP; Q99M37; I191.
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DR SMR; P03976; 1-113.
DR Ensembl; ENSMUSG00000055315; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 39
FT REGION 40 54
FT REGION 55 61
FT REGION 62 93
FT REGION 94 102
FT REGION 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 71.6%; Score 58; DB 1; Length 113;
Best Local Similarity 73.3%; Pred. No. 0.037;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYL 15
Db 24 RSSKSLHSGNGITYL 38

RESULT 14
Q9UL80_HUMAN
ID Q9UL80_HUMAN PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1322670;
RA Stuber P., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
RA Gaskin F., Fu S.M.;
RT "A rheumatoid factor from a normal individual encoded by VH2 and V
RT kappa II gene segments.";
RL Arthritis Rheum. 35:900-904(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1601042;
RA Huber C., Klobeck H.G., Zachau H.G.;
RT "Oncogenic V kappa-J kappa recombination after formation of a productive
RT V kappa-J kappa coding joint.";
RL Eur. J. Immunol. 22:1561-1565(1992).
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DR EMBL; AF035034; AAD56270.1; -; mRNA.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSSP; P01625; ILVE.
DR SMR; Q9UL80; 1-114.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 71.6%; Score 58; DB 2; Length 114;
Best Local Similarity 80.0%; Pred. No. 0.037;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYL 15
Db 24 RSSQSPVSDGNTYL 38

RESULT 15
KV2E_HUMAN
ID KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 309:73-76(1984).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS; Genomic_DNA.
CC PIR; A01889; K2HUGM.
CC HSSP; Q99M37; 1I91.
CC SMR; P06309; 5-117.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL <1 4
FT CHAIN 5 117 Ig kappa chain V-II region GM607.
FT REGION 5 27 Framework-1.
FT REGION 28 43 Complementarity-determining-1.
FT REGION 44 58 Framework-2.
FT REGION 59 65 Complementarity-determining-2.
FT REGION 66 97 Framework-3.
FT REGION 98 106 Complementarity-determining-3.
FT REGION 107 116 Framework-4.
FT DISULFID 27 97 By similarity.

FT NON TER 1
FT NON TER 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 71.6%; Score 58; DB 1; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.038;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYL 15
Db 28 RSSQSLHSHNGNTYL 42

Search completed: December 30, 2005, 13:33:20
Job time : 146 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:15:20 ; Search time 31.5 Seconds  
(without alignments)  
41.994 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIHNGNYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 7712

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/PCITUS COMB.pep.\*

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	96.3	16	1	US-08-053-171-27
2	78	96.3	16	1	US-07-977-696C-30
3	78	96.3	16	1	US-08-129-930B-30
4	78	96.3	16	2	US-08-134-346A-17
5	78	96.3	16	2	US-08-976-288A-30
6	78	96.3	16	2	US-10-226-795-28
7	78	96.3	16	2	US-09-947-839B-30
8	76	93.8	16	2	US-08-563-222C-29
9	74	91.4	16	1	US-08-244-626-4
10	74	91.4	16	2	US-09-914-695-20
11	74	91.4	16	2	US-09-518-737-8
12	73	90.1	16	1	US-08-560-558E-29
13	70	86.4	16	2	US-09-724-409-3
14	70	86.4	16	2	US-09-724-530-3
15	70	86.4	16	2	US-09-328-296-3
16	68	84.0	16	1	US-07-977-696C-68
17	68	84.0	16	1	US-08-129-930B-68
18	68	84.0	16	2	US-08-976-288A-68
19	68	84.0	16	2	US-09-947-839B-68
20	67	82.7	16	1	US-08-438-123-1
21	61	75.3	16	2	US-09-406-532-18
22	61	75.3	16	2	US-09-563-222C-8
23	51	63.0	16	1	US-08-672-345C-43
24	51	63.0	16	2	US-09-214-095D-43
25	51	63.0	16	2	US-09-940-727B-43
26	46	56.8	16	2	US-08-672-345C-22
27	46	56.8	16	1	US-08-672-345C-25

Sequence 22, Appl  
Sequence 25, Appl  
Sequence 22, Appl  
Sequence 25, Appl  
Sequence 19, Appl  
Sequence 28, Appl  
Sequence 19, Appl  
Sequence 28, Appl  
Sequence 19, Appl  
Sequence 28, Appl  
Sequence 79, Appl  
Sequence 79, Appl  
Sequence 79, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 515, App  
Sequence 515, App  
Sequence 515, App

## ALIGNMENTS

RESULT 1  
US-08-053-171-27  
; Sequence 27, Application US/08053171  
; Patent No. 5562903  
; GENERAL INFORMATION:  
; APPLICANT: Co, Loibner  
; TITLE OF INVENTION: Antibody Derivatives  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,171  
; FILING DATE: 22-APR-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-54-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..16  
; OTHER INFORMATION: /note= "First  
; OTHER INFORMATION: Complementarity-determining region (CDR1) of  
; OTHER INFORMATION: BR55-1 antibody light chain"

Query Match 96.3%; Score 78; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16  
Db 1 RSSQSIHNSNGNTYLE 16

## RESULT 2

US-07-977-696C-30  
; Sequence 30, Application US/07977696C  
; Patent No. 5792852  
; GENERAL INFORMATION:  
; APPLICANT: do Couto, Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides with Specificity  
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination  
; TITLE OF INVENTION: and Therapeutic Methods.  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/977,696C  
; FILING DATE: 11-16-92  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anzel Ph.D., Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: P66 38227  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 748-6868  
; TELEFAX: (510) 748-6688  
; TELEX: n.a.  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-977-696C-30

Query Match 96.3%; Score 78; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16  
Db 1 RSSQSIHNSNGNTYLE 16

## RESULT 3

US-08-129-930B-30  
; Sequence 30, Application US/08129930B  
; Patent No. 5804187  
; GENERAL INFORMATION:  
; APPLICANT: do Couto Dr., Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides With Broad  
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
; TITLE OF INVENTION: Diagnostic Vaccination and  
; TITLE OF INVENTION: Therapeutic Methods  
; NUMBER OF SEQUENCES: 96

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: V. AMZEL & ASSOC.  
; STREET: 2055 No. 5804187th Broadway, Suite 201  
; CITY: Walnut Creek  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94596  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/129,930B  
; FILING DATE: September 30, 1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anzel Ph.D., Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: CRPCC-008A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 521-1333  
; TELEFAX: (510) 521-3541  
; TELEX: n.a.  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-129-930B-30

Query Match 96.3%; Score 78; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16  
Db 1 RSSQSIHNSNGNTYLE 16

## RESULT 4

US-08-134-346A-17  
; Sequence 17, Application US/08134346A  
; Patent No. 6281335  
; GENERAL INFORMATION:  
; APPLICANT: do Couto, F.J.R.  
; APPLICANT: Ceriani, R.L.C.  
; APPLICANT: Petersen, J.A.  
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrager, Chong & Flaherty  
; STREET: 300 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10022-7499

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/134,346A  
; FILING DATE: 08-OCT-1993  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Onofrio, Dara L.  
; REGISTRATION NUMBER: 34,889  
; REFERENCE/DOCKET NUMBER: CLT 149,608

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-826-6565  
TELEFAX: 212-826-5909  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-134-346A-17

Query Match 96.3%; Score 78; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16  
| | | | | | | | | | | | | | | | | |  
Db 1 RSSQSIVHSGNGTYLQ 16

## RESULT 5

US-08-976-288A-30  
Sequence 30, Application US/08976288A  
Patent No. 6315997

## GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.  
APPLICANT: Ceriani Dr., Roberto L.  
APPLICANT: Peterson Dr., Jerry A.  
APPLICANT: Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Broad  
TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
TITLE OF INVENTION: Diagnostic Vaccination and  
TITLE OF INVENTION: Therapeutic Methods  
NUMBER OF SEQUENCES: 96

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder & Poplawski  
STREET: 444 South Flower St., 19th Floor  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: Patent In Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,288A  
FILING DATE: No. 6315997ember 21, 1997

## CLASSIFICATION: 424

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/129,930  
FILING DATE: September 30, 1993

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/977,696  
FILING DATE: No. 6315997ember 16, 1992

## ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel Ph.D.  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P6639938

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 622-7700  
TELEFAX: (213) 489-4210  
TELEX: n.a.

## INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-976-288A-30

Query Match 96.3%; Score 78; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16  
| | | | | | | | | | | | | | | | | |  
Db 1 RSSQSIVHSGNGTYLQ 16

## RESULT 6

US-10-226-795-28  
Sequence 28, Application US/10226795  
Patent No. 6875433

## GENERAL INFORMATION:

APPLICANT: HART, MARY KATE  
APPLICANT: WILSON, JULIE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING  
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN  
FILE REFERENCE: ARMY 166

CURRENT APPLICATION NUMBER: US/10/226,795

CURRENT FILING DATE: 2002-11-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 28

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic light  
OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence

US-10-226-795-28

Query Match 96.3%; Score 78; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16  
| | | | | | | | | | | | | | | | | |  
Db 1 RSSQSIVHSGNGTYLQ 16

## RESULT 7

US-09-947-839B-30

Sequence 30, Application US/09947839B

Patent No. 6936706

## GENERAL INFORMATION:

APPLICANT: do Couto, Fernando J.R.  
Ceriani Dr., Roberto L.  
Peterson Dr., Jerry A.

Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Specificity  
for Carcinomas and Kit and Diagnostic Vaccination  
and Therapeutic Methods.

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: V. Amzel & Assoc.

STREET: P.O.Box 159

CITY: Gladwyne

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19035

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,839B

FILING DATE: 06-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Amzel Viviana

REGISTRATION NUMBER: 30,930

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/
/ REFERENCE/DOCKET NUMBER: CRFC-083
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-649-0609
/ TELEFAX: 240-359-0299
/ TELEX: n.a.
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-947-839B-30

Query Match          96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHSGNTYLQ 16
Db 1 RSSQSIHVHSGNTYLE 16

RESULT 8
US-09-563-222C-29
; Sequence 29, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-29

Query Match          93.8%; Score 76; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.4e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHSGNTYLQ 16
Db 1 RSSQSIHVHSGNTYLE 16

RESULT 9
US-08-244-626-4
; Sequence 4, Application US/08244626
; Patent No. 5502167
; GENERAL INFORMATION:
; APPLICANT: Walldmann, Herman
; APPLICANT: Walsh, Louise
; APPLICANT: Crowe, James Scott
; APPLICANT: Lewis, Alan Peter
; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
; STREET: 555 Thirteenth Street, N. W.
; CITY: Washington
; STATE: D. C.
```

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/
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/244,626
/ FILING DATE: July 15, 1994
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB92/02251
/ FILING DATE: December 4, 1992
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ernst, Barbara G.
/ REGISTRATION NUMBER: 30,377
/ REFERENCE/DOCKET NUMBER: 1808-153A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 783-6040
/ TELEFAX: (202) 783-6031
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-244-626-4

Query Match          91.4%; Score 74; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHSGNTYL 15
Db 1 RSSQSIHVHSGNTYL 15

RESULT 10
US-09-914-695-20
; Sequence 20, Application US/09914695
; Patent No. 6706487
; GENERAL INFORMATION:
; APPLICANT: Abdel-Meguid, Sherin
; APPLICANT: Ho, Yen Sen
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Taylor, Alexander H.
; TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
; FILE REFERENCE: P50897
; CURRENT APPLICATION NUMBER: US/09/914,695
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/07349
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,299
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 20
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-695-20

Query Match          91.4%; Score 74; DB 2; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHSGNTYL 15
Db 1 RSSQSIHVHSGNTYL 15
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RESULT 11  
US-09-518-737-8  
; Sequence 8, Application US/09518737  
; Patent No. 6709833  
; GENERAL INFORMATION:  
; APPLICANT: FUKUI, YASUHIRO  
; APPLICANT: NAGATA, SATOSHI  
; APPLICANT: SHIRAI, RYUICHI  
; APPLICANT: SAITO, NAOAKI  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING  
; FILE REFERENCE: 1965/49618  
; CURRENT APPLICATION NUMBER: US/09/518,737  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-518-737-8  
Query Match 91.4%; Score 74; DB 2; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.8e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 RSSQSIHVHSGNTYL 15  
Db 1 RSSQSLVHSGNTYL 15  
|||||:|||||:  
RESULT 12  
US-08-560-558E-29  
; Sequence 29, Application US/08560558E  
; Patent No. 5891996  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Humanized and chimeric monoclonal  
; TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor  
; TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA  
; STREET: P.O. Box 2250  
; CITY: Salt Lake City  
; STATE: Utah  
; COUNTRY: United States of America  
; ZIP: 84110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: WINDOWS95  
; SOFTWARE: WordPerfect 5.1/5.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/560,558E  
; FILING DATE: No. 5891996ember 17, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Turner, Allen C.  
; REGISTRATION NUMBER: 33,041  
; REFERENCE/DOCKET NUMBER: 2720US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (801) 532-1922  
; TELEFAX: (801) 531-9168  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein

HYPOTHEICAL: NO  
US-08-560-558E-29  
Query Match 90.1%; Score 73; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.6e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 RSSQSIHVHSGNTYL 15  
Db 1 RSSQSLVHSGNTYL 15  
|||||:|||||:  
RESULT 13  
US-09-724-409-3  
; Sequence 3, Application US/09724409  
; Patent No. 6838261  
; GENERAL INFORMATION:  
; APPLICANT: Siegal, Clay  
; APPLICANT: Wahl, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005  
; CURRENT APPLICATION NUMBER: US/09/724,409  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-724-409-3

Query Match 86.4%; Score 70; DB 2; Length 16;  
Best Local Similarity 86.7%; Pred. No. 7.7e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 RSSQSIHVHSGNTYL 15  
Db 1 RSSQSLVHSGNTYL 15  
|||||:|||||:  
RESULT 14  
US-09-724-530-3  
; Sequence 3, Application US/09724530  
; Patent No. 6843989  
; GENERAL INFORMATION:  
; APPLICANT: Siegal, Clay  
; APPLICANT: Wahl, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005  
; CURRENT APPLICATION NUMBER: US/09/724,530  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-724-530-3

Query Match 86.4%; Score 70; DB 2; Length 16;  
Best Local Similarity 86.7%; Pred. No. 7.7e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 RSSQSIHVHSGNTYL 15  
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Db 1 RSSQSLVHNGNTFL 15

RESULT 15  
US-09-328-296-3  
; Sequence 3, Application US/09328296  
; Patent No. 6946129  
; GENERAL INFORMATION:  
; APPLICANT: Siegal, Clay  
; APPLICANT: Wahl, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005  
; CURRENT APPLICATION NUMBER: US/09/328,296  
; CURRENT FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-328-296-3

Query Match 86.4%; Score 70; DB 2; Length 16;  
Best Local Similarity 86.7%; Pred. No. 7,7e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSLVHNGNTYL 15  
Db 1 RSSQSLVHNGNTFL 15

Search completed: December 30, 2005, 14:26:44  
Job time : 32.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 35.871 Seconds  
(without alignments)  
36.877 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSVHNGNYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgm2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	96.3	16	1	US-08-053-171-27
2	78	96.3	16	1	US-07-977-696C-30
3	78	96.3	16	1	US-08-129-930B-30
4	78	96.3	16	2	US-08-134-346A-17
5	78	96.3	16	2	US-08-976-288A-30
6	78	96.3	16	2	US-10-226-795-28
7	78	96.3	16	2	US-09-947-839B-30
8	78	96.3	100	2	US-09-840-459-26
9	78	96.3	100	2	US-09-840-459-28
10	78	96.3	100	2	US-09-497-625A-26
11	78	96.3	100	2	US-09-497-625A-28
12	78	96.3	110	2	US-10-114-716A-42
13	78	96.3	111	2	US-09-823-746-12
14	78	96.3	112	1	US-08-053-171-15
15	78	96.3	112	1	US-08-752-844-15
16	78	96.3	112	1	US-08-888-366-16
17	78	96.3	112	1	US-08-591-196-15
18	78	96.3	112	2	US-08-815-190A-14
19	78	96.3	112	2	US-09-293-533-15
20	78	96.3	112	2	US-09-823-746-8
21	78	96.3	125	1	US-08-331-398A-67
22	78	96.3	125	1	US-08-331-397B-67
23	78	96.3	125	1	US-08-759-804A-66
24	78	96.3	131	1	US-08-053-171-5
25	78	96.3	131	1	US-08-053-171-9
26	78	96.3	131	1	US-08-129-930B-95
27	78	96.3	131	2	US-08-134-346A-50

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Sequence 2, Appli  
Sequence 27, Appl  
Sequence 4, Appli  
Sequence 190, App  
Sequence 66, Appl  
Sequence 66, Appl  
Sequence 29, Appl  
Sequence 18, Appl  
Sequence 12, Appl  
Sequence 21, Appl  
Sequence 12, Appl  
Sequence 21, Appl

78 96.3 131 2 US-08-976-288A-95  
78 96.3 149 1 US-08-752-844-2  
78 96.3 149 1 US-08-591-196-2  
78 96.3 149 2 US-09-192-838B-2  
78 96.3 149 2 US-09-293-533-2  
78 96.3 149 2 US-09-324-191-2  
78 96.3 149 2 US-10-226-795-27  
78 96.3 238 2 US-09-192-545-4  
78 96.3 249 2 US-09-726-219A-190  
78 96.3 249 2 US-09-196-522-190  
78 96.3 263 1 US-08-752-844-66  
78 96.3 263 2 US-09-293-533-66  
76 93.8 16 2 US-09-563-222C-29  
75 93.8 112 1 US-08-888-366-18  
75 92.6 238 1 US-08-224-591-12  
75 92.6 238 1 US-08-392-338A-21  
75 92.6 238 1 US-08-926-789-12  
75 92.6 238 2 US-09-166-750-21

## ALIGNMENTS

RESULT 1  
US-08-053-171-27  
; Sequence 27, Application US/08053171  
; Patent No. 5562903  
; GENERAL INFORMATION:  
; APPLICANT: Co, Loibner  
; TITLE OF INVENTION: Antibody Derivatives  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,171  
; FILING DATE: 22-APR-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-54-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..16  
; OTHER INFORMATION: /note= "First  
; OTHER INFORMATION: complementarity-determining region (CDR1) of  
; OTHER INFORMATION: BR55-1 antibody light chain"  
US-08-053-171-27

Query Match 96.3%; Score 78; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4e-06;  
Matches 15; Conservative 1; Mismatches 0; Gaps 0;

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QY 1 RSSQSIHNSNGNTYLQ 16
Db 1 RSSQSIHNSNGNTYLE 16

RESULT 2
US-07-977-696C-30
; Sequence 30, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-30

Query Match 96.3%; Score 78; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16
Db 1 RSSQSIHNSNGNTYLE 16

RESULT 3
US-08-129-930B-30
; Sequence 30, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRPCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-30

Query Match 96.3%; Score 78; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16
Db 1 RSSQSIHNSNGNTYLE 16

RESULT 4
US-08-134-346A-17
; Sequence 17, Application US/08134346A
; Patent No. 6281335
; GENERAL INFORMATION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Ceriani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
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## TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-826-6565

TELEFAX: 212-826-5909

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-134-346A-17

Query Match 96.3%; Score 78; DB 2; Length 16;

Best Local Similarity 93.8%; Pred. No. 4e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16

Db 1 RSSQSIVHSGNGTYLQ 16

## RESULT 5

US-08-976-288A-30

Sequence 30, Application US/08976288A

Patent No. 6315997

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.

APPLICANT: Ceriani Dr., Roberto L.

APPLICANT: Peterson Dr., Jerry A.

APPLICANT: Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides With Broad

TITLE OF INVENTION: Carcinoma Specificity, and Kit and

TITLE OF INVENTION: Diagnostic Vaccination and

TITLE OF INVENTION: Therapeutic Methods

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder &amp; Poplawski

STREET: 444 South Flower St., 19th Floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,288A

FILING DATE: No. 6315997ember 21, 1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/129,930

FILING DATE: September 30, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/977,696

FILING DATE: No. 6315997ember 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Anzel Ph.D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P6639938

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 622-7700

TELEFAX: (213) 489-4210

TELEX: n.a.

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-976-288A-30

Query Match 96.3%; Score 78; DB 2; Length 16;

Best Local Similarity 93.8%; Pred. No. 4e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16

Db 1 RSSQSIVHSGNGTYLQ 16

## RESULT 6

US-10-226-795-28

Sequence 28, Application US/10226795

Patent No. 6875433

GENERAL INFORMATION:

APPLICANT: HART, MARY KATE

APPLICANT: WILSON, JULIE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING

TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN

FILE REFERENCE: ARMY 166

CURRENT APPLICATION NUMBER: US/10/226,795

CURRENT FILING DATE: 2002-11-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 28

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic light

OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence

US-10-226-795-28

Query Match 96.3%; Score 78; DB 2; Length 16;

Best Local Similarity 93.8%; Pred. No. 4e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16

Db 1 RSSQSIVHSGNGTYLQ 16

## RESULT 7

US-09-947-839B-30

Sequence 30, Application US/09947839B

Patent No. 6936706

GENERAL INFORMATION:

APPLICANT: do Couto, Fernando J.R.

Ceriani Dr., Roberto L.

Peterson Dr., Jerry A.

Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Specificity  
for Carcinomas and Kit and Diagnostic Vaccination  
and Therapeutic Methods.

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: V. Amzel &amp; Assoc.

STREET: P.O.Box 159

CITY: Gladwyne

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19035

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,839B

FILING DATE: 06-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Amzel Viviana

REGISTRATION NUMBER: 30,930



```

; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-497-625A-28

Query Match          96.3%; Score 78; DB 2; Length 100;
Best Local Similarity 93.8%; Pred. No. 2.9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIHVSNGNTYIQ 16
Db 24 RSSQSIHVSNGNTYLE 39

RESULT 12
US-10-114-716A-42
; Sequence 42, Application US/10114716A
; Patent No. 6855804
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Yasuhiro Nishiyama
; TITLE OF INVENTION: Covalently Reactive Transition State
; TITLE OF INVENTION: Analogs and Methods of Use Thereof
; FILE REFERENCE: UTH001HB
; CURRENT APPLICATION NUMBER: US/10/114,716A
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/862,849
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/046,373
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/280,624
; PRIOR FILING DATE: 2001-03-31
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus musculus domesticus
; US-10-114-716A-42

Query Match          96.3%; Score 78; DB 2; Length 110;
Best Local Similarity 93.8%; Pred. No. 3.2e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIHVSNGNTYIQ 16
Db 24 RSSQSIHVSNGNTYLE 39

RESULT 13
US-09-823-746-12
; Sequence 12, Application US/09823746
; Patent No. 6962702
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS J.
; APPLICANT: GRIFFITHS, GARY L.
; APPLICANT: MCBRIDE, WILLIAM J.
; APPLICANT: LEUNG, SHUI-ON
; APPLICANT: QU, ZHENGXING
; TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR
; TITLE OF INVENTION: USE WITH BI-SPECIFIC ANTIBODIES
; FILE REFERENCE: 40923-0074US4
; CURRENT APPLICATION NUMBER: US/09/823,746
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/337,756
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized
; OTHER INFORMATION: Mu-9 amino acid sequence
; US-09-823-746-12

Query Match          96.3%; Score 78; DB 2; Length 111;
Best Local Similarity 93.8%; Pred. No. 3.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIHVSNGNTYIQ 16
Db 24 RSSQSIHVSNGNTYLE 39

RESULT 14
US-08-053-171-15
; Sequence 15, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..112
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/ OTHER INFORMATION: /note= "Sequence of the Light Chain
/ Patent No. 5562903
/ OTHER INFORMATION: of Humanized BR55-2 Antibody"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 24..39
/ OTHER INFORMATION: /note= "Complementarity-determining
/ OTHER INFORMATION: region"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 55..61
/ OTHER INFORMATION: /note= "Complementarity-determining
/ OTHER INFORMATION: region"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 94..102
/ OTHER INFORMATION: /note= "Complementarity-determining
/ OTHER INFORMATION: region"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 54
/ OTHER INFORMATION: /note= "Residue that has been
/ OTHER INFORMATION: replaced with mouse amino acid in the humanized
/ OTHER INFORMATION: antibody."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 108
/ OTHER INFORMATION: /note= "Residue in the framework
/ OTHER INFORMATION: that is replaced with mouse amino acid in the
/ OTHER INFORMATION: humanized antibody."
/
US-08-053-171-15
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Query Match 96.3%; Score 78; DB 1; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RSSQSIVHSGNGNTYLQ 16
| | | | | | | | | | | | | | | |
DB 24 RSSQSIVHSGNGNTYLE 39
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RESULT 15
US-08-752-844-15
/ Sequence 15, Application US/08752844
/ Patent No. 5935821
/ GENERAL INFORMATION:
/ APPLICANT: Chatterjee, Malaya
/ APPLICANT: Foon, Kenneth A.
/ TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
/ TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 755 PAGE MILL ROAD
/ CITY: PALO ALTO
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/752,844
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Schiff, J. Michael
/ REGISTRATION NUMBER: 40,253
/ REFERENCE/DOCKET NUMBER: 30414-20002.21
/ TELECOMMUNICATION INFORMATION:
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/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 112 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-752-844-15
Query Match 96.3%; Score 78; DB 1; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
| | | | | | | | | | | | | | | |
DB 24 RSSQSIVHSGNGNTYLE 39

Search completed: December 30, 2005, 13:37:16
Job time : 36.871 secs
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GenCore version 5.1.6  
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QM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 118.968 Seconds  
(without alignments)  
56.194 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIVHSGNTYLQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	81	100.0	16	5	US-10-735-916A-2
2	81	100.0	112	5	US-10-735-916A-54
3	81	100.0	112	5	US-10-735-916A-61
4	81	100.0	112	5	US-10-735-916A-65
5	81	100.0	122	5	US-10-735-916A-49
6	81	100.0	131	5	US-10-735-916A-63
7	81	100.0	131	5	US-10-735-916A-67
8	78	96.3	16	3	US-09-995-529-32
9	78	96.3	16	3	US-09-947-839-30
10	78	96.3	16	3	US-09-995-529-32
11	78	96.3	16	4	US-10-226-795-28
12	78	96.3	16	4	US-10-470-045-53
13	78	96.3	16	6	US-11-070-697-1
14	78	96.3	60	4	US-10-470-045-91
15	78	96.3	100	3	US-09-840-459-26
16	78	96.3	100	3	US-09-840-459-28
17	78	96.3	100	4	US-10-766-773-26
18	78	96.3	100	4	US-10-766-773-28
19	78	96.3	100	4	US-10-766-610-26
20	78	96.3	100	4	US-10-766-610-28
21	78	96.3	100	4	US-10-733-563-26
22	78	96.3	100	4	US-10-733-563-28
23	78	96.3	100	5	US-10-729-441-56
24	78	96.3	100	5	US-10-897-406-56
25	78	96.3	105	5	US-10-764-730-4
26	78	96.3	110	4	US-10-114-716A-42
27	78	96.3	110	5	US-10-930-548-42

28	78	96.3	112	3	US-09-995-529-10	Sequence 10, Appl
29	78	96.3	112	3	US-09-995-529-10	Sequence 10, Appl
30	78	96.3	112	4	US-10-153-401-15	Sequence 15, Appl
31	78	96.3	112	4	US-10-258-728-4	Sequence 4, Appl
32	78	96.3	112	4	US-10-258-728-25	Sequence 25, Appl
33	78	96.3	112	4	US-10-258-728-27	Sequence 27, Appl
34	78	96.3	112	4	US-10-258-728-28	Sequence 28, Appl
35	78	96.3	112	5	US-10-735-916A-55	Sequence 55, Appl
36	78	96.3	112	5	US-10-735-916A-56	Sequence 56, Appl
37	78	96.3	112	5	US-10-858-855-7	Sequence 7, Appl
38	78	96.3	112	6	US-11-070-697-32	Sequence 32, Appl
39	78	96.3	113	5	US-10-729-441-59	Sequence 59, Appl
40	78	96.3	113	5	US-10-729-441-61	Sequence 61, Appl
41	78	96.3	113	5	US-10-897-406-59	Sequence 59, Appl
42	78	96.3	113	5	US-10-897-406-61	Sequence 61, Appl
43	78	96.3	113	6	US-11-070-697-36	Sequence 36, Appl
44	78	96.3	113	6	US-11-070-697-40	Sequence 40, Appl
45	78	96.3	116	5	US-10-787-219A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1  
US-10-735-916A-2  
; Sequence 2, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFIOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-2

Query Match 100.0%; Score 81; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.1e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RSSQSIVHSGNTYLQ 16  
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Db 1 RSSQSIVHSGNTYLQ 16

RESULT 2  
US-10-735-916A-54  
; Sequence 54, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier

APPLICANT: DUFLOS, Alain  
APPLICANT: BECK, Alain  
APPLICANT: HAEUW, Jean-Francois  
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
FILE REFERENCE: 017753-183  
CURRENT APPLICATION NUMBER: US/10/735,916A  
CURRENT FILING DATE: 2003-12-16  
PRIOR APPLICATION NUMBER: FR 03/08 538  
PRIOR FILING DATE: 2003-07-11  
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
PRIOR FILING DATE: 2003-01-20  
PRIOR APPLICATION NUMBER: FR 02/00 653  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: FR 02/00 654  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: FR 02/05 753  
PRIOR FILING DATE: 2002-05-07  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 54  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-735-916A-54

Query Match 100.0%; Score 81; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16  
|||||

DB 24 RSSQSIVHSGNGTYLQ 39  
|||||

RESULT 3  
US-10-735-916A-61  
Sequence 61, Application US/10735916A  
Publication No. US20050084906A1  
GENERAL INFORMATION:  
APPLICANT: GOETSCH, Liliane  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: LEGER, Olivier  
APPLICANT: DUFLOS, Alain  
APPLICANT: BECK, Alain  
APPLICANT: HAEUW, Jean-Francois  
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
FILE REFERENCE: 017753-183  
CURRENT APPLICATION NUMBER: US/10/735,916A  
CURRENT FILING DATE: 2003-12-16  
PRIOR APPLICATION NUMBER: FR 03/08 538  
PRIOR FILING DATE: 2003-07-11  
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
PRIOR FILING DATE: 2003-01-20  
PRIOR APPLICATION NUMBER: FR 02/00 653  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: FR 02/00 654  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: FR 02/05 753  
PRIOR FILING DATE: 2002-05-07  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 61  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-735-916A-61

Query Match 100.0%; Score 81; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16  
|||||

DB 24 RSSQSIVHSGNGTYLQ 39  
RESULT 4  
US-10-735-916A-65  
Sequence 65, Application US/10735916A  
Publication No. US20050084906A1  
GENERAL INFORMATION:  
APPLICANT: GOETSCH, Liliane  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: LEGER, Olivier  
APPLICANT: DUFLOS, Alain  
APPLICANT: BECK, Alain  
APPLICANT: HAEUW, Jean-Francois  
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
FILE REFERENCE: 017753-183  
CURRENT APPLICATION NUMBER: US/10/735,916A  
CURRENT FILING DATE: 2003-12-16  
PRIOR APPLICATION NUMBER: FR 03/08 538  
PRIOR FILING DATE: 2003-07-11  
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
PRIOR FILING DATE: 2003-01-20  
PRIOR APPLICATION NUMBER: FR 02/00 653  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: FR 02/00 654  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: FR 02/05 753  
PRIOR FILING DATE: 2002-05-07  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 65  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-735-916A-65

Query Match 100.0%; Score 81; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16  
|||||

DB 24 RSSQSIVHSGNGTYLQ 39  
|||||

RESULT 5  
US-10-735-916A-49  
Sequence 49, Application US/10735916A  
Publication No. US20050084906A1  
GENERAL INFORMATION:  
APPLICANT: GOETSCH, Liliane  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: LEGER, Olivier  
APPLICANT: DUFLOS, Alain  
APPLICANT: BECK, Alain  
APPLICANT: HAEUW, Jean-Francois  
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
FILE REFERENCE: 017753-183  
CURRENT APPLICATION NUMBER: US/10/735,916A  
CURRENT FILING DATE: 2003-12-16  
PRIOR APPLICATION NUMBER: FR 03/08 538  
PRIOR FILING DATE: 2003-07-11  
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
PRIOR FILING DATE: 2003-01-20  
PRIOR APPLICATION NUMBER: FR 02/00 653  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: FR 02/00 654  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: FR 02/05 753  
PRIOR FILING DATE: 2002-05-07  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 49



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; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-49

Query Match      100.0%; Score 81; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 34 RSSQSIVHSNGNTYLQ 49

RESULT 6
US-10-735-916A-63
; Sequence 63, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-63

Query Match      100.0%; Score 81; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 43 RSSQSIVHSNGNTYLQ 58

RESULT 7
US-10-735-916A-67
; Sequence 67, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
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; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-67

Query Match      100.0%; Score 81; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 43 RSSQSIVHSNGNTYLQ 58

RESULT 8
US-09-995-529-32
; Sequence 32, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-32

Query Match      96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 1 RSSQSIVHSNGNTYLQ 16

RESULT 9
US-09-947-839-30
; Sequence 30, Application US/09947839
; Publication No. US20030138428A1
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; Carcinoma Specificity, and Kit and
; Diagnostic Vaccination and
; Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
```

STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/947,839  
FILING DATE: 06-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/976,288  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 07/977,696  
FILING DATE: No. US20030138428Aember 16, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Viviana Anzel Ph.D.  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P6639938  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 622-7700  
TELEFAX: (213) 489-4210  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-947-839-30

Query Match 96.3%; Score 78; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3e-06; Indels 0; Gaps 0;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16  
|||||  
Db 1 RSSQSIVHSGNGNTYLE 16

RESULT 10  
US-09-995-529-32  
Sequence 32, Application US/09995529  
Publication No. US20040091482A9  
GENERAL INFORMATION:  
APPLICANT: Watkins, Jeffrey D.  
APPLICANT: Huse, William D.  
APPLICANT: Tang, Ying  
TITLE OF INVENTION: Humanized Collagen Antibodies and  
FILE REFERENCE: P-IX 4976  
CURRENT APPLICATION NUMBER: US/09/995,529  
CURRENT FILING DATE: 2001-11-26  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-995-529-32

Query Match 96.3%; Score 78; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3e-06; Indels 0; Gaps 0;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16  
|||||  
Db 1 RSSQSIVHSGNGNTYLE 16

RESULT 11  
US-10-226-795-28  
Sequence 28, Application US/10226795  
Publication No. US20040053865A1  
GENERAL INFORMATION:  
APPLICANT: HART, MARY KATE  
APPLICANT: WILSON, JULIE  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING  
FILE REFERENCE: ARMY 166  
CURRENT APPLICATION NUMBER: US/10/226,795  
CURRENT FILING DATE: 2002-11-18  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 28  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic light  
OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence  
US-10-226-795-28

Query Match 96.3%; Score 78; DB 4; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3e-06; Indels 0; Gaps 0;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16  
|||||  
Db 1 RSSQSIVHSGNGNTYLE 16

RESULT 12  
US-10-470-045-53  
Sequence 53, Application US/10470045  
Publication No. US20040146505A1  
GENERAL INFORMATION:  
APPLICANT: Scancell Limited  
APPLICANT: Durrant, Linda Gillian  
APPLICANT: Parsons, Tina  
TITLE OF INVENTION: Substances  
FILE REFERENCE: P32181WO/NJL  
CURRENT APPLICATION NUMBER: US/10/470,045  
CURRENT FILING DATE: 2003-07-24  
PRIOR APPLICATION NUMBER: GB 0102145.0  
PRIOR FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 53  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-470-045-53

Query Match 96.3%; Score 78; DB 4; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3e-06; Indels 0; Gaps 0;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16  
|||||  
Db 1 RSSQSIVHSGNGNTYLE 16

RESULT 13  
US-11-070-697-1  
Sequence 1, Application US/11070697  
Publication No. US20050169926A1  
GENERAL INFORMATION:  
APPLICANT: QU, ZHENGXING  
APPLICANT: HANSEN, HANS  
APPLICANT: GOLDENBERG, DAVID M.  
TITLE OF INVENTION: CHIMERIC, HUMAN AND HUMANIZED ANTI-CSAP MONOCLONAL  
ANTIBODIES

; FILE REFERENCE: 018733/1064  
; CURRENT APPLICATION NUMBER: US/11/070,697  
; CURRENT FILING DATE: 2005-03-03  
; PRIOR APPLICATION NUMBER: US/10/116,116  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/823,746  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 09/337,756  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 60/104,156  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/090,142  
; PRIOR FILING DATE: 1998-06-22  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-11-070-697-1

Query Match 96.3%; Score 78; DB 6; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16  
| | | | | | | | | | | | | | | |  
Db 1 RSSQSIVHSGNGTYLE 16

RESULT 14

US-10-470-045-91  
; Sequence 91, Application US/10470045  
; Publication No. US20040146505A1  
; GENERAL INFORMATION:  
; APPLICANT: Scancell Limited  
; APPLICANT: Durrant, Linda Gillian  
; APPLICANT: Parsons, Tina  
; TITLE OF INVENTION: Substances  
; FILE REFERENCE: P32181WO/NJL  
; CURRENT APPLICATION NUMBER: US/10/470,045  
; CURRENT FILING DATE: 2003-07-24  
; PRIOR APPLICATION NUMBER: GB 0102145.0  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 91  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-470-045-91

Query Match 96.3%; Score 78; DB 4; Length 60;  
Best Local Similarity 93.8%; Pred. No. 1.3e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16  
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Db 24 RSSQSIVHSGNGTYLE 39

RESULT 15

US-09-840-459-26  
; Sequence 26, Application US/09840459  
; Patent No. US20020150576A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-840-459-26

Query Match 96.3%; Score 78; DB 3; Length 100;  
Best Local Similarity 93.8%; Pred. No. 2.3e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16  
| | | | | | | | | | | | | | | |  
Db 24 RSSQSIVHSGNGTYLE 39

Search completed: December 30, 2005, 14:14:50  
Job time : 118.968 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 5.93548 Seconds  
(without alignments)  
20.187 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIVHSNGNTYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	16	7	US-11-012-353-2
2	81	100.0	112	7	US-11-012-353-54
3	81	100.0	112	7	US-11-012-353-61
4	81	100.0	112	7	US-11-012-353-65
5	81	100.0	122	7	US-11-012-353-49
6	81	100.0	131	7	US-11-012-353-63
7	81	100.0	131	7	US-11-012-353-67
8	78	96.3	100	6	US-10-932-334-56
9	78	96.3	112	7	US-11-012-353-55
10	78	96.3	112	7	US-11-012-353-56
11	78	96.3	113	6	US-10-932-334-59
12	78	96.3	113	6	US-10-932-334-61
13	78	96.3	116	7	US-11-065-943-49
14	78	96.3	251	6	US-10-512-184-30
15	78	96.3	320	6	US-10-512-184-67
16	78	96.3	569	6	US-10-512-184-66
17	78	96.3	618	6	US-10-512-184-48
18	76	93.8	112	7	US-11-012-353-57
19	75	92.6	113	6	US-10-932-334-60
20	74	91.4	112	6	US-10-502-145-19
21	74	91.4	113	6	US-10-932-334-69
22	74	91.4	131	6	US-10-789-273-14
23	74	91.4	144	7	US-11-055-163-15
24	73	90.1	112	6	US-10-502-145-15
25	72	88.9	113	6	US-10-932-334-62

26	72	88.9	113	6	US-10-932-334-67	Sequence 67, Appl
27	71	87.7	16	7	US-11-125-837-13	Sequence 13, Appl
28	71	87.7	131	7	US-11-125-837-23	Sequence 23, Appl
29	70	86.4	16	7	US-11-102-743-3	Sequence 3, Appl
30	70	86.4	112	7	US-11-102-743-2	Sequence 2, Appl
31	69	85.2	16	6	US-10-932-334-4	Sequence 4, Appl
32	69	85.2	100	7	US-11-054-669-81	Sequence 81, Appl
33	69	85.2	100	7	US-11-084-554-112	Sequence 112, App
34	69	85.2	100	7	US-11-084-554-118	Sequence 118, App
35	69	85.2	112	6	US-10-502-145-23	Sequence 23, Appl
36	69	85.2	113	6	US-10-932-334-8	Sequence 8, Appl
37	69	85.2	113	6	US-10-932-334-9	Sequence 9, Appl
38	69	85.2	113	6	US-10-932-334-10	Sequence 10, Appl
39	69	85.2	113	6	US-10-932-334-11	Sequence 11, Appl
40	69	85.2	113	6	US-10-932-334-12	Sequence 12, Appl
41	69	85.2	113	6	US-10-932-334-58	Sequence 58, Appl
42	69	85.2	113	6	US-10-932-334-66	Sequence 66, Appl
43	69	85.2	113	6	US-10-932-334-68	Sequence 68, Appl
44	69	85.2	113	6	US-10-932-334-82	Sequence 82, Appl
45	69	85.2	113	6	US-10-932-334-83	Sequence 83, Appl

#### ALIGNMENTS

##### RESULT 1

US-11-012-353-2  
; Sequence 2, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-1 HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: Patent in Ver. 3.3  
; SEQ ID NO 2  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-11-012-353-2

Query Match 100.0%; Score 81; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16

Db 1 RSSQSIVHSNGNTYLQ 16

##### RESULT 2

US-11-012-353-54  
; Sequence 54, Application US/11012353

```
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-012-353-54

Query Match      100.0%; Score 81; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLQ 39

RESULT 3
US-11-012-353-61
; Sequence 61, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 61
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-012-353-54

Query Match      100.0%; Score 81; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLQ 39

RESULT 4
US-11-012-353-65
; Sequence 65, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 65
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-012-353-65

Query Match      100.0%; Score 81; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSQSIVHSNGNTYLQ 16
Db      24 RSSQSIVHSNGNTYLQ 39

RESULT 5
US-11-012-353-49
; Sequence 49, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
```

; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 49  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-49

Query Match 100.0%; Score 81; DB 7; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16  
Db 34 RSSQSIVHSNGNTYLQ 49  
|||||

RESULT 6  
US-11-012-353-63  
; Sequence 63, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFIOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 63  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-63

Query Match 100.0%; Score 81; DB 7; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16  
Db 34 RSSQSIVHSNGNTYLQ 49  
|||||

Db 43 RSSQSIVHSNGNTYLQ 58

RESULT 7  
US-11-012-353-67  
; Sequence 67, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFIOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 67  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-67

Query Match 100.0%; Score 81; DB 7; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16  
Db 43 RSSQSIVHSNGNTYLQ 58  
|||||

RESULT 8  
US-10-932-334-56  
; Sequence 56, Application US/10932334  
; Publication No. US20050249728A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunogen, Inc.  
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY  
; FILE REFERENCE: A8689  
; CURRENT APPLICATION NUMBER: US/10/932,334  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR FILING DATE: US/10/729,441  
; PRIOR FILING DATE: 2003-12-08  
; PRIOR FILING DATE: 2003-12-08  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 56  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-932-334-56

Query Match 96.3%; Score 78; DB 6; Length 100;  
Best Local Similarity 93.8%; Pred. No. 3.2e-07;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 9
US-11-012-353-55
; Sequence 55, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GORTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-55

Query Match 96.3%; Score 78; DB 7; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.6e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 10
US-11-012-353-56
; Sequence 56, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GORTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20

QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 11
US-10-932-334-59
; Sequence 59, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-59

Query Match 96.3%; Score 78; DB 6; Length 113;
Best Local Similarity 93.8%; Pred. No. 3.7e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 12
US-10-932-334-61
; Sequence 61, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
```



```
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-61

Query Match          96.3%; Score 78; DB 6; Length 113;
Best Local Similarity 93.8%; Pred. No. 3.7e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
   |||||:|||||:
Db 24 RSSQSIVHSGNGNTYLE 39

RESULT 13
US-11-065-943-49
; Sequence 49, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-065-943-49

Query Match          96.3%; Score 78; DB 7; Length 116;
Best-Local Similarity 93.8%; Pred. No. 3.8e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
   |||||:|||||:
Db 27 RSSQSIVHSGNGNTYLE 42

RESULT 14
US-10-512-184-30
; Sequence 30, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VD2 with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
```

US-10-512-184-30

```
Query Match          96.3%; Score 78; DB 6; Length 251;
Best Local Similarity 93.8%; Pred. No. 9.1e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
   |||||:|||||:
Db 161 RSSQNIHVHSGNGNTYLQ 176

RESULT 15
US-10-512-184-67
; Sequence 67, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising AG - linker - scFv VD2.
US-10-512-184-67
```

```
Query Match          96.3%; Score 78; DB 6; Length 320;
Best Local Similarity 93.8%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
   |||||:|||||:
Db 230 RSSQNIHVHSGNGNTYLQ 245
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Search completed: December 30, 2005, 14:15:20  
Job time : 6.93548 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:37:27 ; Search time 132.5 Seconds  
(without alignments)  
53.057 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIHNSGNTYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 19975

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	16	7	ADJ76836 CDR seque
2	81	100.0	16	9	ADZ67006 Murine in
3	78	96.3	16	2	AAR70451 VL sequen
4	78	96.3	16	5	ABP52343 Fv region
5	78	96.3	16	7	ADC03151 Colon spe
6	78	96.3	16	7	ADD94147 Mouse HUI
7	78	96.3	16	7	ADH61992 Mouse ant
8	78	96.3	16	8	ADL27487 CDR from
9	78	96.3	16	8	ADM78123 Human SJB
10	78	96.3	16	8	ADM78129 Human SJB
11	78	96.3	16	8	ADM78081 Human SJB
12	78	96.3	16	8	ADP84865 Complemen
13	78	96.3	16	8	ADR19270 Glycosyla
14	78	96.3	16	8	ADS87339 Humanised
15	76	93.8	16	5	AAU70349 Mouse Kap
16	76	93.8	16	8	ADP84887 Complemen
17	76	93.8	16	9	ADZ08831 Mammalian
18	75	92.6	16	7	ADD94234 Mouse HUI
19	74	91.4	16	2	AAR75487 Mouse ant
20	74	91.4	16	3	AAB21364 Mouse ant
21	74	91.4	16	4	AAB97198 Murine an
22	74	91.4	16	6	ABP58276 Murine mo
23	74	91.4	16	7	ADD94233 Mouse HUI
24	74	91.4	16	8	ADP84888 Complemen

25	74	91.4	16	8	ADR19288	Adri9288 Glycosyla
26	74	91.4	16	8	ADS94307	AdS94307 Antibody
27	74	91.4	16	9	ADY80101	Ady80101 Anti-ghre
28	74	91.4	16	9	ADY80084	Ady80084 Anti-ghre
29	74	91.4	16	9	ARB21685	Aeb21685 Anti-Nogo
30	74	91.4	16	9	ARB08720	Aeb08720 antibody
31	73	90.1	16	8	ADP84893	Adp84893 Complemen
32	73	90.1	16	8	ADP84886	Adp84886 Complemen
33	73	90.1	16	8	ADR19287	Adri9287 Glycosyla
34	72	88.9	16	2	AAR40216	Aar40216 Humanised
35	72	88.9	16	7	ADD94261	Add94261 Mouse HUI
36	72	88.9	16	7	ADD94225	Add94225 Mouse HUI
37	72	88.9	16	8	ADP84891	Adp84891 Complemen
38	71	87.7	16	2	AAW58534	Aaw58534 CDR-1 of
39	71	87.7	16	3	AAV51154	Aay51154 Murine CD
40	71	87.7	16	7	ADD94229	Add94229 Mouse HUI
41	71	87.7	16	7	ADD94226	Add94226 Mouse HUI
42	71	87.7	16	8	ADP84866	Adp84866 Complemen
43	71	87.7	16	8	ADP84889	Adp84889 Complemen
44	71	87.7	16	9	AEA45027	Aea45027 Apolipop
45	70	86.4	16	2	AAW31747	Aaw31747 CDRL1 reg

## ALIGNMENTS

### RESULT 1

ADJ76836	ID	ADJ76836 standard; peptide; 16 AA.
XX	AC	ADJ76836;
XX	AC	ADJ76836;
DT	06-MAY-2004	(first entry)
XX	XX	CDR sequence for anti-IGF-1R antibody.
DE	XX	cytostatic; antipsoriatic; antibody;
KW	KW	insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW	KW	or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW	KW	ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW	KW	CDR.
OS	OS	Mus musculus.
XX	XX	WO2003059951-A2.
PN	PN	24-JUL-2003.
XX	XX	20-JAN-2003; 2003WO-FR000178.
PF	PF	18-JAN-2002; 2002FR-00000653.
XX	XX	18-JAN-2002; 2002FR-00000654.
PR	PR	07-MAY-2002; 2002FR-00005753.
XX	XX	(FABR ) FABRE MEDICAMENT SA PIERRE.
PA	PA	Goetsch L, Corvaia N, Leger O;
XX	XX	WPI; 2003-569653/53.
PI	PI	N-PSDB; ADJ76835.
XX	XX	New antibodies that bind to human insulin-like growth factor receptor,
DR	DR	useful for treatment, prevention and diagnosis of cancers.
XX	XX	Claim 1; SEQ ID NO 2; 164pp; French.
XX	XX	The invention relates to an isolated antibody (Ab), and its functional
CC	CC	fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC	CC	IR) and optionally: (i) inhibit natural binding of insulin-like growth
CC	CC	factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC	CC	kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC	CC	treat diseases associated with overexpression and/or abnormal activity of
CC	CC	IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 81; DB 7; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-07; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0;

QY 1 RSSQSIVHSGNTYLQ 16  
 |||||  
 DB 1 RSSQSIVHSGNTYLQ 16  
 |||||

RESULT 2  
 ADZ67006  
 ID ADZ67006 standard; peptide; 16 AA.  
 XX  
 AC ADZ67006;  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:2.  
 XX  
 KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2005084906-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 PF 16-DEC-2003; 2003US-00735916.  
 XX  
 PR 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 PR 20-JAN-2003; 2003WO-FR000178.  
 PR 11-JUL-2003; 2003FR-00008538.  
 XX  
 PA (GOET/) GOETSCH L.  
 PA (CORV/) CORVAIA N.  
 PA (LEGE/) LEGER O.  
 PA (DUFL/) DUFLOS A.  
 PA (HAEU/) HAEUW J.  
 PA (BECK/) BECK A.  
 XX  
 PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 XX  
 DR WPI; 2005-321968/33.  
 DR N-PSDB; ADZ67005.  
 XX  
 PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX  
 PS Claim 1; SEQ ID NO 2; 125pp; English.  
 XX  
 CC The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 81; DB 9; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-07; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0;

QY 1 RSSQSIVHSGNTYLQ 16  
 |||||  
 DB 1 RSSQSIVHSGNTYLQ 16  
 |||||

RESULT 3  
 AAR70451  
 ID AAR70451 standard; peptide; 16 AA.  
 XX  
 AC AAR70451;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-OCT-1995 (first entry)  
 XX  
 DE VL sequence of anti-KC-4 monoclonal antibody (kII-Jk2) corresp. to.  
 DE complementarity determining region 1 (CDR1).  
 XX  
 KW Anti-KC-4 antibody; monoclonal antibody; cancer; VL chain.  
 XX  
 OS Synthetic.  
 XX  
 FN WO9510776-A1.  
 XX  
 PD 20-APR-1995.  
 XX  
 PF 16-NOV-1993; 93WO-US011444.  
 XX  
 PR 08-OCT-1993; 93US-00134346.  
 XX  
 PA (CANC-) CANCER RES FUND CONTRA COSTA.  
 XX  
 PI Do Couto JJR, Ceriani RL, Peterson JA;  
 XX  
 DR WPI; 1995-161912/21.

DR N-PSDB; AAQ87531.

XX New humanised anti-KC-4 monoclonal antibody - used for detection of

PT cancer cells, in vivo imaging, ex-vivo purging and treatment of cancers.

XX Example; Table 14, Page 31; 61pp; English.

XX The cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL were

CC prepared by PCR from polyadenylated RNA isolated from 100 million KC-4

CC hybridoma cells. All clones were obtd. from independent PCRs. The

CC sequences of the primers are given in AAQ87519-Q87526. The PCR products

CC were cloned, without prior purificn., into pCR1000 (Invitrogen) and

CC sequenced in both directions. The VL DNA sequence and its derived protein

CC sequences are shown in AAQ87531 and AAR70449-R70457. The mature VL chain

CC begins at AA D of framework 1 (FR1). VL is a group II kappa chain. Part

CC of the CDR3 and all of the FR4 are encoded by JK2. There is a an

CC asparagine glycosylation site in the light chain in FR3. The site reads

CC NIS. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-

CC 2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 16 AA;

Query Match 96.3%; Score 78; DB 2; Length 16;

Best Local Similarity 93.8%; Pred. No. 1.6e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16

DB 1 RSSQSIVHSGNGNTYLE 16

RESULT 4

ABP52343

ID ABP52343 standard; peptide; 16 AA.

XX

AC ABP52343;

XX

DT 17-OCT-2002 (first entry)

XX

DE Fv region SC100 antibody CDR-L1 amino acid sequence.

XX

KW Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;

KW tumour; immune response; cancer; vaccine; antibody.

XX

OS Mus musculus.

OS Synthetic.

XX

PN WO200258728-A2.

XX

PD 01-AUG-2002.

XX

PF 28-JAN-2002; 2002WO-GB0000354.

XX

PR 26-JAN-2001; 2001GB-00002145.

XX

PA (SCAN-) SCANCEL LTD.

PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX

PI Durrant LG, Parsons T, Robins A;

XX

DR WPI; 2002-608418/65.

XX

PT Use of polypeptides and nucleic acids encoding the polypeptides, in

PT manufacturing medicament for stimulating a cytotoxic T cell response and

PT for preventing or treating cancer, e.g. colorectal, lung, breast or

PT ovarian cancer.

XX

PS Example 11; Page 45; 87pp; English.

XX

CC The present invention describes the use of a polypeptide (I) in the

CC manufacture of a medicament for stimulating a cytotoxic T cell response,

CC where (I) comprises a first portion comprising the part of human PC that

CC binds to CD64 and a second portion comprising one or more heterologous T.

CC cell epitopes. Also described is a method of stimulating a cytotoxic T

CC cell response in a patient such as a mammal, preferably human, by

CC administering (I) to the patient. (I) has cytostatic activity and can be

CC used in vaccine production. (I) and the nucleic acid encoding (I) are

CC useful in the manufacture of a medicament for stimulating cytotoxic T

CC cell response. The medicament is useful for preventing and/or treating

CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The

CC medicament stimulates cytotoxic and helper T cell responses. The

CC antibodies are useful as vaccines to stimulate helper and cytotoxic T

CC cell responses. The polypeptides and nucleic acids are useful in

CC optimising immunisation schedules for enhancing a protective immune

CC response against cancer. The present sequence represents an Fv region

CC SC100 antibody CDR-L1 amino acid sequence which is used in an example

CC from the present invention

XX

SQ Sequence 16 AA;

Query Match 96.3%; Score 78; DB 5; Length 16;

Best Local Similarity 93.8%; Pred. No. 1.6e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16

DB 1 RSSQSIVHSGNGNTYLE 16

RESULT 5

ADC03151

ID ADC03151 standard; peptide; 16 AA.

XX

AC ADC03151;

XX

DT 18-DEC-2003 (first entry)

XX

DE Colon specific antigen-p mucin murine antibody light chain CDRI.

XX

KW cytostatic; antitumour; antibody; colon specific antigen-p mucin;

KW hapten binding site; immunoconjugate; close-range lesion; tumour; ovary;

KW thymus; parathyroid; spleen; carcinoma; gastrointestinal cancer;

KW colorectal cancer; pancreatic cancer; ovarian cancer;

KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO200282041-A2.

XX

PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US010235.

XX

PR 03-APR-2001; 2001US-00823746.

XX

PA (IMMU-) IMMUNOMEDICS INC.

XX

PI Hansen HU, Griffiths GL, Leung S, McBride WJ, Qu Z;

PI Goldenberg DM;

XX

DR WPI; 2003-167089/16.

XX

XX Novel multivalent, multispecific antibody for detecting/treating tumors

XX expressing colon specific antigen-p mucin in mammal, comprises antigen

XX and hapten binding sites.

XX Claim 9; Page 132; 202pp; English.

XX

PS The invention relates to a multivalent, multispecific antibody or its

XX fragment comprising one more antigen binding sites having affinity

XX towards colon specific antigen-p mucin (CSAp) target antigen and one or

XX more hapten binding sites having affinity towards hapten molecules. The

XX antibody is useful for screening a targetable conjugate. A therapeutic

XX immunoconjugate comprising the antibody is useful for detecting close-

XX range lesion. The antibody or immunoconjugate are also useful for

XX delivering a diagnostic/detection or therapeutic agent, or their

CC combination, to a target. The antibody or a targetable conjugate are  
 CC useful for detecting or treating tumours expressing CSAP in a mammal, for  
 CC imaging malignant tissue or normal tissue or cells in a mammal expressing  
 CC CSAP, where the normal tissue is from ovary, thymus, parathyroid or  
 CC spleen, for intraoperatively identifying/disclosing the diseased tissues  
 CC expressing CSAP in a subject, and for endoscopic identification of  
 CC diseased tissues expressing CSAP. They are also useful for intravascular  
 CC identification of diseased tissues expressing CSAP, for detecting lesions  
 CC during an endoscopic, laparoscopic, intravascular catheter or surgical  
 CC procedure, and for detecting and treating target cells, tissues or  
 CC pathogens in a mammal. A method using the antibody is useful for  
 CC diagnosing or detecting a malignancy in a subject, where the malignancy  
 CC is carcinoma, gastrointestinal cancer, colorectal or pancreatic cancer or  
 CC ovarian cancer, the subject is human or a domestic pet. This sequence  
 CC represents the light chain complementarity determining region 1 (CDR1)  
 CC from the antibodies of the invention.

XX Sequence 16 AA;  
 SQ

Query Match 96.3%; Score 78; DB 7; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16  
 Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 6  
 ADD94147  
 ID ADD94147 standard; peptide; 16 AA.  
 AC ADD94147;  
 XX 29-JAN-2004 (first entry)  
 DT  
 DE Mouse HUI77 light chain CDR1 partial amino acid sequence SeqID32.  
 XX  
 KW grafted antibody; complementarity determining region; CDR; light CDR;  
 KW heavy CDR; cryptic collagen epitope; solid tumour;  
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
 KW collagen agonist; collagen antagonist; cancer metastasis;  
 KW anti-cryptic collagen; antibody; HUI77; variable region light chain;  
 KW mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003046204-A2.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 26-NOV-2002; 2002WO-US038147.  
 XX  
 PR 26-NOV-2001; 2001US-00995529.  
 PR 06-DEC-2001; 2001US-00011250.  
 XX  
 PA (CELL-) CELL MATRIX INC.  
 XX  
 PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;  
 XX  
 DR WPI; 2003-513649/48.  
 DR N-PSDB; ADD94146.  
 XX  
 XX New cryptic collagen antibody with one or more complementarity  
 PT determining regions, useful for diagnosing and treating disorders  
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
 XX  
 PS Claim 25; SEQ ID NO 32; 232pp; English.  
 XX  
 XX This invention relates to a novel grafted antibody or its functional  
 CC fragment comprising one or more complementarity determining regions  
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
 CC acid (aa) substitution where the antibody has specific binding activity

CC for a cryptic collagen epitope. The growth of all solid tumours requires  
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
 CC to limiting tumour growth. The invention may allow development of  
 CC therapeutics with a cytostatic activity as a collagen agonist or  
 CC antagonist. The invention is useful for diagnosing and treating disorders  
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
 CC present sequence is the partial amino acid sequence of a mouse anti-  
 CC cryptic collagen site antibody HUI77 variable region light chain CDR  
 CC which is related to the invention.

XX Sequence 16 AA;  
 SQ

Query Match 96.3%; Score 78; DB 7; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16  
 Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 7  
 ADH61992  
 ID ADH61992 standard; peptide; 16 AA.  
 XX  
 AC ADH61992;  
 XX  
 DT 25-MAR-2004 (first entry)  
 DE Mouse antibody 2K1 VL region CDR1 SEQ ID NO:24.  
 XX  
 KW osteopontin; antibody; integrin; OPN; immunosuppressive; anti-arthritis;  
 KW anti-rheumatic; osteopathic; autoimmune disease; rheumatism;  
 KW rheumatoid arthritis; arthritis deformans; mouse; 2K1; CDR1.  
 XX  
 OS Mus sp.  
 XX  
 PN WO2003027151-A1.  
 XX  
 PD 03-APR-2003.  
 XX  
 PF 25-SEP-2002; 2002WO-JP009868.  
 XX  
 PR 25-SEP-2001; 2001JP-00290700.  
 XX  
 PA (IMMU-) IMMUNO BIOLOGICAL LAB CO LTD.  
 PA (FUJI) FUJISAWA PHARM CO LTD.  
 XX  
 PI Ueda T, Kon S, Yamamoto N, Higuchi H, Torikai M, Tokieda Y;  
 PI Nakashima T, Maeda H;  
 XX  
 DR WPI; 2003-393331/37.  
 XX  
 PT Recombinant anti-osteopontin antibodies with human-origin heavy and light  
 PT chain constant regions, useful in diagnosis and developing drugs for  
 PT autoimmune diseases, rheumatism and rheumatoid arthritis.  
 XX  
 PS Claim 14; SEQ ID NO 24; 111pp; Japanese.  
 XX  
 CC The invention relates to a novel anti-osteopontin antibody or antibody  
 CC fragment which inhibits the binding of and integrin recognising the RGD  
 CC sequence to osteopontin (OPN) or its fragment and inhibits the binding of  
 CC an integrin recognising the SVYGLR sequence to osteopontin or its  
 CC fragment. An antibody of the invention has immunosuppressive, anti-  
 CC arthritic, anti-rheumatic, and osteopathic activity. The antibodies are  
 CC useful in diagnostics and developing drugs for autoimmune diseases,  
 CC rheumatism, rheumatoid arthritis and arthritis deformans. With these  
 CC antibodies, it is possible to distinguish rheumatoid arthritis from  
 CC arthritis deformans. The present sequence is used in the exemplification  
 CC of the invention.

XX Sequence 16 AA;  
 SQ

Query Match 96.3%; Score 78; DB 7; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16  
Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 8  
ADL27487  
ID ADL27487 standard; peptide; 16 AA.  
XX  
AC ADL27487;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE CDR from the light chain of antibody EGP6D8-1-2.  
XX  
KW glycoprotein; EGP6D8-1-1; EGP13F6-1-2; EGP13C6-1-1;  
KW Ebola virus infection; antibody; light chain;  
KW Complementarity determining region; CDR.  
XX  
OS Mus sp.  
XX  
XX WO2004018649-A2.  
XX  
XX 04-MAR-2004.  
XX  
XX 21-AUG-2003; 2003WO-US027450.  
XX  
XX 23-AUG-2002; 2002US-00226795.  
XX  
XX (USSA) US ARMY MEDICAL RES INST INFECTIOUS DISE.  
XX  
XX Hart MK, Wilson JA;  
XX WPT; 2004-226835/21.  
XX  
XX New isolated monoclonal antibody that binds Ebola virus GP, which  
PT monoclonal antibody comprises a heavy chain variable region, useful for  
PT treating or ameliorating Ebola virus infection.  
XX  
XX Claim 33; Page 65; 68pp; English.  
XX  
XX The specification describes monoclonal antibodies that bind Ebola virus  
CC glycoprotein. The antibodies are EGP6D8-1-1, EGP13F6-1-2, and EGP13C6-1-1.  
CC 1. The monoclonal antibodies of the invention are useful for treating or  
CC ameliorating an Ebola virus infection. The antibodies were found to be  
CC effective when administered 2 days after challenge, after significant  
CC viral replication had occurred. ADL27487-ADL27489 represent  
CC complementarity determining regions (CDRs) from the light chain of a  
CC monoclonal antibody of the invention.  
XX  
SQ Sequence 16 AA;

Query Match 96.3%; Score 78; DB 8; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16  
Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 9  
ADM78123  
ID ADM78123 standard; peptide; 16 AA.  
XX  
AC ADM78123;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
XX

DE Human SUB3-38 antibody variable light chain CDR1 peptide region.  
XX monoclonal antibody; adenylate kinase isozyme 3;  
KW complementarity determining region; CDR; heart disease; marker AK3;  
KW biochemical; human; variable; light chain.  
XX  
XX Homo sapiens.  
XX  
XX WO2004029094-A1.  
XX  
XX 08-APR-2004.  
PD  
XX 27-SEP-2003; 2003WO-KR001979.  
XX  
XX 28-SEP-2002; 2002KR-00059211.  
XX  
XX (KIMH/) KIM H.  
XX  
XX Kim H;  
XX WPT; 2004-316088/29.  
XX  
XX New monoclonal antibody specific to human mitochondrial adenylate kinase  
PT isozyme 3, useful for preparing a composition for detecting a heart  
PT disease marker AK3.  
XX  
XX Claim 1; SEQ ID NO 86; 126pp; English.  
XX  
XX The invention relates to a novel monoclonal antibody specific to  
CC adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity  
CC determining regions (CDRs) of a sequence having 6-18 amino acids. The  
CC invention further relates to: a composition comprising the monoclonal  
CC antibody for detecting a heart disease marker AK3; a kit comprising the  
CC monoclonal antibody for the diagnosis of heart disease; and a method of  
CC detecting a heart disease marker AK3. The monoclonal antibody is useful  
CC for preparing a composition for detecting a heart disease marker AK3. The  
CC monoclonal antibody reduces false positive results of the conventional  
CC biochemical markers. This sequence represents a human antibody variable  
CC light chain CDR peptide region of the invention.  
XX  
SQ Sequence 16 AA;

Query Match 96.3%; Score 78; DB 8; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16  
Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 10  
ADM78129  
ID ADM78129 standard; peptide; 16 AA.  
XX  
XX ADM78129;  
XX  
XX 01-JUL-2004 (first entry)  
DT  
XX  
XX Human SUB3-39 antibody variable light chain CDR1 peptide region.  
XX  
XX monoclonal antibody; adenylate kinase isozyme 3;  
KW complementarity determining region; CDR; heart disease; marker AK3;  
KW biochemical; human; variable; light chain.  
XX  
XX Homo sapiens.  
XX  
XX WO2004029094-A1.  
XX  
XX 08-APR-2004.  
PD  
XX 27-SEP-2003; 2003WO-KR001979.  
XX  
XX

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PR 28-SEP-2002; 2002KR-00059211.
XX (KIMH/) KIM H.
XX Kim H;
XX WPI; 2004-316088/29.
XX New monoclonal antibody specific to human mitochondrial adenylate kinase
PT isozyme 3, useful for preparing a composition for detecting a heart
PT disease marker AK3.
XX Claim 1; SEQ ID NO 92; 126pp; English.
XX The invention relates to a novel monoclonal antibody specific to
CC adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity
CC determining regions (CDRs) of a sequence having 6-18 amino acids. The
CC invention further relates to: a composition comprising the monoclonal
CC antibody for detecting a heart disease marker AK3; a kit comprising the
CC monoclonal antibody for the diagnosis of heart disease; and a method of
CC detecting a heart disease marker AK3. The monoclonal antibody is useful
CC for preparing a composition for detecting a heart disease marker AK3. The
CC monoclonal antibody reduces false positive results of the conventional
CC biochemical markers. This sequence represents a human antibody variable
CC light chain CDR peptide region of the invention.
XX Sequence 16 AA;
XX Query Match 96.3%; Score 78; DB 8; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 1.6e-06;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
DB 1 RSSQSIVHSGNGNTYLE 16

RESULT 12
ADP84865
ID ADP84865 standard; peptide; 16 AA.
XX AC ADP84865;
XX DT 09-SEP-2004 (first entry)
XX DE Complementarity determining region SEQ ID NO 7.
XX antibody; Core-1 antigen; framework region; immunoglobulin superfamily;
KW protease inhibitor; lectin; helix-bundle protein; lipocalin;
KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;
KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;
KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
KW metastasis.
XX OS Unidentified.
XX PN WO2004050707-A2.
XX PD 17-JUN-2004.
XX PF 01-DEC-2003; 2003WO-DE003994.
XX PR 29-NOV-2002; 2002DE-01056900.
XX PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
XX PI Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;
XX Christensen PA;
XX WPI; 2004-461095/43.
XX New recognition molecules, e.g. antibodies (and nucleic acids) that bind
PT specifically to Core-1 antigens, useful for diagnosis, treatment and
PT prevention of tumors and metastases.
XX Claim 2; SEQ ID NO 7; 136pp; German.
XX This invention describes novel recognition molecules, especially
CC antibodies that bind specifically to the Core-1 antigen. The recognition
CC molecules are used to make constructs containing the framework regions
CC that separate, include and/or flank the specified sequences, especially
CC where the framework regions are from the immunoglobulin (Ig) superfamily,
CC protease inhibitors, lectins, helix-bundle proteins and/or lipocalins.
CC Most especially the framework regions are from antibodies, particularly
CC the variable heavy chain (VH) and the variable light chain (VL) of human
CC and/or murine origin. The constructs may also include a His or myc tag, a
CC lysine-rich region and/or a multimerisation domain, most particularly it

```



CC is a single-chain antibody fragment, multibody, Fab fragment, fusion  
 CC protein of an antibody fragment with peptide or protein, and/or an Ig of  
 CC types G, M, A, E or D and/or their subclasses. It may be human,  
 CC humanised, murine or chimeric, e.g. IgM without the J chain. The  
 CC additional sequences/structures in the constructs are Ig domains of  
 CC various species, interacting or stabilising domains, signal sequences,  
 CC fluorescent dyes, toxins, antibodies with catalytic activity or other  
 CC specificities, cytolytic agents, enzymes, immuno-modulators or -  
 CC effectors, MHC molecules, antigens, chelators for radioactive labels,  
 CC liposomes, transmembrane domains, viruses and/or cells, specifically  
 CC macrophages. The antibodies, also constructs containing them, nucleic  
 CC acid encoding them, and related vectors and host cells, are useful for  
 CC prevention (e.g. as vaccine), diagnosis, alleviation, treatment,  
 CC monitoring and/or secondary treatment of tumours (specifically of breast,  
 CC colon, stomach, pancreas, large/small intestine, ovary, cervix, lung,  
 CC prostate, kidney and/or liver) and/or metastases (particularly to liver),  
 CC specifically where these are positive for the C1 antigen. The products of  
 CC the invention provide simple, reliable and efficient detection of  
 CC tumours. They are specific for carcinoma and show almost no binding to  
 CC healthy tissue.

XX Sequence 16 AA;  
 SQ Query Match 96.3%; Score 78; DB 8; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16  
 |||||  
 Db 1 RSSQSIVHSNGNTYLE 16

## RESULT 13

ADRI9270  
 ID ADRI9270 standard; peptide; 16 AA.

XX AC ADRI9270;

XX DT 21-OCT-2004 (first entry)

XX DE Glycosylated MUC1 tumour epitope recognition peptide, SEQ ID 7.

XX KW Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1;  
 XX KW tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary;  
 XX KW liver; kidney cell; intestinal; lung cancer; multiple myeloma.

XX OS Unidentified.

XX PN WO2004065423-A2.

XX PD 05-AUG-2004.

XX PF 23-JAN-2004; 2004WO-DE000132.

XX PR 23-JAN-2003; 2003DE-01003664.

XX PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.

XX PI Goletz S, Danielczyk A, Stahn R, Karsten U;

XX DR WPI; 2004-593433/57.

XX PT New recognition molecules that bind the glycosylated MUC1 tumour epitope,  
 XX PT useful for prevention, diagnosis, treatment and monitoring of tumors.

XX PS Claim 4; SEQ ID NO 7; 158pp; German.

XX CC The invention relates to novel recognition molecules comprising sequences  
 CC that bind specifically to a glycosylated MUC1 tumour epitope. The novel  
 CC recognition molecules comprise: sequences ADRI9264 or ADRI9265; sequences  
 CC ADRI9266 or ADRI9267 and sequences ADRI9268 and ADRI9269, and bind  
 CC specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The  
 CC invention further comprises: a construct comprising the recognition

CC molecule fused, chemically coupled or non-covalently associated with  
 CC additional sequences and/or structures; an isolated nucleic acid that  
 CC encodes the recognition molecule or construct; expression cassettes or  
 CC vector that contains the isolated nucleic acid, operatively linked to a  
 CC promoter; virus or host cell comprising at least one cassette or vector  
 CC of ADRI9266; an organism containing at least one host cell of ADRI9267; a  
 CC method for preparing the recognition molecule and construct; and a kit  
 CC containing the recognition molecule and/or construct. The recognition  
 CC molecules have cytostatic activity. The recognition molecules, constructs  
 CC containing them, the nucleic acid encoding them, and derived viruses,  
 CC cells and organisms, are used for prevention, diagnosis, treatment and  
 CC monitoring of tumours and/or metastases, specifically where MUC1  
 CC positive, particularly carcinoma of breast, colon, stomach, pancreas,  
 CC ovary, liver or kidney cells; (gastro)intestinal or lung cancers and  
 CC multiple myeloma. The recognition molecules show little or no binding to  
 CC MUC1 in either the serum or normal tissue, so provides simple, safe and  
 CC efficient detection of tumours, even at an early stage (carcinoma in  
 CC situ), and can differentiate between tumours and benign diseases. This  
 CC sequence represents one of the novel glycosylated MUC1 tumour epitope  
 CC recognition molecules of the invention.

XX Sequence 16 AA;

Query Match 96.3%; Score 78; DB 8; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16  
 |||||  
 Db 1 RSSQSIVHSNGNTYLE 16

## RESULT 14

ADS87339  
 ID ADS87339 standard; peptide; 16 AA.

XX AC ADS87339;

XX DT 18-NOV-2004 (first entry)

XX DE Humanised antibody MN3 light chain variable region CDR1.

XX KW cytostatic; vasotropic; antimicrobial; antinflammatory; antipyretic;  
 XX KW antiatherosclerotic; cardiant; monoclonal antibody; NCA90; NCA95;  
 XX KW chimeric antibody; humanized antibody; inflammation; appendicitis;  
 XX KW inflammatory bowel disease; pelvic inflammatory disease; fever;  
 XX KW cystic fibrosis; granulocyte related disorder; atherosclerosis;  
 XX KW infarction; cancer; ischemic lesion; complementarity determining region.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Chimeric.

XX PN WO2004029093-A2.

XX PD 08-APR-2004.

XX PF 30-SEP-2003; 2003WO-GB004229.

XX PR 30-SEP-2002; 2002US-0414341P.

XX PA (IMMU-) IMMUNOMEDICS INC.

XX PA (MCCA/) MCCALL J D.

XX PI Goldenberg DM, Hansen H, Leung S;

XX DR WPI; 2004-329873/30.

XX PT Monoclonal anti-granulocyte antibody that binds NCA90 and NCA95 antigens,  
 XX PT useful for treating malignancy, inflammation, atherosclerosis,  
 XX PT infarction, or other granulocyte related disorders.

XX PS Claim 4; Page 105; 134pp; English.

XX CC The invention relates to a monoclonal antibody (Mab) (I) or its fragment  
CC that binds NCA90 or NCA95, where when the Mab or its fragment binds NCA90  
CC the Mab or its fragment is chimeric, partially humanized or fully  
CC humanized and where when the Mab or its fragment binds NCA95 the Mab or  
CC its fragment is either fully humanized or chimeric, partially humanized  
CC or fully humanized BW 250/183. (I) is useful for treating, detecting or  
CC imaging sites of inflammation resulting from appendicitis, inflammatory  
CC bowel disease, pelvic inflammatory disease, fever and cystic fibrosis and  
CC treating granulocyte related disorders, atherosclerosis and infarction.  
CC (I) is useful for detecting or treating cancer or ischemic lesion. This  
CC sequence corresponds to the complementarity determining region 1 (CDR1)  
CC of the light chain of the antibody of the invention.

XX SQ Sequence 16 AA;  
SQ Query Match 96.3%; Score 78; DB 8; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16  
| | | | | | | | | | | | | | | |  
Db 1 RSSQSIVHSGNGNTYLE 16

RESULT 15  
AAU70349  
ID AAU70349 standard; peptide; 16 AA.  
AC AAU70349;  
XX  
XX 14-FEB-2002 (first entry)  
DT  
DE Mouse Kappa II light chain CDR1.  
DE  
DE Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KW complementarity determining region; framework region; IgBP;  
KW transgenic plant; immunoglobulin binding protein array; IgW; IgG; IgA;  
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.  
XX  
XX Mus musculus.  
XX  
XX WO200183806-A1.  
FN  
XX  
XX 08-NOV-2001.  
PD  
XX  
XX 02-MAY-2001; 2001WO-US014349.  
PF  
XX  
XX 02-MAY-2000; 2000US-00563222.  
PR  
XX  
XX (EPIC-) EPICYTE PHARM INC.  
PA  
XX  
XX Hiatt AC, Hein MB;  
PI  
XX  
XX WPI; 2002-055482/07.  
DR  
XX  
XX Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding  
PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array.  
XX  
XX  
XX Disclosure; Page 14; 129pp; English.

XX CC The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IgBP that binds to  
CC a ligand, and transformed plant cells are selected, and preparing an IgBP  
CC array in plant cells. At least one peptide sequence has at least 75%  
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,  
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is  
CC useful for preparing an immunoglobulin binding protein array, preferably

CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
CC discovery of e.g. screening assays of IGBPs having desired  
CC characteristics. The present sequence is a mammalian immunoglobulin  
CC derived peptide that may be incorporated into an IgBP of the invention

XX SQ Sequence 16 AA;  
SQ Query Match 93.8%; Score 76; DB 5; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.6e-06;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16  
| | | | | | | | | | | | | | | |  
Db 1 RSSQSIVHSGNGNTYLE 16

Search completed: December 30, 2005, 14:19:57  
Job time : 139.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 14:07:14 ; Search time 22.5 Seconds  
(without alignments)  
68.421 Million cell updates/sec

Title: US-10-735-916A-2  
Perfect score: 81  
Sequence: 1 RSSQSIHNGNTYLQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	28	34.6	16	2 A36285	site-specific meth
2	21	25.9	16	2 B45895	T-cell surface gly
3	18	22.2	16	2 A59046	alpha-conotoxin MI
4	18	22.2	16	2 G24304	ribosomal protein
5	18	22.2	16	2 A44352	candidapepsin (EC
6	18	22.2	16	2 H49039	T-cell receptor be
7	18	22.2	16	2 S42237	hypothetical prote
8	18	22.2	16	2 D89854	conserved hypotet
9	18	22.2	16	2 PD0002	inulin fructotrans
10	17	21.0	16	2 S51610	hypothetical prote
11	16.5	20.4	16	2 E28027	protein P8 - curle
12	16	19.8	16	2 C39509	mannose-specific l
13	16	19.8	16	2 G45681	orf 61.1 - phage I
14	16	19.8	16	2 S23184	redoxendonuclease
15	16	19.8	16	2 A49226	major outer membra
16	16	19.8	16	2 S09732	photosystem I prot
17	16	19.8	16	2 A36889	leu operon leader
18	15	18.5	16	2 S01689	rRNA N-glycosidase
19	15	18.5	16	2 PH1778	T cell receptor al
20	15	18.5	16	2 G49039	T-cell receptor be
21	15	18.5	16	2 PH0777	T-cell receptor al
22	15	18.5	16	2 E58501	25K kidney and gal
23	14	17.3	16	1 MTDFRS	melanotropin beta
24	14	17.3	16	2 C45133	casein kinase II (
25	14	17.3	16	2 C45143	protein-tyrosine-p
26	14	17.3	16	2 F4908	chitinase (EC 3.2.
27	14	17.3	16	2 A39109	hypothetical prote
28	14	17.3	16	2 C49655	T-cell-receptor be
29	14	17.3	16	2 G53284	T-cell receptor be

30	14	17.3	16	2 PH1622	Ig H chain V-D-J r
31	14	17.3	16	2 S33589	beta-crystallin A4
32	14	17.3	16	2 S69361	carbamoyl-phosphat
33	14	17.3	16	2 B44820	7K protein - Eache
34	13	16.0	16	2 S00123	dihydrolipoamide S
35	13	16.0	16	2 S10807	protein kinase C 1
36	13	16.0	16	2 A36300	T-cell receptor ga
37	13	16.0	16	2 A45133	casein kinase II (
38	13	16.0	16	2 C58503	proteoglycan assoc
39	13	16.0	16	2 B24099	crystal protein, 7
40	13	16.0	16	2 PH1770	T cell receptor al
41	13	16.0	16	2 H41299	T-cell receptor be
42	13	16.0	16	2 PH0137	T-cell receptor be
43	13	16.0	16	2 E49255	T-cell receptor be
44	13	16.0	16	2 E53284	T-cell receptor be
45	13	16.0	16	2 PH1588	Ig H chain V-D-J r

ALIGNMENTS

RESULT 1

A36285  
Site-specific methyltransferase (EC 2.1.1.-) - Escherichia coli (fragment)  
C;Species: Escherichia coli  
C;Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 21-Mar-1996  
C;Accession: A36285  
R;Reich, N.O.; Everett, E.A.  
J. Biol. Chem. 265, 8929-8934, 1990  
A;Title: Identification of peptides involved in S-adenosylmethionine binding in the Eco  
A;Reference number: A36285; MUID:90256827; PMID:2341412  
A;Accession: A36285  
A;Status: preliminary  
A;Molecule type: Protein  
A;Residues: 1-16 <REI>  
A;Cross-references: UNIPARC:UPI000017AA66  
C;Keywords: methyltransferase

Query Match 34.6%; Score 28; DB 2; Length 16;  
Best Local Similarity 30.8%; Pred. No. 1.8e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 SQSIHVSNGNTYL 15  
::: : |||| :  
DB 2 TEAXIDSNGNXII 14

RESULT 2

B45895  
T-cell surface glycoprotein CD28 short form - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Feb-1994  
C;Accession: B45895  
R;Lee, K.P.; Taylor, C.; Petryniak, B.; Turka, L.A.; June, C.H.; Thompson, C.B.  
J. Immunol. 145, 344-352, 1990  
A;Title: The genomic organization of the CD28 gene. Implications for the regulation of  
A;Reference number: A45895; MUID:90293482; PMID:2162892  
A;Accession: B45895  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-16 <LEE>  
A;Cross-references: UNIPARC:UPI000017C3C5; GB:M37813  
C;Keywords: glycoprotein

Query Match 25.9%; Score 21; DB 2; Length 16;  
Best Local Similarity 37.5%; Pred. No. 2.7e+03; Indels 1; Gaps 0;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVH 8  
::: : ||:  
DB 9 KSNGTIH 16

```
RESULT 3
A59046
C:Species: Conus magus (Conus magus)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: A59046
R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.
J. Biol. Chem. 271, 7522-7528, 1996
A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptors
A:Reference number: A59046; MUID:96205934; PMID:8631783
A:Accession: A59046
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <CAR>
A:Cross-references: UNIPROT:P56636; UNIPARC:UPI00001287CA
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin
F:1-16/Product: alpha-conotoxin MII #status experimental <NAR>
F:2-8,3-16/Disulfide bonds: #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 HSN 10
Db 12 HSN 14

RESULT 4
G24304
ribosomal protein H [validated] - Haloarcula marismortui (fragment)
C:Species: Haloarcula marismortui
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000
C:Accession: G24304
R:Shoham, M.; Dijk, J.; Reinhardt, R.; Wittmann-Liebold, B.
FEBS Lett. 204, 323-330, 1986
A:Title: Purification and characterization of ribosomal proteins from the 30 S subunit of
A:Reference number: A24304
A:Accession: G24304
A:Molecule type: protein
A:Residues: 1-16 <SHO>
A:Cross-references: UNIPARC:UPI000017ABA2
C:Keywords: protein biosynthesis; ribosome

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GNTY 14
Db 2 GNKY 5

RESULT 5
A44352
candidapepsin (EC 3.4.23.24), white-opaque switching regulated - yeast (Candida albicans)
C:Species: Candida albicans
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Nov-1996
C:Accession: A44352
R:Morrow, B.; Srikantha, T.; Soll, D.R.
Mol. Cell. Biol. 12, 2997-3005, 1992
A:Title: Transcription of the gene for a pepsinogen, PEP1, is regulated by white-opaque
A:Reference number: A44352; MUID:92318916; PMID:1620110
A:Accession: A44352
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-16 <MOR>
A:Cross-references: UNIPARC:UPI000017B22C
C:Keywords: aspartic proteinase; hydrolase

Query Match 22.2%; Score 18; DB 2; Length 16;
```

```
Best Local Similarity 25.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SSQSIHVSNGNT 13
Db 5 TGSVVLDSGTY 16

RESULT 6
H49039
T-cell receptor beta chain V-D-J-C region (V beta 5, J beta 1.4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: H49039
R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A:Reference number: A49039; MUID:92164737; PMID:1311263
A:Accession: H49039
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-16 <ROS>
A:Cross-references: UNIPARC:UPI000017C3B7
A:Note: sequence extracted from NCBI backbone (NCBIP:90720)
C:Keywords: T-cell receptor

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 SNGNT 13
Db 5 ANGQT 9

RESULT 7
S42237
hypothetical protein 2 - Staphylococcus aureus plasmid pNS1
C:Species: Staphylococcus aureus
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S42237
R:Noguchi, N.; Aoki, T.; Sasatsu, M.; Kono, M.; Shishido, K.; Ando, T.
FEMS Microbiol. Lett. 37, 283-288, 1986
A:Title: Determination of the complete nucleotide sequence of pNS1, a staphylococcal tet
A:Reference number: S42236
A:Accession: S42237
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <NOG>
A:Cross-references: UNIPROT:Q51950; UNIPARC:UPI00000B1F13; EMBL:M16217; NID:g150832; PII
C:Genetics:
A:Genome: plasmid pNS1

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GNTY 14
Db 9 GNLY 12

RESULT 8
DB9854
conserved hypothetical protein SAS021 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: DB9854
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
```

A;Reference number: A89758; MUID:21311952; PMID:11418146  
A;Accession: D89954  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-16 <KUR>  
A;Cross-references: UNIPROT:Q99VH9; UNIPARC:UPI00000CA988; GB:BA000018; FID:gl3700694; R  
A;Experimental source: strain N315  
C;Genetics:  
A;Gene: SAS021

Query Match 22.2%; Score 18; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 8.7e+03;  
Matches 6; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 RSSQSIVHNGNTY 14  
||| ||| :|  
DB 3 RSQASI--GTGHY 14

## RESULT 9

PD0002  
inulin fructotransferase (depolymerizing, difructofuranose-1,2':2,3'-dianhydride-forming  
C;Species: Bacillus sp.  
C;Date: 10-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: PD0002  
R;Kang, S.I.; Kim, W.P.; Chang, Y.J.; Kim, S.I.  
Biocli. Biotechnol. Biochem. 82, 628-631, 1998  
A;Title: Purification and properties of inulin fructotransferase (DFA III-producing) fro  
A;Reference number: PD0002  
A;Accession: PD0002  
A;Molecule type: protein  
A;Residues: 1-16 <KAN>  
A;Cross-references: UNIPROT:Q7M0Z5; UNIPARC:UPI000017CD57  
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 22.2%; Score 18; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 NTY 14  
|||  
DB 13 NTY 15

## RESULT 10

S51610  
hypothetical protein - tomato  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
C;Accession: S51610  
R;Krolkiewicz, S.; Saenger, H.L.; Niesbach-Kloesgen, U.  
Mol. Gen. Genet. 245, 565-576, 1994  
A;Title: Structural and functional characterisation of the signal recognition particle-s  
A;Reference number: S51597; MUID:95107255; PMID:7808407  
A;Accession: S51610  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-16 <KRO>  
A;Cross-references: UNIPARC:UPI000017B08B; EMBL:Z34527

Query Match 21.0%; Score 17; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 1.3e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQS 5  
|||  
DB 10 RSSSS 14

## RESULT 11

E28027  
protein P8 - curled-leaved tobacco (fragment)  
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)

C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 09-Jul-2004  
C;Accession: E28027  
R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987  
A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid  
A;Reference number: A94167  
A;Accession: E28027  
A;Molecule type: protein  
A;Residues: 1-16 <BAU>  
A;Cross-references: UNIPROT:Q7M1V7; UNIPARC:UPI000017B09F  
A;Note: 10-Lys was also found

Query Match 20.4%; Score 16.5; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 1.6e+04;  
Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 6 IVHSGNGN-TY 14  
||| :|:|  
DB 7 IVANDGSKTY 16

## RESULT 12

C39509  
mannose-specific lectin B-SJA-II chain b-1, bark - Japanese pagoda tree (fragment)  
C;Species: Sophora japonica (Japanese pagoda tree)  
C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 31-Dec-2004  
C;Accession: C39509  
R;Ueno, M.; Ogawa, H.; Matsumoto, I.; Seno, N.  
J. Biol. Chem. 266, 3146-3153, 1991  
A;Title: A novel mannose-specific and sugar specifically aggregatable lectin from the b  
A;Reference number: A39509; MUID:91131618; PMID:1993686  
A;Accession: C39509  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <UEN>  
A;Cross-references: UNIPROT:P93537; UNIPARC:UPI000017B075  
C;Superfamily: lectin

Query Match 19.8%; Score 16; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 1.9e+04;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 IVHSGNGNTYL 15  
||| :|:  
DB 5 IVAVEFDTYI 14

## RESULT 13

G45681  
orf 61.1 - phage T6 (fragment)  
C;Species: phage T6  
C;Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994  
C;Accession: G45681  
R;Selick, H.E.; Stormo, G.D.; Dyson, R.L.; Alberts, B.M.  
J. Virol. 67, 2305-2316, 1993  
A;Title: Analysis of five presumptive protein-coding sequences clustered between the pr  
A;Reference number: A45681; MUID:93188183; PMID:8383243  
A;Accession: G45681  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-16 <SBL>  
A;Cross-references: UNIPARC:UPI000017A83E  
A;Note: sequence extracted from NCBI backbone (NCBI:P:128349)

Query Match 19.8%; Score 16; DB 2; Length 16;  
Best Local Similarity 11.1%; Pred. No. 1.9e+04;  
Matches 1; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVHS 9  
:|:|:|:|  
DB 6 KXSKNVINT 14

```
RESULT 14
S23184
redoxendonuclease (EC 4.2.99.-) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S23184
R;Huq, I.; Haukanes, B.I.; Helland, D.E.
Eur. J. Biochem. 206, 833-839, 1992
A;Title: Purification to homogeneity and characterization of a redoxendonuclease from
A;Reference number: S23184; MUID:92299012; PMID:1376689
A;Accession: S23184
A;Molecule type: protein
A;Residues: 1-16 <HUQ>
A;Cross-references: UNIPARC:UPI000017C559
A;Experimental source: thymus
C;Function:
A;Description: recognizes and induces cleavage of DNA damaged by UV
C;Keywords: carbon-oxygen lyase

Query Match      19.8%; Score 16; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 SNGNTY 14
Db 1 SSGPAY 6

RESULT 15
A49226
major outer membrane protein - Haemophilus somnus (fragment)
C;Species: Haemophilus somnus
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49226
R;Tagawa, Y.; Ishikawa, H.; Yuasa, N.
Infect. Immun. 61, 91-96, 1993
A;Title: Purification and partial characterization of the major outer membrane protein o
A;Reference number: A49226; MUID:93114910; PMID:8418069
A;Contents: 8025
A;Accession: A49226
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <TAG>
A;Cross-references: UNIPROT:Q9R5E9; UNIPARC:UPI00000BE2A7
A;Note: sequence extracted from NCBI backbone (NCBIP:121595)

Query Match      19.8%; Score 16; DB 2; Length 16;
Best Local Similarity 28.6%; Pred. No. 1.9e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 SIVHSNG 11
Db 2 TVINQNG 8

Search completed: December 30, 2005, 14:25:36
Job time : 24.5 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 14:06:48 ; Search time 141.5 Seconds  
(without alignments)  
79.777 Million cell updates/sec

Title: US-10-735-916A-2  
Perfect score: 81  
Sequence: 1 RSSQSIVHSNGNTYLQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 1144

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	29.6	16	2	Q8MUV9 SCHMA
2	22	27.2	16	2	Q9N235_9PRIM
3	21	25.9	16	2	Q7YOM3 MAIZE
4	20	24.7	16	2	Q8MJT2 HORSE
5	20	24.7	16	2	Q9LAP2 ENTFC
6	20	24.7	16	2	O89560 HHV8
7	19	23.5	16	2	O4YGP0 PLABE
8	19	23.5	16	2	Q8MBB6_PINTA
9	19	23.5	16	2	Q8MBB7_PINEL
10	19	23.5	16	2	Q9S8Y6 LUPAR
11	19	23.5	16	2	Q8MBB5_PINEC
12	19	23.5	16	2	Q78377_9HIV1
13	18	22.2	16	1	PPAC_BACNE
14	18	22.2	16	2	Q9UCR2 HUMAN
15	18	22.2	16	2	Q7RJ25 FLAYO
16	18	22.2	16	2	O4YQ63 PLABE
17	18	22.2	16	2	Q9TR82_PIG
18	18	22.2	16	2	O51950_92ZZZ
19	18	22.2	16	2	Q5DUAL_98TAP
20	18	22.2	16	2	Q7M025_BACSP
21	18	22.2	16	2	Q6GB29_STAAS
22	18	22.2	16	2	O6GI19_STAAR
23	18	22.2	16	2	O7A6N0_STAAN
24	18	22.2	16	2	Q99VH9_STAAM
25	17.5	21.6	16	2	Q9R4Z5_STRSU
26	17	21.0	16	1	C146_CYPDO
27	17	21.0	16	2	Q16183 HUMAN
28	17	21.0	16	2	Q9UC55 HUMAN
29	17	21.0	16	2	O7PDD5_PLAYO
30	17	21.0	16	2	O4G403_macaca mula
31	17	21.0	16	2	Q9S940_BETVU

32	17	21.0	16	2	Q80XZ9_9MURI	Q80XZ9 rattus sp.
33	16.5	20.4	16	2	Q7M1V7_NICPL	Q7M1V7 nicotiana p
34	16	19.8	16	1	CFAB_BOVIN	P81187 bos taurus
35	16	19.8	16	1	NEP_HV1J3	P12480 human immun
36	16	19.8	16	2	P79034_EMENI	P79034 emericella
37	16	19.8	16	2	Q7S0C4_NEUCR	Q7S0C4 neurospora
38	16	19.8	16	2	Q86UF7_HUMAN	Q86UF7 homo sapien
39	16	19.8	16	2	Q9UC75_HUMAN	Q9UC75 homo sapien
40	16	19.8	16	2	O5C0J9_SCHJA	O5C0J9 schistosoma
41	16	19.8	16	2	P79137_CERAE	P79137 cercopithec
42	16	19.8	16	2	Q6Q142_BOVIN	Q6Q142 bos taurus
43	16	19.8	16	2	Q7JFV3_SHEEP	Q7JFV3 ovis aries
44	16	19.8	16	2	Q9TR88_BOVIN	Q9TR88 bos taurus
45	16	19.8	16	2	Q9TSK2_VULVU	Q9TSK2 vulpes vulp

ALIGNMENTS

RESULT 1

Q8MUV9 SCHMA PRELIMINARY; PRT; 16 AA.  
ID Q8MUV9;  
AC Q8MUV9;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Elastase 2a (Fragment).  
GN NamesCE-2a;  
OS Schistosoma mansoni (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6183;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22086216; PubMed=11986325; DOI=10.1074/jbc.M202364200;  
RA Salter J.P., Choe Y., Albrecht H., Franklin C., Lim K.C., Craik C.S.,  
RA McKerrow J.H.;  
RT "Cercarial elastase is encoded by a functionally conserved gene family  
RT across multiple species of schistosomes";  
RL J. Biol. Chem. 277:24618-24624(2002).  
DR EMBL; AF510333; AAM43940.1; -; Genomic\_DNA.  
FT NON TER 16  
SQ SEQUENCE 16 AA; 1910 MW; 88B1DFA0AF61AE5 CRC64;  
Query Match 29.6%; Score 24; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred.No. 4.1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 NGNTYL 15

Db 3 NGRTFL 8

RESULT 2

Q9N235\_9PRIM PRELIMINARY; PRT; 16 AA.  
ID Q9N235\_9PRIM  
AC Q9N235\_9PRIM  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Cytochrome c oxidase polypeptide VIIa-heart (Fragment).  
OS Nycticebus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini; Loridae;  
OC Nycticebus.  
OX NCBI\_TaxID=108082;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92268136; PubMed=10335655;  
RA Schmidt T.R., Goodman M., Grossman L.I.;  
RA "Molecular evolution of the COX7A gene family in primates.";  
RL Mol. Biol. Evol. 16:619-626(1999).  
DR EMBL; AF127786; AAF72744.1; -; Genomic\_DNA.

```
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1822 MW; E586241C602C15E8 CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 2; Length 16;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSQSIVHS 9
   |||::|
Db 5 RVSQLIRS 13

RESULT 3
QYOM3 MAIZE
ID Q7YOM3 MAIZE PRELIMINARY; PRT; 16 AA.
AC Q7YOM3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Starch branching enzyme IIB (Fragment).
GN Name=acl;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1537761; DOI=10.1105/tpc.104.025700;
RA Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
RA Buckler E.S.;
RT "Dissection of maize kernel composition and starch production by
RT candidate gene association.";
RL Plant Cell 16:2719-2733(2004).
DR EMBL; AY290277; AAP44840.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1656 MW; AA2246F178EDD5A4 CRC64;

Query Match
Best Local Similarity 25.9%; Score 21; DB 2; Length 16;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 HSGNNT 13
   |||::|
Db 1 HASSNT 6

RESULT 4
Q8MJT2 HORSE
ID Q8MJT2 HORSE PRELIMINARY; PRT; 16 AA.
AC Q8MJT2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Laminin 5 gamma 2 (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Spirito F., Meneguzzi G.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292647; AM54459.1; -; mRNA.
DR InterPro; IPR000034; Laminin_B.1.
DR ProDom; PD003031; Laminin_B.1.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1751 MW; 10CCECB38DCAB5C8 CRC64;

Query Match
Best Local Similarity 24.7%; Score 20; DB 2; Length 16;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 HSGN 12
   |||::|
Db 2 HSSGD 6

RESULT 5
Q9LAP2 ENTFC
ID Q9LAP2 ENTFC PRELIMINARY; PRT; 16 AA.
AC Q9LAP2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VanY (Fragment).
GN Name=vanYb;
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TUH7-15;
RX MEDLINE=20307504; PubMed=10846225;
RA Dahl K.H., Lundblad E.W., Rokenes T.P., Olavik O., Sundsfjord A.;
RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin-
RT resistant enterococci and characterization of two novel insertion
RT sequences.";
RL Microbiology 146:1469-1479(2000).
DR EMBL; AF125554; AAP73102.1; -; Genomic_DNA.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1991 MW; 30402510516D5F9A CRC64;

Query Match
Best Local Similarity 24.7%; Score 20; DB 2; Length 16;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 QSVHSGN 12
   |||::|
Db 3 KSNYHSNAD 11

RESULT 6
O89560 HHV8
ID O89560 HHV8 PRELIMINARY; PRT; 16 AA.
AC O89560;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Minor capsid protein (Fragment).
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99034644; PubMed=9815212; DOI=10.1086/314514;
RA Labuca J.R., Love J.L., Abbott L.Z., Dube S., Freidman-Kien A.E.,
RA Polesz B.J.;
RT "Detection of human herpesvirus 8 DNA sequences in tissues and bodily
RT fluids.";
RL J. Infect. Dis. 178:1610-1615(1998).
DR EMBL; AF042149; AAC25060.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1787 MW; 2B505B0137E39DFF CRC64;

Query Match
Best Local Similarity 24.7%; Score 20; DB 2; Length 16;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 IVHSNG 11
   |||::|
Db 1 VLESNG 6
```



```
RESULT 7
QAYGPO PLABE
ID QAYGPO PLABE PRELIMINARY; PRT; 16 AA.
AC QAYGPO;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB403344.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]_TaxID=5821;
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01005266; CAI02827.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1971 MW; 9282A5EC21B7B5C1 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 3.1e+04;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGN 12
DB 3 RKINIFHPNIN 14

RESULT 8
Q8M8B6 PINTA
ID Q8M8B6 PINTA PRELIMINARY; PRT; 16 AA.
AC Q8M8B6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 3 (Fragment).
GN Name=nad3;
OS Pinus taeda (Loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=3352;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Tauer C., Huang Y.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF426453; AM21490.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1854 MW; FF3839987FD93A91 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NGNTYLQ 16
DB '4 NGRRLVQ 10

RESULT 9
Q8M8B7 PINEL
ID Q8M8B7 PINEL PRELIMINARY; PRT; 16 AA.
AC Q8M8B7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 3 (Fragment).
GN Name=nad3;
OS Pinus ellottii (Slash pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=42064;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Tauer C., Huang Y.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF426452; AM21488.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1854 MW; FF3839987FD93A91 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NGNTYLQ 16
DB 4 NGRRLVQ 10

RESULT 10
Q9S8Y6 LUPAR
ID Q9S8Y6 LUPAR PRELIMINARY; PRT; 16 AA.
AC Q9S8Y6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
OS Lupinus arboreus (Tree lupin).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3872;
RN [1]_
RP PROTEIN SEQUENCE.
RA MEDLINE=92344803; PubMed=1368361; DOI=10.1016/0031-9422(92)83098-J;
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
RA Farnden K.J.;
RA Phytochemistry 31:1519-1527(1992).
DR GO; GO:0004067; F:asparaginase activity; IEA.
SQ SEQUENCE 16 AA; 1499 MW; 90136390E527BF0B CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 VHSNGN 12
DB 7 VDSQGN 12

RESULT 11
Q8M8B5 PINEC
ID Q8M8B5 PINEC PRELIMINARY; PRT; 16 AA.
AC Q8M8B5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 3 (Fragment).
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Tauer C., Huang Y.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF426453; AM21490.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1854 MW; FF3839987FD93A91 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NGNTYLQ 16
DB '4 NGRRLVQ 10
```

```

GN Name=nad3;
OS Pinus echinata (Shortleaf pine).
OC Mitochondrion.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=71631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Tauer C., Huang Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF426454; AAM21492.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1854 MW; FF3839987FD93A91 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 NGNTYLQ 16
|||
Db 4 NGRVLIQ 10

RESULT 12
Q78377_9HIV1 PRELIMINARY; PRT; 16 AA.
AC Q78377
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Immunodeficiency virus type 1, viral sample FLPR4C (Florida patient
DE B), partial env cds, V4 region. (Fragment).
DE Human immunodeficiency virus 1.
OC Viruses; Retrovirus; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.-Y., Ciecielski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
RA Jaffe H.W.;
RT "Molecular epidemiology of HIV transmission in a dental practice.";
RL Science 256:1165-1171(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: M92120; AAA44490.1; -; Genomic_RNA.
FT NON TER
FT NON TER
SQ SEQUENCE 16 AA; 1745 MW; 72260DC174FF6428 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 3.1e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 IVHNGNT 13
:|:|
Db 1 LFHTANNT 8

RESULT 13
PPAC_BACME STANDARD; PRT; 16 AA.
AC PPAC_BACME
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)

```

```

DE (Pyrophosphate phospho-hydrolase) (PPase) (Fragment).
GN Name=ppac;
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=98455825; PubMed=9782505;
RA Young T.W., Kuhn N.J., Wadeson A., Ward S., Burges D., Cooke G.D.;
RL "Bacillus subtilis ORF YyBQ encodes a manganese-dependent inorganic
RT pyrophosphatase with distinctive properties: the first of a new class
RT of soluble pyrophosphatase?";
RL Microbiology 144:2563-2571(1998).
CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -1- COFACTOR: Binds 2 manganese ions per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the PPase class C family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR HAMAP; MF_00207; -; 1.
KW Direct protein sequencing; Hydrolase; Manganese; Metal-binding.
FT METAL 8
FT METAL 12 12 Manganese 1 (By similarity).
FT METAL 14 14 Manganese 1 (By similarity).
FT METAL 16 16 Manganese 2 (By similarity).
FT NON TER
FT NON TER
SQ SEQUENCE 16 AA; 1828 MW; 3C0E6735D98B38A0 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.7e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 HSNQNT 13
|||
Db 8 HKNPDT 13

RESULT 14
Q9UCR2_HUMAN PRELIMINARY; PRT; 16 AA.
ID Q9UCR2_HUMAN PRELIMINARY; PRT; 16 AA.
AC Q9UCR2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Kruttsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON TER
FT NON TER
FT NON TER
SQ SEQUENCE 16 AA; 1775 MW; 0B851FF76214DBD6 CRC64;

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 30.8%; Pred. No. 4.7e+04;
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SSQIVHNGNTY 14
|::|
Db 3 SMQIVFGYGYTF 15

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RESULT 15
Q7RJ25 PLAYO
ID Q7RJ25 PLAYO PRELIMINARY; PRT; 16 AA.
AC Q7RJ25;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY03439;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sadegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000989; EAA23013.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 16 AA; 1892 MW; 711E4AA20D1D0958 CRC64;

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 NTY 14
DB 3 NTY 5

Search completed: December 30, 2005, 14:24:46
Job time : 144.5 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 14:25:05 ; Search time 110 Seconds  
(without alignments)  
60.775 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIVHSNGNTYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 11256

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	16	5	US-10-735-916A-2
2	78	96.3	16	3	US-09-995-529-32
3	78	96.3	16	3	US-09-947-839-30
4	78	96.3	16	3	US-09-995-529-32
5	78	96.3	16	4	US-10-226-795-28
6	78	96.3	16	4	US-10-470-045-53
7	78	96.3	16	6	US-11-070-697-1
8	76	93.8	16	3	US-09-563-222-29
9	76	93.8	16	4	US-10-783-950-29
10	76	93.8	16	5	US-10-810-881A-56
11	75	92.6	16	3	US-09-995-529-119
12	75	92.6	16	3	US-09-995-529-119
13	74	91.4	16	3	US-09-518-737-8
14	74	91.4	16	3	US-09-995-529-118
15	74	91.4	16	3	US-09-995-529-118
16	74	91.4	16	4	US-10-762-629-20
17	74	91.4	16	5	US-10-723-748-8
18	74	91.4	16	5	US-10-687-035-6
19	74	91.4	16	5	US-10-497-475-1
20	72	88.9	16	3	US-09-995-529-110
21	72	88.9	16	3	US-09-995-529-146
22	72	88.9	16	3	US-09-995-529-110
23	72	88.9	16	3	US-09-995-529-146
24	71	87.7	16	3	US-09-995-529-111
25	71	87.7	16	3	US-09-995-529-114
26	71	87.7	16	3	US-09-995-529-111
27	71	87.7	16	3	US-09-995-529-114

28 70 86.4 16 3 US-09-995-529-115 Sequence 115, App  
29 70 86.4 16 3 US-09-995-529-117 Sequence 117, App  
30 70 86.4 16 3 US-09-995-529-115 Sequence 115, App  
31 70 86.4 16 3 US-09-995-529-117 Sequence 117, App  
32 70 86.4 16 4 US-10-434-469-10 Sequence 10, Appl  
33 70 86.4 16 5 US-10-846-981-3 Sequence 3, Appl  
34 70 86.4 16 5 US-10-482-105-8 Sequence 8, Appl  
35 70 86.4 16 5 US-10-409-611-79 Sequence 79, Appl  
36 70 86.4 16 5 US-10-919-923-3 Sequence 3, Appl  
37 70 86.4 16 5 US-10-409-608A-21 Sequence 21, Appl  
38 70 86.4 16 5 US-10-500-207A-10 Sequence 10, Appl  
39 69 85.2 16 3 US-09-972-656-5 Sequence 5, Appl  
40 69 85.2 16 3 US-09-995-529-113 Sequence 113, App  
41 69 85.2 16 3 US-09-995-529-113 Sequence 113, App  
42 69 85.2 16 5 US-10-706-852-16 Sequence 16, Appl  
43 69 85.2 16 5 US-10-729-441-4 Sequence 4, Appl  
44 69 85.2 16 5 US-10-877-773-101 Sequence 101, App  
45 69 85.2 16 5 US-10-877-774-101 Sequence 101, App

#### ALIGNMENTS

RESULT 1  
US-10-735-916A-2  
; Sequence 2, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-2

Query Match 100.0%; Score 81; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.1e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16  
Db 1 RSSQSIVHSNGNTYLQ 16

RESULT 2  
US-09-995-529-32  
; Sequence 32, Application US/09995529  
; Publication No. US20030099655A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying

```
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-32

Query Match          96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSSQSIVHSNGNTYLQ 16
        |||||
Db      1 RSSQSIVHSNGNTYLE 16
        |||||

RESULT 3
US-09-947-839-30
; Sequence 30, Application US/09947839
; Publication No. US20030138428A1
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; CERTIFIANT: Ceriani Dr., Roberto L.
; PETERSON DR., JERRY A.
; PADIAN DR., EDUARDO A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; Carcinoma Specificity, and Kit and
; Diagnostic Vaccination and
; Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,839
; FILING DATE: 06-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/976,288
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. US20030138428A1ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-947-839-30
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Query Match          96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSSQSIVHSNGNTYLQ 16
        |||||
Db      1 RSSQSIVHSNGNTYLE 16
        |||||

RESULT 4
US-09-995-529-32
; Sequence 32, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-32

Query Match          96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSSQSIVHSNGNTYLQ 16
        |||||
Db      1 RSSQSIVHSNGNTYLE 16
        |||||

RESULT 5
US-10-226-795-28
; Sequence 28, Application US/10226795
; Publication No. US20040053865A1
; GENERAL INFORMATION:
; APPLICANT: HART, MARY KATE
; APPLICANT: WILSON, JULIE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
; FILE REFERENCE: ARMY 166
; CURRENT APPLICATION NUMBER: US/10/226,795
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic light
; OTHER INFORMATION: chain of Mab EGPd8-1-2 amino acid sequence
US-10-226-795-28

Query Match          96.3%; Score 78; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSSQSIVHSNGNTYLQ 16
        |||||
Db      1 RSSQSIVHSNGNTYLE 16
        |||||

RESULT 6
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US-10-470-045-53  
; Sequence 53, Application US/10470045  
; Publication No. US20040146505A1  
; GENERAL INFORMATION:  
; APPLICANT: Scancell Limited  
; APPLICANT: Durrant, Linda Gillian  
; APPLICANT: Parsons, Tina  
; TITLE OF INVENTION: Substances  
; FILE REFERENCE: P32181WO/NUL  
; CURRENT APPLICATION NUMBER: US/10/470,045  
; CURRENT FILING DATE: 2003-07-24  
; PRIOR APPLICATION NUMBER: GB 0102145.0  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-470-045-53

Query Match 96.3%; Score 78; DB 4; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RSSQSIVHSNGNTYLQ 16  
|||||:|||||:  
DB 1 RSSQSIVHSNGNTYL 16

RESULT 7  
US-11-070-697-1  
; Sequence 1, Application US/11070697  
; Publication No. US20050169926A1  
; GENERAL INFORMATION:  
; APPLICANT: OU, ZHENGXING  
; APPLICANT: HANSEN, HANS  
; APPLICANT: GOLDENBERG, DAVID M.  
; TITLE OF INVENTION: CHIMERIC, HUMAN AND HUMANIZED ANTI-CSAP MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: 018733/1064  
; CURRENT APPLICATION NUMBER: US/11/070,697  
; CURRENT FILING DATE: 2005-03-03  
; PRIOR APPLICATION NUMBER: US/10/116,116  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/823,746  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 09/337,756  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 60/104,156  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/090,142  
; PRIOR FILING DATE: 1998-06-22  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-11-070-697-1

Query Match 96.3%; Score 78; DB 6; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RSSQSIVHSNGNTYLQ 16  
|||||:|||||:  
DB 1 RSSQSIVHSNGNTYL 16

RESULT 8  
US-09-563-222-29  
; Sequence 29, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-29

Query Match 93.8%; Score 76; DB 3; Length 16;  
Best Local Similarity 87.5%; Pred. No. 6.5e-06;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RSSQSIVHSNGNTYLQ 16  
|||||:|||||:  
DB 1 RSSQSIVHSNGNTYL 16

RESULT 9  
US-10-783-950-29  
; Sequence 29, Application US/10783950  
; Publication No. US20040199945A1  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICHAEL B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/10/783,950  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US/09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-783-950-29

Query Match 93.8%; Score 76; DB 4; Length 16;  
Best Local Similarity 87.5%; Pred. No. 6.5e-06;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RSSQSIVHSNGNTYLQ 16  
|||||:|||||:  
DB 1 RSSQSIVHSNGNTYL 16

RESULT 10  
US-10-810-881A-56  
; Sequence 56, Application US/10810881A  
; Publication No. US20050129695A1  
; GENERAL INFORMATION:  
; APPLICANT: Mercken, Marc; Benson, Jacqueline M.  
; TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN5021 NP  
; CURRENT APPLICATION NUMBER: US/10/810,881A

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; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(16)
; OTHER INFORMATION: LC CDR1
US-10-810-881A-56
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Query Match 93.8%; Score 76; DB 5; Length 16;
Best Local Similarity 87.5%; Pred. No. 6.5e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RSSQSIVHSNGNTYLQ 16
| | | | | | | | | | | | | | | |
Db 1 RSSQSLVHSNGNTYLE 16
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RESULT 11
US-09-995-529-119
; Sequence 119, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-119
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Query Match 92.6%; Score 75; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 9.5e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RSSQSIVHSNGNTYLQ 16
| | | | | | | | | | | | | | | |
Db 1 RSSQSLVHSNGNTYLE 16
```

```
RESULT 12
US-09-995-529-119
; Sequence 119, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
```

```
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-119
```

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Query Match 92.6%; Score 75; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 9.5e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RSSQSIVHSNGNTYLQ 16
| | | | | | | | | | | | | | | |
Db 1 RSSQSLVHSNGNTYLE 16
```

```
RESULT 13
US-09-518-737-8
; Sequence 8, Application US/09518737
; Publication No. US2003008321A1
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIKA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOAKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-8
```

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Query Match 91.4%; Score 74; DB 3; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RSSQSIVHSNGNTYL 15
| | | | | | | | | | | | | |
Db 1 RSSQSLVHSNGNTYL 15
```

```
RESULT 14
US-09-995-529-118
; Sequence 118, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Tang, Ying
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
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```
; FEATURES:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-118

Query Match      91.4%; Score 74; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 RSSQSIVHSGNGTYLQ 16
   |||||
Db 1 RSSQSIVHSGNGTYFE 16
```

```
RESULT 15
US-09-995-529-118
; Sequence 118, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-118
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```
Query Match      91.4%; Score 74; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 RSSQSIVHSGNGTYLQ 16
   |||||
Db 1 RSSQSIVHSGNGTYFE 16
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Search completed: December 30, 2005, 14:43:48  
Job time : 111 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 14:25:45 ; Search time 8 Seconds  
(without alignments)  
14.978 Million cell updates/sec

Title: US-10-735-916A-2  
Perfect score: 81  
Sequence: 1 RSSQSIHVSNGNTYLQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.New:\*  
1: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	16	7 US-11-012-353-2	Sequence 2, Appli
2	71	87.7	16	7 US-11-125-837-13	Sequence 13, Appli
3	70	86.4	16	7 US-11-102-743-3	Sequence 3, Appli
4	69	85.2	16	6 US-10-932-334-4	Sequence 4, Appli
5	66	81.5	16	7 US-11-125-837-1	Sequence 1, Appli
6	61	75.3	16	7 US-11-009-939-18	Sequence 18, Appli
7	59	72.8	16	7 US-11-105-708-17	Sequence 17, Appli
8	25	30.9	16	6 US-10-726-554-13	Sequence 13, Appli
9	25	30.9	16	6 US-10-507-662-5	Sequence 5, Appli
10	22	27.2	16	6 US-10-999-866-59	Sequence 59, Appli
11	22	27.2	16	7 US-11-055-163-20	Sequence 20, Appli
12	21	25.9	16	7 US-11-010-748A-77	Sequence 77, Appli
13	21	25.9	16	7 US-11-010-748A-89	Sequence 89, Appli
14	21	25.9	16	7 US-11-010-748A-126	Sequence 126, App
15	21	25.9	16	7 US-11-010-748A-138	Sequence 138, App
16	21	25.9	16	7 US-11-060-646-10	Sequence 10, Appli
17	20	24.7	16	7 US-11-087-812-92	Sequence 92, Appli
18	19	23.5	16	7 US-11-009-939-24	Sequence 24, Appli
19	18.5	22.8	16	7 US-11-127-677-87	Sequence 87, Appli
20	18	22.2	16	6 US-10-507-662-6	Sequence 6, Appli
21	18	22.2	16	6 US-10-467-657-9175	Sequence 9175, App
22	18	22.2	16	6 US-10-485-788A-495	Sequence 495, App
23	18	22.2	16	6 US-10-919-492-3	Sequence 3, Appli
24	18	22.2	16	6 US-10-919-492-10	Sequence 10, Appli
25	18	22.2	16	7 US-11-052-168A-32	Sequence 32, Appli

26	18	22.2	16	7 US-11-090-908-5	Sequence 5, Appli
27	18	22.2	16	7 US-11-060-005-34	Sequence 34, Appli
28	18	22.2	16	7 US-11-167-710-12	Sequence 12, Appli
29	17	21.0	16	7 US-11-089-764-3	Sequence 3, Appli
30	17	21.0	16	7 US-11-089-764-4	Sequence 4, Appli
31	17	21.0	16	7 US-11-089-764-7	Sequence 7, Appli
32	17	21.0	16	7 US-11-089-764-10	Sequence 10, Appli
33	17	21.0	16	7 US-11-089-764-11	Sequence 11, Appli
34	17	21.0	16	7 US-11-089-764-12	Sequence 12, Appli
35	17	21.0	16	7 US-11-089-764-33	Sequence 33, Appli
36	17	21.0	16	7 US-11-054-515-2728	Sequence 2728, Ap
37	17	21.0	16	7 US-11-054-515-2868	Sequence 2868, Ap
38	17	21.0	16	7 US-11-054-515-3212	Sequence 3212, Ap
39	17	21.0	16	7 US-11-060-646-4	Sequence 4, Appli
40	17	21.0	16	7 US-11-044-899-44	Sequence 44, Appli
41	17	21.0	16	7 US-11-009-939-34	Sequence 34, Appli
42	16	19.8	16	6 US-10-467-657-8935	Sequence 8935, Ap
43	16	19.8	16	6 US-10-467-657-9115	Sequence 9115, Ap
44	16	19.8	16	6 US-10-649-229-18	Sequence 18, Appli
45	16	19.8	16	6 US-10-929-988-281	Sequence 281, App

ALIGNMENTS

RESULT 1  
US-11-012-353-2  
; Sequence 2, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION: GORTSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFILOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 2  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-2

Query Match 100.0%; Score 81; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVSNGNTYLQ 16  
| | | | | | | | | | | | | | | |  
Db 1 RSSQSIHVSNGNTYLQ 16

RESULT 2  
US-11-125-837-13  
; Sequence 13, Application US/11125837

```
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-13

Query Match      87.7%; Score 71; DB 7; Length 16;
Best Local Similarity 87.5%; Pred. No. 6.5e-07;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 1 RSSQSIVHSNGNTYLE 16

RESULT 3
US-11-102-743-3
; Sequence 3, Application US/11/102743
; Publication No. US20050266002A1
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/11/102,743
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-102-743-3

Query Match      86.4%; Score 70; DB 7; Length 16;
Best Local Similarity 86.7%; Pred. No. 9.8e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYL 15
Db 1 RSSQSLVHSNGNTFL 15

RESULT 4
US-10-932-334-4
; Sequence 4, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08

; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-13

Query Match      85.2%; Score 69; DB 6; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 1 RSSQSIVHSNVNTYLE 16

RESULT 5
US-11-125-837-1
; Sequence 1, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-1

Query Match      81.5%; Score 66; DB 7; Length 16;
Best Local Similarity 75.0%; Pred. No. 4.9e-06;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 1 RSSQSIVHNDGNTYFE 16

RESULT 6
US-11-009-939-18
; Sequence 18, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 16
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; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-009-939-18

Query Match 75.3%; Score 61; DB 7; Length 16;  
Best Local Similarity 80.0%; Pred. No. 3.7e-05;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVHNGNTYL 15  
|||||:|||||  
DB 1 RSSQSLENSGNTYL 15

## RESULT 7

US-11-105-708-17  
; Sequence 17, Application US/11105708  
; Publication No. US20050281821A1  
; GENERAL INFORMATION:  
; APPLICANT: Pernaletti, Flavia  
; APPLICANT: Freimark, Bruce  
; APPLICANT: Van Epps, Dennis  
; APPLICANT: Brooks, Peter C  
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition  
; FILE REFERENCE: 30797-704.501  
; CURRENT APPLICATION NUMBER: US/11/105,708  
; CURRENT FILING DATE: 2005-04-13  
; PRIOR APPLICATION NUMBER: 09/478,977  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: 60/152,496  
; PRIOR FILING DATE: 1999-09-02  
; PRIOR APPLICATION NUMBER: 60/143,534  
; PRIOR FILING DATE: 1999-09-02  
; PRIOR APPLICATION NUMBER: 60/114,878  
; PRIOR FILING DATE: 1999-01-06  
; PRIOR APPLICATION NUMBER: 60/114,877  
; PRIOR FILING DATE: 1999-01-06  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-105-708-17

Query Match 72.8%; Score 59; DB 7; Length 16;  
Best Local Similarity 81.2%; Pred. No. 8.2e-05;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSQSIVHNGNTYLQ 16  
|||||:|||||  
DB 1 RSSQSIVSSWGNTYLE 16

## RESULT 8

US-10-726-554-13  
; Sequence 13, Application US/10726554  
; Publication No. US20050249753A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, Jong Wook et al.  
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST  
; TITLE OF INVENTION: THE HBV S-SURFACE  
; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME  
; FILE REFERENCE: 1599-0197P  
; CURRENT APPLICATION NUMBER: US/10/726,554  
; CURRENT FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: US/09/865,483  
; PRIOR FILING DATE: PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 16

; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-726-554-13

Query Match 30.9%; Score 25; DB 6; Length 16;  
Best Local Similarity 50.0%; Pred. No. 72;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 IVHSNGNT 13  
:::|||||  
DB 1 VIWSGNT 8

## RESULT 9

US-10-507-662-5  
; Sequence 5, Application US/10507662  
; Publication No. US20050255102A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES  
; FILE REFERENCE: AL36PCT  
; CURRENT APPLICATION NUMBER: US/10/507,662  
; CURRENT FILING DATE: 2004-09-13  
; PRIOR APPLICATION NUMBER: 60/364,991  
; PRIOR FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: 60/426,286  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-507-662-5

Query Match 30.9%; Score 25; DB 6; Length 16;  
Best Local Similarity 50.0%; Pred. No. 72;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 VHSNGNTY 14  
:|:|:  
DB 2 ISSGGSTY 9

## RESULT 10

US-10-999-866-59  
; Sequence 59, Application US/10999866  
; Publication No. US20050266004A1  
; GENERAL INFORMATION:  
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann  
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS A  
; FILE REFERENCE: CEN5042NP  
; CURRENT APPLICATION NUMBER: US/10/999,866  
; CURRENT FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: 60/527,794  
; PRIOR FILING DATE: 2003-12-08  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 59  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(16)  
; OTHER INFORMATION: HC CDR 2  
US-10-999-866-59

Query Match 27.2%; Score 22; DB 6; Length 16;  
Best Local Similarity 37.5%; Pred. No. 2.4e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy      6 IVHNGNT 13
      : : : |||
Db      1 VIVAGNT 8

RESULT 11
US-11-055-163-20
; Sequence 20, Application US/11055163
; Publication No. US20050271655A1
; GENERAL INFORMATION:
; APPLICANT: LEE, DANIEL H. S.
; APPLICANT: PEPINSKY, R. BLAKE
; APPLICANT: LI, WEIWEI
; APPLICANT: RABACCHI, SYLVIA A.
; APPLICANT: RELTON, JANE K.
; APPLICANT: WORLEY, DANE S.
; APPLICANT: STRITTMATTER, STEPHEN M.
; APPLICANT: SAH, DINAH Y.W.
; TITLE OF INVENTION: NOGO RECEPTOR ANTAGONISTS
; FILE REFERENCE: A170 CON (00455.271)
; CURRENT APPLICATION NUMBER: US/11/055.163
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: PCT/US03/25004
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 60/402,866
; PRIOR FILING DATE: 2002-08-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: heavy chain peptide sequence
US-11-055-163-20

Query Match      27.2%; Score 22; DB 7; Length 16;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      6 IVHNGNTY 14
      : : : ||| |
Db      1 LIYSNDTKY 9

RESULT 12
US-11-010-748A-77
; Sequence 77, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-77

Query Match      25.9%; Score 21; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TYLQ 16
      : : : |||
Db      2 TYLQ 5

RESULT 13
US-11-010-748A-89
; Sequence 89, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-89

Query Match      25.9%; Score 21; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TYLQ 16
      : : : |||
Db      2 TYLQ 5

RESULT 14
US-11-010-748A-126
; Sequence 126, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-126

Query Match      25.9%; Score 21; DB 7; Length 16;
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Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 13 TYLQ 16  
|||  
Db 2 TYLQ 5

RESULT 15  
US-11-010-748A-138  
; Sequence 138, Application US/11010748A  
; Publication No. US2005024421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMAYER, Wolfgang  
; APPLICANT: MOLL, Heidrun  
; APPLICANT: SCHARM, Burkhard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 138  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CD15 peptide fragment  
US-11-010-748A-138

Query Match 25.9%; Score 21; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 13 TYLQ 16  
|||  
Db 2 TYLQ 5

Search completed: December 30, 2005, 14:44:10  
Job time : 9 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 62.2097 Seconds  
(without alignments)  
49.440 Million cell updates/sec

Title: US-10-735-916A-4  
Perfect score: 35  
Sequence: 1 KVSFRLY 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	7	ADJ76838	Adj76838 CDR seque
2	35	100.0	7	ADZ67008	Adz67008 Murine in
3	35	100.0	112	ADJ76888	Adj76888 Anti-IGF-
4	35	100.0	112	ADJ76899	Adj76899 Anti-IGF-
5	35	100.0	112	ADJ76895	Adj76895 Anti-IGF-
6	35	100.0	112	ADZ67058	Adz67058 Murine in
7	35	100.0	112	ADZ67069	Adz67069 Human ant
8	35	100.0	112	ADZ67065	Adz67065 Human ant
9	35	100.0	122	ADJ76883	Adj76883 Anti-IGF-
10	35	100.0	122	ADZ67053	Adz67053 Murine in
11	35	100.0	111	ADJ76901	Adj76901 Anti-IGF-
12	35	100.0	131	ADJ76897	Adj76897 Anti-IGF-
13	35	100.0	131	ADZ67071	Adz67071 Human ant
14	35	100.0	131	ADZ67067	Adz67067 Human ant
15	35	100.0	841	ADQ08646	Adq08646 Clona int
16	34	97.1	435	AAG09372	Aag09372 Arabidops
17	34	97.1	571	AAG09371	Aag09371 Arabidops
18	34	97.1	576	AAG09370	Aag09370 Arabidops
19	31	88.6	374	ABR53373	AbR53373 Protein s
20	31	88.6	374	ADK63348	Adk63348 Disease t
21	31	88.6	687	AAY58997	Aay58997 Soybean s
22	30	85.7	176	ADT56879	Adt56879 Plant pol
23	30	85.7	323	ADA33883	Ada33883 Acinetoba
24	30	85.7	380	ABM73096	Abm73096 Staphyloc

25	30	85.7	388	5	ABP38975	Abp38975 Staphyloc
26	30	85.7	388	8	ADJ06741	Adj06741 Staphyloc
27	30	85.7	419	6	ABJ26662	Abj26662 Human pro
28	30	85.7	439	5	ABB75887	Abb75887 Human dip
29	30	85.7	463	2	AAW04360	Aaw04360 Human cat
30	30	85.7	463	2	AAW04360	Aaw04360 Human cat
31	30	85.7	463	4	AAW04360	Aaw04360 Human cat
32	30	85.7	463	5	AAO21724	Aao21724 Human all
33	30	85.7	463	5	ADZ58744	Adz58744 Human cat
34	30	85.7	463	6	ABP71988	Abp71988 Human cat
35	30	85.7	463	6	ABU57625	Abu57625 Different
36	30	85.7	463	7	ADN95622	Adn95622 Human BEC
37	30	85.7	463	7	ADN95622	Adn95622 Human cat
38	30	85.7	463	7	ADP65152	Adp65152 Human cat
39	30	85.7	463	8	ADZ67989	Adz67989 Human pro
40	30	85.7	463	8	ADJ75482	Adj75482 Marker ge
41	30	85.7	463	8	ADJ75390	Adj75390 Marker ge
42	30	85.7	463	8	ADN03739	Adn03739 Antipsori
43	30	85.7	463	8	ADO55149	Ado55149 Protein #
44	30	85.7	463	8	ADO20355	Ado20355 Human PRO
45	30	85.7	463	8	ADR67272	Adr67272 Human bla
						Adr97344 Human CTS

ALIGNMENTS

RESULT 1  
ADJ76838  
ID ADJ76838 standard; peptide; 7 AA.  
XX  
AC ADJ76838;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE CDR sequence for anti-IGF-1R antibody.  
XX  
KW cytostatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX  
OS Mus musculus.  
XX  
PN WO2003059951-A2.  
XX  
PD 24-JUL-2003.  
XX  
PP 20-JAN-2003; 2003WO-FR000178.  
XX  
PR 18-JAN-2002; 2002FR-00000653.  
PR 18-JAN-2002; 2002FR-00000654.  
PR 07-MAY-2002; 2002FR-00005753.  
XX  
PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
PI Goetsch L, Corvaia N, Leger O;  
XX  
DR WPI; 2003-569653/53.  
XX  
PS N-PSDB; ADJ76837.  
XX  
PT New antibodies that bind to human insulin-like growth factor receptor,  
XX useful for treatment, prevention and diagnosis of cancers.  
XX  
PS Claim 1; SEQ ID NO 4; 164pp; French.  
XX  
CC The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7  
 |||||  
 Db 1 KVSNNRLY 7

RESULT 2

ADZ67008  
 ID ADZ67008 standard; peptide; 7 AA.

XX AC ADZ67008;

DT 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:4.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

OS Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUFL/) DUFIOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

DR N-PSDB; ADZ67007.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

PT antibody or its functional fragment, being capable of binding human IGF-

PT IR and specifically inhibiting tyrosine kinase activity of receptor,

PT useful for treating cancer.

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7  
 |||||  
 Db 1 KVSNNRLY 7

RESULT 3

ADJ76888

ID ADJ76888 standard; protein; 112 AA.

XX AC ADJ76888;

XX 06-MAY-2004 (first entry)

DT Anti-IGF-IR related protein #5.

XX cytostatic; antipsoriatic; antibody;

XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;

XX or epidermal growth factor receptor; EGFR; signal transduction pathway;

XX ligand; tumor; cancer; osteosarcoma; complementarity determining region;

XX CDR.

XX Mus musculus.

XX WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;  
XX WPI; 2003-569653/53.  
XX New antibodies that bind to human insulin-like growth factor receptor,  
XX useful for treatment, prevention and diagnosis of cancers.  
XX PS Disclosure; SEQ ID NO 54; 164pp; French.  
XX CC The invention relates to an isolated antibody (Ab), and its functional  
XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
XX 1R) and optionally; (i) inhibit natural binding of insulin-like growth  
XX factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
XX kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
XX treat diseases associated with overexpression and/or abnormal activity of  
XX IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
XX hyperactivity of signal transduction pathways mediated by interaction of  
XX these receptors with their ligands. Especially they inhibit  
XX transformation of normal cells to tumor cells, inhibit growth and/or  
XX proliferation of tumor cells, so are useful against cancers of the  
XX prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
XX also for treating psoriasis. Ab are also used to diagnose diseases caused  
XX by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
XX protein sequence used to generate the Ab of the invention.  
XX SQ Sequence 112 AA;  
Query Match 100.0%; Score 35; DB 7; Length 112;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVSNNRLY 7  
DB 55 KVSNNRLY 61  
|||||  
RESULT 4  
ADJ76899  
ID ADJ76899 standard; protein; 112 AA.  
XX AC ADJ76899;  
XX DT 06-MAY-2004 (first entry)  
XX DE Anti-IGF-1R related protein #14.  
XX KW cytostatic; antipsoriatic; antibody;  
XX IGF-1-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
XX or epidermal growth factor receptor; EGFR; signal transduction pathway;  
XX ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
XX CDR.  
XX OS Homo sapiens.  
XX PN WO2003059951-A2.  
XX PR 18-JAN-2002; 2002FR-00000653.  
XX DT 07-MAY-2002; 2002FR-00005753.  
XX PD 24-JUL-2003.  
XX PF 20-JAN-2003; 2003WO-FR000178.  
XX PR 18-JAN-2002; 2002FR-00000653.  
XX PR 18-JAN-2002; 2002FR-00000654.  
XX PR 07-MAY-2002; 2002FR-00005753.  
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX PI Goetsch L, Corvaia N, Leger O;  
XX WPI; 2003-569653/53.  
XX New antibodies that bind to human insulin-like growth factor receptor,  
XX useful for treatment, prevention and diagnosis of cancers.

XX PS Disclosure; SEQ ID NO 65; 164pp; French.  
XX CC The invention relates to an isolated antibody (Ab), and its functional  
XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
XX 1R) and optionally; (i) inhibit natural binding of insulin-like growth  
XX factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
XX kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
XX treat diseases associated with overexpression and/or abnormal activity of  
XX IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
XX hyperactivity of signal transduction pathways mediated by interaction of  
XX these receptors with their ligands. Especially they inhibit  
XX transformation of normal cells to tumor cells, inhibit growth and/or  
XX proliferation of tumor cells, so are useful against cancers of the  
XX prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
XX also for treating psoriasis. Ab are also used to diagnose diseases caused  
XX by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
XX protein sequence used to generate the Ab of the invention.  
XX SQ Sequence 112 AA;  
Query Match 100.0%; Score 35; DB 7; Length 112;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVSNNRLY 7  
DB 55 KVSNNRLY 61  
|||||  
RESULT 5  
ADJ76895  
ID ADJ76895 standard; protein; 112 AA.  
XX AC ADJ76895;  
XX DT 06-MAY-2004 (first entry)  
XX DE Anti-IGF-1R related protein #12.  
XX KW cytostatic; antipsoriatic; antibody;  
XX IGF-1-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
XX or epidermal growth factor receptor; EGFR; signal transduction pathway;  
XX ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
XX CDR.  
XX OS Homo sapiens.  
XX PN WO2003059951-A2.  
XX PR 24-JUL-2003.  
XX PF 20-JAN-2003; 2003WO-FR000178.  
XX PR 18-JAN-2002; 2002FR-00000653.  
XX PR 18-JAN-2002; 2002FR-00000654.  
XX PR 07-MAY-2002; 2002FR-00005753.  
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX PI Goetsch L, Corvaia N, Leger O;  
XX WPI; 2003-569653/53.  
XX New antibodies that bind to human insulin-like growth factor receptor,  
XX useful for treatment, prevention and diagnosis of cancers.  
XX PS Disclosure; SEQ ID NO 61; 164pp; French.  
XX CC The invention relates to an isolated antibody (Ab), and its functional  
XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
XX 1R) and optionally; (i) inhibit natural binding of insulin-like growth  
XX factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 35; DB 7; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 7.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
 |||||  
 Db 55 KVSNNRLY 61

RESULT 6  
 ADZ67058  
 ID ADZ67058 standard; protein; 112 AA.

AC ADZ67058;

XX 30-JUN-2005 (first entry)

XX Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:54.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; androgen; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW immunoglobulin; light chain variable region.

XX Mus musculus.

OS US2005084906-A1.

PN 21-APR-2005.

PD 16-DEC-2003; 2003US-00735916.

PF 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR0001178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOETZ) GOETSCH L.

PA (CORV) CORVAIA N.

PA (LEGE) LEGER O.

PA (DUFLO) DUFLOS A.

PA (HAUW) HAEUW J.

PA (BECK) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.

XX Example 12; SEQ ID NO 54; 125pp; English.

XX

CC The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 35; DB 9; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 7.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
 |||||  
 Db 55 KVSNNRLY 61

RESULT 7  
 ADZ67069

ID ADZ67069 standard; protein; 112 AA.

AC ADZ67069;

XX 30-JUN-2005 (first entry)

XX Human antibody 7C10 2 light chain variable region SEQ ID NO:65.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; androgen; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW light chain variable region.

XX Homo sapiens.

OS US2005084906-A1.

PN 21-APR-2005.

PD 16-DEC-2003; 2003US-00735916.

XX



CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX  
 SQ Sequence 112 AA;

Query Match 100.0%; Score 35; DB 9; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 7.7; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;

Qy 1 KVSNNLY 7  
 Db 55 KVSNNLY 61  
 |||||

## RESULT 9

ADJ76883  
 ID ADJ76883 standard; protein; 122 AA.

AC ADJ76883;

DT 06-MAY-2004 (first entry)

DE Anti-IGF-IR related protein #3.

XX Cytostatic; antipsoriatic; antibody;

KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX Mus musculus.

PN WO2003059951-A2.

PD 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

PR 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

PI Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 49; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth

CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-IR. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

SQ Sequence 122 AA;

Query Match 100.0%; Score 35; DB 7; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7  
 Db 65 KVSNNLY 71  
 |||||

## RESULT 10

ADZ67053  
 ID ADZ67053 standard; protein; 122 AA.

AC ADZ67053;

DT 30-JUN-2005 (first entry)

DE Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:49.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW immunoglobulin; light chain variable region.

XX Mus musculus.

Key Location/Qualifiers  
 FT Peptide 1..10  
 FT Region 34..49 /note= "leader peptide"

FT Region 65..71 /note= "CDR1"

FT Region 104..111 /note= "CDR2"

FT Region 104..111 /note= "CDR3"

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFLOS A.

PA (HAEU/) HAEUW J.

XX (BECK/) BECK A.

PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 XX WPI; 2005-321968/33.  
 DR N-PSDB; AD267052.  
 XX  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX  
 XX Example 8; SEQ ID NO 49; 125pp; English.  
 XX  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (AD267006 and AD267014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1- and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 35; DB 9; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7  
 |||||  
 DB 65 KVSNNRLY 71

RESULT 11

ADJ76901  
 ID ADJ76901 standard; protein; 131 AA.

XX AC ADJ76901;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #15.

XX KW cytotatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;

KW CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000179.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX DR WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,

PT useful for treatment, prevention and diagnosis of cancers.

XX PS Disclosure; SEQ ID NO 67; 164pp; French.

XX CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 7; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 9.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7  
 |||||  
 DB 74 KVSNNRLY 80

RESULT 12

ADJ76897

ID ADJ76897 standard; protein; 131 AA.

XX AC ADJ76897;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #13.

XX KW cytotatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

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XX 20-JAN-2003; 2003WO-FR000178.
PF 18-JAN-2002; 2002FR-00000653.
XX 18-JAN-2002; 2002FR-00000653.
PR 07-MAY-2002; 2002FR-00005753.
XX (FABR ) FABRE MEDICAMENT SA PIERRE.
PA Goetsch L, Corvaia N, Leger O;
XX WPI; 2003-569653/53.
XX New antibodies that bind to human insulin-like growth factor receptor,
PT useful for treatment, prevention and diagnosis of cancers.
XX Disclosure; SEQ ID NO 63; 164pp; French.
PS The invention relates to an isolated antibody (Ab), and its functional
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC treat diseases associated with overexpression and/or abnormal activity of
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
CC hyperactivity of signal transduction pathways mediated by interaction of
CC these receptors with their ligands. Especially they inhibit
CC transformation of normal cells to tumor cells, inhibit growth and/or
CC proliferation of tumor cells, so are useful against cancers of the
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
CC also for treating psoriasis. Ab are also used to diagnose diseases caused
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
CC protein sequence used to generate the Ab of the invention.
XX Sequence 131 AA;
SQ
Query Match 100.0%; Score 35; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVSNNRLY 7
DB 74 KVSNNRLY 80
RESULT 13
ADZ67071
ID ADZ67071 standard; protein; 131 AA.
XX AC ADZ67071;
XX 30-JUN-2005 (first entry)
XX Human antibody 7C10 2 light chain variable region SEQ ID NO:67.
XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
KW musculoskeletal disease; respiratory disease; lung tumor;
KW endocrine disease; gynecology and obstetrics; breast tumor;
KW endometrial carcinoma; gastrointestinal disease; colon tumor;
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
KW light chain variable region.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..19 /note= "leader peptide"
FT Region 43..58 /note= "CDR1"
FT Region 74..80 /note= "CDR2"
FT Region 113..121 /note= "CDR3"

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FT /note= "CDR3"
XX US2005084906-A1.
XX 21-APR-2005.
XX 16-DEC-2003; 2003US-00735916.
XX 18-JAN-2002; 2002FR-00000653.
PR 18-JAN-2002; 2002FR-00000654.
PR 07-MAY-2002; 2002FR-00005753.
PR 20-JAN-2003; 2003WO-FR000178.
PR 11-JUL-2003; 2003FR-00008538.
XX (GOET/) GOETSCH L.
PA (CORV/) CORVAIA N.
PA (LEGE/) LEGER O.
PA (DUFL/) DUFLOS A.
PA (HAEU/) HAEUW J.
PA (BECK/) BECK A.
XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
XX WPI; 2005-321968/33.
XX N-PSDB; ADZ67070.
XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
XX antibody or its functional fragment, being capable of binding human IGF-
XX IR and specifically inhibiting tyrosine kinase activity of receptor,
XX useful for treating cancer.
XX Example 12; SEQ ID NO 67; 125pp; English.
XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
XX capable of binding to human IGF-IR and, if necessary, capable of
XX specifically inhibiting tyrosine kinase activity of the receptor,
XX comprising a light or heavy chain having at least one complementary
XX determining region (CDR) consisting of one of two fully defined 16 amino
XX acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
XX the preparation of a medicament intended for the prevention or treatment
XX of an illness connected with an overexpression and/or an abnormal
XX activation of the IGF-IR and/or EGFR, and/or connected with a
XX hyperactivation of the transduction pathway of the signal mediated by the
XX interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
XX the administration of the medicament does not induce or only slightly
XX induces secondary effects connected with inhibition of the insulin
XX receptor. The antibody is useful for preparation of a medicament intended
XX to inhibit the transformation of normal cells into cells with tumoral
XX character, preferably IGF-dependent, especially IGF1 and/or IGF2-
XX dependent and/or EGF-dependent and/or HBR2/neu-dependent cells. (I) is
XX useful for preparation of a medicament intended to inhibit the growth
XX and/or the proliferation of tumor cells, preferably IGF-dependent,
XX especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
XX HER2/neu-dependent cells. (I) is useful in the preparation of a
XX medicament intended for prevention or for the treatment of cancer, where
XX the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
XX breast cancer, endometrial cancer or colon cancer. (I) is useful in the
XX preparation of a medicament intended for the prevention or for the
XX treatment of psoriasis. (I) is useful in preparation of a medicament
XX intended for the specific targeting of a biologically active compound to
XX cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
XX is useful for in vitro diagnosis of illnesses induced by an
XX overexpression or an underexpression of the IGF-IR and/or EGFR receptor
XX starting from a biological sample in which the abnormal presence, of IGF-
XX IR and/or EGFR receptor is suspected, which involves contacting the
XX biological sample with (I), which is optionally labeled. The present
XX sequence is used in the exemplification of the invention.
XX Sequence 131 AA;
Query Match 100.0%; Score 35; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 9.1;

```



Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
 DB 74 KVSRLY 80

RESULT 14  
 ID ADZ67067 standard; protein; 131 AA.  
 AC ADZ67067;  
 DT 30-JUN-2005 (first entry)  
 XX Human antibody 7C10 1 light chain variable region SEQ ID NO:63.  
 XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW light chain variable region.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /note= "leader peptide"  
 FT Region 43..62  
 FT /note= "CDR1"  
 FT Region 74..80  
 FT /note= "CDR2"  
 FT Region 113..121  
 FT /note= "CDR3"  
 XX US2005084906-A1.  
 XX 21-APR-2005.  
 XX 16-DEC-2003; 2003US-00735916.  
 XX 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 PR 20-JAN-2003; 2003WO-FR000178.  
 PR 11-JUL-2003; 2003FR-00008538.  
 XX (GOET/) GOETSCH L.  
 PA (CORV/) CORVAIA N.  
 PA (LEGE/) LEGER O.  
 PA (DUFL/) DUFLOS A.  
 PA (HAEU/) HAEUW J.  
 PA (BECK/) BECK A.  
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 XX WPI; 2005-321968/33.  
 DR N-PSDB; ADZ67066.  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX Example 12; SEQ ID NO 63; 125pp; English.  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary

determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a hyperactivation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for the preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.

Sequence 131 AA;  
 Query Match 100.0%; Score 35; DB 9; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 9.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
 DB 74 KVSRLY 80

RESULT 15  
 ADQ08646  
 ID ADQ08646 standard; protein; 841 AA.  
 XX AC ADQ08646;  
 XX DT 26-AUG-2004 (first entry)  
 XX Ciona intestinalis nervous system associated protein SeqID48.  
 DE gene cluster; nervous system; sea-squirt tailbud; embryo; larva;  
 KW nervous system disease.  
 XX Ciona intestinalis.  
 OS JP2004057127-A.  
 XX 26-FEB-2004.  
 XX 31-JUL-2002; 2002JP-00222532.  
 XX 31-JUL-2002; 2002JP-00222532.  
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 XX WPI; 2004-208712/20.  
 DR N-PSDB; ADQ08645.  
 XX Novel genes derived from Ciona intestinalis (sea squirt), expressed in nervous system in the tailbud embryo or larva, useful for studying the development of nervous system.

XX PS Claim 4; SEQ ID NO 48; 897pp; Japanese.  
XX CC This invention relates to a novel gene cluster, where the encoded  
CC proteins are expressed in the nervous system of sea-squirt tailbud embryo  
CC or larva. The invention is useful for studying the development of the  
CC nervous system of the sea-squirt and for research purposes. The genes may  
CC be used for determining the disease-development mechanisms in the nervous  
CC system. In addition, novel gene clusters expressed in nervous system of  
CC sea-squirt tailbud embryo or larva allows development of diagnostics and  
CC therapeutics related to nervous system diseases. The present sequence is  
CC that of a protein encoded by a C intestinalis gene of the invention.  
XX SQ Sequence 841 AA;

Query Match 100.0%; Score 35; DB 8; Length 841;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVSRLY 7  
Db 801 KVSRLY 807

Search completed: December 30, 2005, 13:23:57  
Job time : 64.2097 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 9.93548 Seconds  
(without alignments)  
67.789 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	31	88.6	108	E32530	Ig kappa chain V r
2	31	88.6	112	D28195	Ig kappa chain V r
3	31	88.6	374	A57583	histone acetyltran
4	30	85.7	64	JS0299	cytotoxin homolog
5	30	85.7	216	PQ0299	hypothetical prote
6	30	85.7	305	AI2079	hypothetical prote
7	30	85.7	375	G89972	conserved hypotet
8	30	85.7	405	A41252	heat shock protein
9	30	85.7	435	E69820	conserved hypotet
10	30	85.7	463	S66504	dipeptidyl-peptida
11	30	85.7	600	AI2454	ATP-binding protei
12	30	85.7	845	I48176	synaptonemal compl
13	30	85.7	993	S49461	synaptonemal compl
14	30	85.7	1102	AD2136	microcyatin synth
15	29	82.9	184	G97182	hypothetical secre
16	29	82.9	264	E90500	lipopate-protein li
17	29	82.9	233	D90153	cobalamin biosynth
18	29	82.9	329	T04710	peroxidase (EC 1.1
19	29	82.9	379	A24241	leukocyte elastase
20	29	82.9	379	S27383	elastase inhibitor
21	29	82.9	407	I39859	germination respon
22	29	82.9	528	AI2121	hypothetical prote
23	29	82.9	566	S07508	DNA primase - phag
24	29	82.9	588	E71802	penicillin-binding
25	29	82.9	588	E64715	penicillin-binding
26	29	82.9	809	S33533	heat shock protein
27	29	82.9	832	E71492	hypothetical prote
28	29	82.9	1003	C71139	hypothetical prote
29	29	82.9	2144	T21712	hypothetical prote

hypothetical prote  
Ig kappa chain V r  
conserved hypotet  
hypothetical prote  
hypothetical prote  
ORF MSV146 hypotet  
repressor - Staphy  
ribosome-phosphate d  
ribose-phosphate d  
phosphoribosylpyro  
ribose-phosphate d  
phosphoribosylpyro  
ribose-phosphate d  
class I histocompa  
membrane associate  
hypothetical prote

ALIGNMENTS

RESULT 1

E32530  
Ig kappa chain V region (DB3) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jul-2004  
C:Accession: E32530  
R:Deverson, E.; Berek, C.; Taussig, M.; Feinstein, A.  
Eur. J. Immunol. 17, 9-13, 1987  
A:Title: Monoclonal BALB/c anti-progesterone antibodies use family IX variable region h  
A:Reference number: A32530; MUID:87133855; PMID:3102254  
A:Accession: E32530  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-108 <DEV>  
A:Cross-references: UNIPROT:Q8VC16; UNIPARC:UPI0000176B00; GB:M27587  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:16-95/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 31; DB 2; Length 108;  
Best Local Similarity 85.7%; Pred. No. 7.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNLY 7  
DB 55 KVSNNRY 61  
|||||

RESULT 2

D28195  
Ig kappa chain V region (anti-haloperidol antibody D) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
C:Accession: D28195  
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
J. Biol. Chem. 263, 4059-4063, 1988  
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid  
A:Reference number: A28195; MUID:88153717; PMID:3267217  
A:Accession: D28195  
A:Molecule type: mRNA  
A:Residues: 1-112 <SHE>  
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B01; GB:M19769  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 31; DB 2; Length 112;  
Best Local Similarity 85.7%; Pred. No. 7.7;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNLY 7  
|||||

Db 55 KVSNNRFP 61

RESULT 3

A57583

histone acetyltransferase (EC 2.3.1.48) HAT1 - yeast (Saccharomyces cerevisiae)

NlAlternate names: protein LPA15w; protein YP8132.12; protein YPL001w

C:Species: Saccharomyces cerevisiae

C>Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

C:Accession: A57583; S52530; S59692

R:Kleff, S.; Andrusis, E.D.; Anderson, C.W.; Sternglanz, R.

J. Biol. Chem. 270, 24674-24677, 1995

A:Title: Identification of a gene encoding a yeast histone H4 acetyltransferase.

A:Reference number: A57583; MUID:96027552; PMID:7559580

A:Accession: A57583

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-374 <KLB>

A:Cross-references: UNIPROT:Q12341; UNIPARC:UPI00000530B2; GB:Z48483; NID:G683777; PIDN:G683777; PIDN:

R:Badcock, K.; Churcher, C.

submitted to the EMBL Data Library, February 1995

A:Reference number: S52519

A:Accession: S52530

A:Molecule type: DNA

A:Residues: 1-374 <BAD>

A:Cross-references: UNIPARC:UPI00000530B2; EMBL:Z48483; NID:G683777; PIDN:CAA88385.1; PI

A:Experimental source: strain AB972

R:Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wa

submitted to the EMBL Data Library, August 1995

A:Description: The sequence of Saccharomyces cerevisiae chromosomes XVI left arm.

A:Reference number: S59677

A:Accession: S59692

A:Molecule type: DNA

A:Residues: 1-374 <HAL>

A:Cross-references: UNIPARC:UPI00000530B2; EMBL:U33335; NID:G965076; PIDN:AAB68104.1; PI

C:Genetics:

A:Gene: SGD:HAT1

A:Cross-references: SGD:S0005922; MIPS:YPL001w

A:Map position: 16L

C:Keywords: acyltransferase; coenzyme A

Query Match 88.6%; Score 31; DB 2; Length 374;

Best Local Similarity 85.7%; Pred. No. 27;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRFP 7

Db 326 KVSNNRFP 332

RESULT 4

JS0299

cytotoxin homolog S4C8 - shield snake

C:Species: Aspidelaps scutatus (shield snake)

C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004

C:Accession: JS0299

R:Joubert, F.J.

Int. J. Biochem. 20, 337-345, 1988

A:Title: Snake venom toxins II. The primary structures of cytotoxin homologues S3C2 and

A:Reference number: JS0298; MUID:88185648; PMID:3356299

A:Accession: JS0299

A:Molecule type: protein

A:Residues: 1-64 <JOU>

A:Cross-references: UNIPROT:P19004; UNIPARC:UPI00001287FC

A:Experimental source: venom

C:Superfamily: snake toxin

C:Keywords: cytotoxin

Query Match 85.7%; Score 30; DB 2; Length 64;

Best Local Similarity 71.4%; Pred. No. 7.4;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRFP 7

Db 24 KVSNNRFP 30

RESULT 5

PQ0299

hypothetical protein 5 (gldA 3' region) - Bacillus stearothermophilus (fragment)

C:Species: Bacillus stearothermophilus

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Oct-2004

C:Accession: PQ0299

R:Mallinder, P.R.; Pritchard, A.; Moir, A.

Gene 110, 9-16, 1992

A:Title: Cloning and characterization of a gene from Bacillus stearothermophilus var. n.

A:Reference number: JQ1474; MUID:92184120; PMID:1339360

A:Accession: PQ0299

A:Molecule type: DNA

A:Residues: 1-216 <MAL>

A:Cross-references: UNIPROT:P32815; UNIPARC:UPI000013B0F1; GB:M65289; NID:G142976; PIDN:

A:Experimental source: strain var. non-diataticus

F:20-94/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 85.7%; Score 30; DB 2; Length 216;

Best Local Similarity 71.4%; Pred. No. 26;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRFP 7

Db 71 KVSNNRFP 77

RESULT 6

AI2079

hypothetical protein alr2191 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C:Accession: AI2079

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AI2079

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-305 <KUR>

A:Cross-references: UNIPROT:Q8YU20; UNIPARC:UPI00000CE359; GB:BA000019; PIDN:BA073890.1;

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr2191

Query Match 85.7%; Score 30; DB 2; Length 305;

Best Local Similarity 71.4%; Pred. No. 37;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRFP 7

Db 49 KVSNNRFP 55

RESULT 7

G89972

conserved hypothetical protein SA1673 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 05-Oct-2004

C:Accession: G89972

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: G89972

A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-375 <KUR>  
 A;Cross-references: UNIPROT:Q99722; UNIPARC:UPI00000CACF6; GB:BA000018; PID:g13701649; F  
 A;Experimental source: strain N315  
 C;Genetics:  
 A:Gene: SA1673

Query Match 85.7%; Score 30; DB 2; Length 375;  
 Best Local Similarity 71.4%; Pred. No. 45;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7  
 |: |||||

DB 232 KIGNRLY 238

## RESULT 8

A1252  
 heat shock protein 47 precursor - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 03-Apr-1992 #sequence revision 12-Apr-1996 #text\_change 05-Oct-2004  
 C;Accession: A41252; A27656; S16673  
 R;Hirayoshi, K.; Kudo, H.; Takechi, H.; Nakai, A.; Yamada, K.M.; Nagata, K  
 Mol. Cell. Biol. 11, 4036-4044, 1991  
 A;Title: HSP47: a tissue-specific, transformation-sensitive, collagen-binding heat shock  
 A;Reference number: A41252; MUID:91304395; PMID:2072906  
 A;Accession: A41252  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-405 <HIR>  
 A;Cross-references: UNIPROT:P13731; UNIPARC:UPI000012CC27; GB:X57157; NID:G63510; PIDN:Q  
 R;Nagata, K.; Saga, S.; Yamada, K.M.  
 Biochem. Biophys. Res. Commun. 153, 428-434, 1988  
 A;Title: Characterization of a novel transformation-sensitive heat-shock protein (HSP47)  
 A;Reference number: A27656; MUID:88240438; PMID:3377793  
 A;Accession: A27656  
 A:Molecule type: protein  
 A:Residues: 16-51 <NAG>  
 A;Cross-references: UNIPARC:UPI00001731PD  
 R;Nagata, K.

Trends Biochem. Sci. 21, 23-26, 1996  
 A;Title: Hsp47: a collagen-specific molecular chaperone.  
 A;Reference number: A57864  
 A;Contents: annotation; review article  
 C;Comment: This stress-induced glycoprotein of the ER lumen lacks protease inhibitor act  
 C;Genetics:  
 A:Gene: HSP47  
 A;Function:  
 A;Description: Hsp47 associates transiently with procollagen to assist as a molecular ch  
 and is induced by stresses such as heat shock.  
 C;Superfamily: serpin  
 C;Keywords: collagen binding; endoplasmic reticulum; glycoprotein; heat shock; molecular  
 F;1-15/Domain: signal sequence #status predicted <SIG>  
 F;16-405/Product: heat shock protein 47 #status predicted <MAT>  
 F;402-405/Region: endoplasmic reticulum retention signal  
 F;107,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.7%; Score 30; DB 1; Length 405;  
 Best Local Similarity 71.4%; Pred. No. 49;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7  
 |: |||||

DB 116 KIGNRLY 122

## RESULT 9

E69820  
 conserved hypothetical protein yhbA - Bacillus subtilis  
 C;Species: Bacillus subtilis  
 C;Date: 05-Dec-1997 #sequence revision 05-Dec-1997 #text\_change 05-Oct-2004  
 C;Accession: E69820

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
 C.; Bron, S.; Brummet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle  
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F  
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee  
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon  
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero  
 akeuchi, M.; Takakoshi, A.; Tanaka, T.; Terpsstra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,  
 A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A;Reference number: A69580; MUID:98044033; PMID:9384377  
 A;Accession: E69820  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-435 <KUN>  
 A;Cross-references: UNIPROT:P97030; UNIPARC:UPI0000060111; GB:Z99108; GB:AL009126; NID:  
 A;Experimental source: strain 168  
 C;Genetics:  
 A:Gene: yhbA  
 F;230-304/Domain: ferredoxin 2[4Fe-4S] homology <PER>

Query Match 85.7%; Score 30; DB 2; Length 435;  
 Best Local Similarity 71.4%; Pred. No. 53;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7  
 |: |||||

DB 281 KIGNRLY 287

## RESULT 10

S6504  
 dipeptidyl-peptidase I (EC 3.4.14.1) precursor - human  
 C;Species: Homo sapiens (man)  
 C;Date: 19-Mar-1997 #sequence revision 11-Apr-1997 #text\_change 09-Jul-2004  
 C;Accession: S6504  
 R;Paris, A.; Strukelj, B.; Pungercar, J.; Renko, M.; Dolenc, I.; Turk, V.  
 FEBS Lett. 369, 326-330, 1995  
 A;Title: Molecular cloning and sequence analysis of human preprocathepsin C.  
 A;Reference number: S6504; MUID:95377428; PMID:7649281  
 A;Accession: S6504  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A;Residues: 1-463 <PAR>  
 A;Cross-references: UNIPROT:PS3634; UNIPARC:UPI0000127099; EMBL:X87212; NID:gl006656; P  
 C;Genetics:

A:Gene: GDB:CTSC  
 A;Cross-references: GDB:642234  
 A;Map position: 8p22-8p22  
 C;Superfamily: papain  
 C;Keywords: dipeptidylpeptidase hydrolase  
 F;258,405,427/Active site: Cys, His, Asn #status predicted

Query Match 85.7%; Score 30; DB 2; Length 463;  
 Best Local Similarity 85.7%; Pred. No. 56;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7  
 |: |||||

DB 162 KVSNNRLY 168

## RESULT 11

AI2454  
 ATP-binding protein of ABC transporter all5193 [imported] - Nostoc sp. (strain PCC 7120  
 C;Species: Nostoc sp. PCC 7120  
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #sequence revision 14-Dec-2001 #text\_change 09-Jul-2004

C;Accession: A12454  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: A12454  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-600 <KUR>  
A;Cross-references: UNIPROT:Q8YLW3; UNIPARC:UPI00000CEDBE; GB:BA000019; PIDN:BA076892.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all5193  
C;Superfamily: Escherichia coli ABC transporter mla; ATP-binding cassette homology

Query Match 85.7%; Score 30; DB 2; Length 600;  
Best Local Similarity 85.7%; Pred. No. 74;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7  
|||  
Db 115 KVSNNLY 121

RESULT 12  
I48176  
synaptonemal complex protein - golden hamster (fragment)  
C;Species: Mesocricetus auratus (Golden hamster)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48176  
R;Dobson, M.J.; Pearlman, R.E.; Karaizakis, A.; Spyropoulos, B.; Moens, P.B.  
J. Cell Sci. 107, 2749-2760, 1994  
A;Title: Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disju  
A;Reference number: I48176; MUID:95181577; PMID:7876343  
A;Accession: I48176  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-845 <RES>  
A;Cross-references: UNIPROT:Q60563; UNIPARC:UPI000013567E; GB:IL32978; NID:G598124; PIDN:  
C;Genetics:  
A;Gene: synl

Query Match 85.7%; Score 30; DB 2; Length 845;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7  
:|||  
Db 781 EISNNLY 787

RESULT 13  
S49461  
synaptonemal complex protein 1 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S49461; S59599  
R;Julien, S.; Luc, M.; Francois, C.  
submitted to the EMBL Data Library, October 1994  
A;Description: Cloning and sequencing of the murine SCP1 cDNA.  
A;Reference number: S49461  
A;Accession: S49461  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-993 <JUL>  
A;Cross-references: UNIPROT:Q62209; UNIPARC:UPI0000028B49; EMBL:Z38118; NID:gl360015; PI  
R;Sage, J.; Martin, L.; Cuzin, F.; Rassoulzadegan, M.  
Biochim. Biophys. Acta 1263, 258-260, 1995  
A;Title: cDNA sequence of the murine synaptonemal complex protein 1 (SCP1).  
A;Reference number: S59599; MUID:96004899; PMID:7548215  
A;Accession: S59599  
A;Status: preliminary

A;Molecule type: mRNA  
A;Residues: 1-993 <SAG>  
A;Cross-references: UNIPARC:UPI0000028B49; EMBL:Z38118; NID:gl360015; PIDN:CAA86262.1; P  
Query Match 85.7%; Score 30; DB 2; Length 993;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNRLY 7  
|||||  
Db 927 VSNRLY 932

RESULT 14  
AD2136  
microcystin synthetase B [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AD2136  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AD2136  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1102 <KUR>  
A;Cross-references: UNIPROT:Q8YTS0; UNIPARC:UPI00000CE4E9; GB:BA000019; PIDN:BA074342.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all2643  
C;Superfamily: peptide synthetase ppsb; acetate-CoA ligase homology; acyl carrier protei  
C;Keywords: carrier protein

Query Match 85.7%; Score 30; DB 2; Length 1102;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNRLY 7  
|||||  
Db 639 VSNRLY 644

RESULT 15  
G97182  
hypothetical secreted protein [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: G97182  
R;Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: G97182  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-184 <KUR>  
A;Cross-references: UNIPROT:Q97GS2; UNIPARC:UPI00000CA495; GB:AE001437; PIDN:AAK80250.1;  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC2293

Query Match 82.9%; Score 29; DB 2; Length 184;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7  
|||||  
Db 60 KVSNNLY 66

Search completed: December 30, 2005, 13:34:53  
Job time : 10.9355 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 63 Seconds  
(without alignments)  
78.392 Million cell updates/sec

Title: US-10-735-916A-4  
Perfect score: 35  
Sequence: 1 KVSRLY 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	97.1	404	Q90420 BRARE	Q90420 brachydanio
2	34	97.1	405	Q61QV2 BRARE	Q61QV2 brachydanio
3	34	97.1	406	Q5DW60 ONCMY	Q5DW60 oncorhynchu
4	34	97.1	576	G6PD1 ARATH	Q43727 arabidopsis
5	32	91.4	355	Q8KKD3 HELPY	Q8KKD3 helicobacte
6	32	91.4	614	Q6BSM3 DEBHA	Q6BSM3 debaryomyce
7	32	91.4	1220	Q4PFH3 USTWA	Q4PFH3 ustilago ma
8	31	88.6	374	HAT1 YEAST	Q12341 saccharomyc
9	31	88.6	573	Q9AWB2 SOYEN	Q9AWB2 glycine max
10	31	88.6	685	Q7SNZ0 PEA	Q7SNZ0 pisum sativ
11	30	85.7	64	CKH48 ASPSC	P19004 aspidelaps
12	30	85.7	130	Q6FSG5 CANGA	Q6FSG5 candida gla
13	30	85.7	161	Q747U3 GEOSL	Q747U3 geobacter s
14	30	85.7	189	Q4U9D3 THEAN	Q4U9D3 thelleria a
15	30	85.7	216	YGL5 BACST	P12815 bacillus st
16	30	85.7	219	Q90XR7 BRARE	Q90XR7 brachydanio
17	30	85.7	219	Q567K6 BRARE	Q567K6 brachydanio
18	30	85.7	238	Q4WH23 ASPFU	Q4WH23 aspergillus
19	30	85.7	238	Q4WH44 ASPFU	Q4WH44 aspergillus
20	30	85.7	248	Q9AJU8 SHIFL	Q9AJU8 shigella fl
21	30	85.7	248	Q8VSA9 SHIFL	Q8VSA9 shigella fl
22	30	85.7	301	Q9AFK9 SHIFL	Q9AFK9 shigella fl
23	30	85.7	305	Q8YU20 ANASP	Q8YU20 anabaena sp
24	30	85.7	331	Q9M425 SPIOL	Q9M425 epinacia ol
25	30	85.7	356	Q50Q58 ENTHI	Q50Q58 entamoeba h
26	30	85.7	375	Q4L7G0 STAHJ	Q4L7G0 staphylococ
27	30	85.7	375	Q6G877 STAA5	Q6G877 staphylococ
28	30	85.7	375	Q6GPK0 STAA8	Q6GPK0 staphylococ
29	30	85.7	375	Q7A4U3 STAA8	Q7A4U3 staphylococ
30	30	85.7	375	Q8NVU0 STAAW	Q8NVU0 staphylococ
31	30	85.7	375	Q99T22 STAAW	Q99T22 staphylococ

32	30	85.7	375	2	Q5HER8 STAA8	Q5HER8 staphylococ
33	30	85.7	376	2	Q5HN80 STAEQ	Q5HN80 staphylococ
34	30	85.7	380	2	Q8CRX0 STAEQ	Q8CRX0 staphylococ
35	30	85.7	380	2	Q5L2R3 GEOKA	Q5L2R3 geobacillus
36	30	85.7	385	2	Q5OME4 ENTHI	Q5OME4 entamoeba h
37	30	85.7	405	1	HSP47 CHICK	P13731 gallus gall
38	30	85.7	435	2	P97030 BACSU	P97030 bacillus su
39	30	85.7	456	2	Q526J5 MAGGR	Q526J5 magnaporthe
40	30	85.7	463	1	CATC HUMAN	P53634 h dipeptid
41	30	85.7	463	1	CATC MACFA	Q60HG6 m dipeptid
42	30	85.7	463	2	Q53G93 HUMAN	Q53G93 homo sapien
43	30	85.7	463	2	Q71E76 HUMAN	Q71E76 homo sapien
44	30	85.7	463	2	Q8WY99 HUMAN	Q8WY99 homo sapien
45	30	85.7	463	2	Q5RB02 PONPY	Q5RB02 pongo pygma

ALIGNMENTS

RESULT 1  
ID Q90420 BRARE PRELIMINARY; PRT; 404 AA.  
AC Q90420;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE 47 kDa heat shock protein.  
GN Name-hsp47; Synonymshsp;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=9626405; PubMed=8634155;  
RA Pearson D.S., Kulyk W.M., Kelly G.M., Krone P.H.;  
RT "Cloning and characterization of a cDNA encoding the collagen-binding  
RT stress protein hsp47 in zebrafish.";  
RL DNA Cell Biol. 15:263-272(1996).  
CC -!- SIMILARITY: Belongs to the serpin family.  
DR EMBL; U31079; AAB06193.1; -; mRNA.  
DR HSP; P01012; IOVA.  
DR Ensembl; ENSDARG0000019949; Danio rerio.  
DR ZFIN; ZDB-GENE-990415-93; hsp47.  
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000886; ER target S.  
DR InterPro; IPR000215; Prot\_inh\_serpin.  
DR Pfam; PF00079; Serpin; 1.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW Heat shock; Serpin.  
SQ SEQUENCE 404 AA; 5225D331FBCFA0F7 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 404;  
Best Local Similarity 85.7%; Pred. No. 42;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7

Db 115 KISRLY 121

RESULT 2

Q61QV2 BRARE  
ID Q61QV2 BRARE PRELIMINARY; PRT; 405 AA.  
AC Q61QV2;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hsp47 protein.  
GN Name=hsp47;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_taxid=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX TISSUE=Embryo;  
R MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Buetow K.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX TISSUE=Embryo;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.  
CC -1- SIMILARITY: Belongs to the serpin family.  
DE EMBL; BC071301; AAH71301.1; -; mRNA.  
DR ZFIN; ZDB-GENE-990415-93; hsp47.  
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
DR InterPro; IPR000886; ER\_target\_S.  
DR InterPro; IPR000215; Prot\_inh\_serpin.  
DR Pfam; PF00079; Serpin; 1.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW Serpin.  
SQ SEQUENCE 405 AA; 45593 MW; 0083BE0AC435184B CRC64;  
Query Match 97.1%; Score 34; DB 2; Length 405;  
Best Local Similarity 85.7%; Pred. No. 42;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVSNNLY 7  
DB 116 KISNNLY 122  
[1]|||||  
[2]|||||

RESULT 3  
QSDW60\_ONCMY  
ID QSDW60\_ONCMY PRELIMINARY; PRT; 406 AA.  
AC QSDW60;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Heat shock protein 47.  
GN Name=HSP47;  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_taxid=8022;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15721272; DOI=10.1016/j.bbrc.2005.01.097;  
RA Ojima N., Yamashita M., Watabe S.;  
RT "Quantitative mRNA expression profiling of heat-shock protein families  
in rainbow trout cells.";  
RL Biochem. Biophys. Res. Commun. 329:51-57 (2005).  
CC -1- SIMILARITY: Belongs to the serpin family.  
DR EMBL; AB196463; FAD90029.1; -; mRNA.  
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000886; ER\_target\_S.  
DR InterPro; IPR000215; Prot\_inh\_serpin.  
DR Pfam; PF00079; Serpin; 1.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW Heat shock; Serpin.  
SQ SEQUENCE 406 AA; 45451 MW; 897A18B5B427877C CRC64;  
Query Match 97.1%; Score 34; DB 2; Length 406;  
Best Local Similarity 85.7%; Pred. No. 42;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVSNNLY 7  
DB 117 KISNNLY 123  
[1]|||||  
[2]|||||

RESULT 4  
G6PD1\_ARATH  
ID G6PD1\_ARATH STANDARD; PRT; 576 AA.  
AC Q43727; O65577; Q9PFMS;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Glucose-6-phosphate 1-dehydrogenase 1, chloroplast precursor  
(EC 1.1.1.49) (G6PD1) (G6PDH).  
GN Name=APG1; OrderedLocNames=At5g35790; ORFNames=MIK22.2, MWP19.3;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_taxid=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99364543; PubMed=10437832; DOI=10.1023/A:1006257230779;  
RA Wendt U.K., Hauschild R., Lange C., Pietersma M., Wenderoth I.,  
RA von Schaewen A.;  
RT "Evidence for functional convergence of redox regulation in G6PDH  
isoforms of cyanobacteria and higher plants.";  
RL Plant Mol. Biol. 40:487-494 (1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=cv. Columbia;  
RX MEDLINE=97471969; PubMed=9330910;  
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,  
RA Miyajima N., Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence  
features of the 1.6 Mb regions covered by twenty physically assigned  
P1 clones.";  
RL DNA Res. 4:215-230 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC STRAIN=cv. Columbia;  
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;  
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,  
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,  
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
Chen M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,  
Chao Q., Choy N., Ene J., Ene A., Goldsmith A.D., Gurjal M., Hansen N.F.,

RA Hayaehizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,  
RA Khan S., Koesena E., Ishida J., Jiang P.X., Jones T., Kawai J.,  
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
RA Satou M., Tame R., Vayaberg E.K., Wallender E.K., Wong C., Yamamura Y.,  
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
RT "Empirical analysis of transcriptional activity in the Arabidopsis  
RT genome";  
RL Science 302:842-846(2003).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. Lu Y.-P., Flavell R.,  
RA Brover V., Trouhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.A.;  
RT "Full-length cDNA from Arabidopsis thaliana";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE OF 17-576.  
RC STRAIN=cv. Columbia;  
RA Fink A., Greppin H., Tacchini P.;  
RT "Nucleotide sequence of a cDNA encoding the glucose-6-phosphate  
RT dehydrogenase from Arabidopsis thaliana";  
RL (er) Plant Gene Register FGR95-021.  
CC -!- FUNCTION: Catalyzes the rate-limiting step of the oxidative  
CC pentose-phosphate pathway, which represents a route for the  
CC dissimilation of carbohydrates besides glycolysis. The main  
CC function of this enzyme is to provide reducing power (NADPH) and  
CC pentose phosphates for fatty acid and nucleic acid synthesis which  
CC are involved in membrane synthesis and cell division.  
CC -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-  
CC 1,5-lactone 6-phosphate + NADPH.  
CC -!- ENZYME REGULATION: Regulated by metabolites. Posttranslationally  
CC inactivated by cysteine-mediated redox modification via the  
CC ferredoxin-thioredoxin system in the light and this avoids futile  
CC cycles with photosynthetic CO2 fixation (by similarity).  
CC -!- PATHWAY: Pentose phosphate pathway; first step.  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Chloroplast.  
CC -!- DEVELOPMENTAL STAGE: Increase of activity in the apex linked to  
CC the early stages of the transition from vegetative to reproductive  
CC growth.  
CC -!- MISCELLANEOUS: There are 6 glucose-6-phosphate 1-dehydrogenase  
CC genes in A.thaliana.  
CC -!- SIMILARITY: Belongs to the glucose-6-phosphate dehydrogenase  
CC family.  
CC -!- CAUTION: Ref.5 sequence differs from that shown due to a  
CC frameshift in position 65.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL: AJ001359; CAA04696.1; -; mRNA.  
CC EMBL: AB005236; BAB09918.1; -; Genomic\_DNA.  
CC EMBL: AV099561; AM20413.1; -; mRNA.  
CC EMBL: BT002133; AAN72144.1; -; mRNA.  
CC EMBL: AY086213; AAM64291.1; -; mRNA.  
CC EMBL: X84230; CAA59012.1; ALT\_FRAME; mRNA.  
CC HSSP: P11413; 1OKI.  
CC InterPro: IPR001282; G6PD.  
CC PANTHER: PTHR10097; G6PD; 1.  
CC Pfam: PF02781; G6PD C; 1.  
CC Pfam: PF00479; G6PD N; 1.  
CC PRINTS: PIRSF000110; G6PD; 1.  
CC PRINTS: PR00079; G6PDHGRNASE.  
CC ProDom: PD001129; G6PD; 1.  
CC TIGRFAMS: TIGR00871; zwf; 1.  
CC PROSITE: PS00069; G6P\_DEHYDROGENASE; 1.  
CC Carbohydrate metabolism; Chloroplast; Glucose metabolism;  
CC KW Carbohydrate metabolism; Oxidoreductase; Transit peptide.  
CC TRANSIT 1 50  
CC FT TRANSIT 1 50  
CC CHAIN 51 576  
CC Glucose-6-phosphate 1-dehydrogenase 1.

FT ACT\_SITE 326 326 Proton acceptor (By similarity).  
FT BINDING 99 99 NADP (By similarity).  
FT BINDING 131 131 NADP (By similarity).  
FT BINDING 284 284 Substrate; phosphate group (By  
FT similarity).  
FT BINDING 268 268 Substrate; phosphate group (By  
FT similarity).  
FT DISULFID 149 157 Redox modulation (By similarity).  
FT CONFLICT 110 110 A -> D (in Ref. 5).  
FT CONFLICT 205 213 IPPNIFVDV -> STPKLIVDE (in Ref. 1).  
FT CONFLICT 297 297 Q -> E (in Ref. 5).  
FT CONFLICT 383 383 G -> A (in Ref. 5).  
FT CONFLICT 485 486 RS -> PR (in Ref. 1).  
FT CONFLICT 514 514 G -> A (in Ref. 1).  
FT CONFLICT 530 530 D -> E (in Ref. 1).  
FT CONFLICT 539 539 L -> R (in Ref. 1).  
SQ SEQUENCE 576 AA; 65428 MW; 6559FFCCF76F44DF CRC64;  
Query Match 97.1%; Score 34; DB 1; Length 576;  
Best Local Similarity 85.7%; Pred. No. 61;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVSNNRY 7  
Db 195 KISNNRY 201  
|:|||||  
RESULT 5.  
Q8KKD3 HELPY PRELIMINARY; PRT; 355 AA.  
AC Q8KKD3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein orf58.  
GN Names-orf58;  
OS Helicobacter pylori (Campylobacter pylori).  
OG Plasmid pHel5.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
OC Helicobacteraceae; Helicobacter.  
ON NCBI\_TaxId=210;  
RX [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21972792; PubMed=11976306;  
RX DOI=10.1128/JB.184.10.2755-2766.2002;  
RA Hofreuter D., Haas R.;  
RT "Characterization of two cryptic Helicobacter pylori plasmids: a  
RT putative source for horizontal gene transfer and gene shuffling.";  
RL J. Bacteriol. 184:2755-2766(2002).  
DR EMBL: AF469113; NAM23664.1; -; Genomic\_DNA.  
KW Hypothetical protein; Plasmid.  
SQ SEQUENCE 355 AA; 41561 MW; C9090A779A04693F CRC64;  
Query Match 91.4%; Score 32; DB 2; Length 355;  
Best Local Similarity 85.7%; Pred. No. 11e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVSNNRY 7  
Db 345 KLSNNRY 351  
|:|||||  
RESULT 6  
Q6BSM3 DEBHA PRELIMINARY; PRT; 614 AA.  
AC Q6BSM3;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to CA3237[CaSPB4 Candida albicans CaSPB4.  
GN OrderedLocusNames=DEHA008470g;  
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).  
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.  
 OX NCBI\_TaxID=4959;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN-ATCC 36239 / CBS 767; DOI=10.1038/nature02579;  
 RX PubMed=1529592; DOI=10.1038/nature02579;  
 RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neveglisse C., Tallia E.,  
 RA Goffard N., Franchou L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boissane A., Boyer J., Cattolico L., Confanioli E., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Kerrest A., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerkast A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Niclaud J.-M., Nikolski M., Ozdas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Weslowski-Louvel M., Westhof E., Wirth B.,  
 RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in yeasts.";  
 RL Nature 430:35-44(2004).  
 CC -1- SIMILARITY: Belongs to the DEAD box helicase family.  
 DR EMBL; CR382136; CAG86941.1; -; Genomic\_DNA.  
 DR GO; GO:000524; F:ATP binding; IEA.  
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR InterPro; IPR001410; DEAD.  
 DR InterPro; IPR011545; DEAD/DEAH\_N.  
 DR InterPro; IPR000629; DEAD box.  
 DR Pfam; PF001650; Helicase\_C.  
 DR Pfam; PF00271; Helicase\_C; 1.  
 DR SMART; SM00487; DEXDC; 1.  
 DR SMART; SM00490; HELIC; 1.  
 DR PROSITE; PS00039; DEAD ATP HELICASE; 1.  
 KW ATP-binding; Complete proteome; Helicase; Hydrolase;  
 KW Nucleotide-binding; RNA-binding.  
 SQ SEQUENCE 614 AA; 70369 MW; 9AB5F7CC840C5D1B CRC64;  
 Query Match 91.4%; Score 32; DB 2; Length 614;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVSRLY 7  
 DB 71 KLSRLY 77  
 ID Q4PH3\_USTWA PRELIMINARY; PRT; 1220 AA.  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DE Hypothetical protein.  
 GN ORFNames=UW01140.1;  
 OS Ustilago maydis S21.  
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
 OX NCBI\_TaxID=237631;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=521;  
 RA Birren B., Nussbaum C., Abebe A., Abouelheil A., Adekoya E.,  
 RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
 RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,  
 RA Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,  
 RA Borowsky M., Bouthgatter B., Brunache A., Butler J., Calixte N.,  
 RA Calvo S., Camarata J., Campo K., Chang J., Cheehatsang Y., Citroen M.,  
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,

RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
 RA Fitzgerald M., Foley K., Gage D., Galaican J., Gearin G., Gnarre S.,  
 RA Girke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,  
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Hubby E., Iliev I.,  
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyseselis M., Karlsson E.,  
 RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,  
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
 RA Lindblad-toh K., Liu X., Lokytsang T., Lokytsang Y., Lucien O.,  
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,  
 RA Manning J., Marabell R., Maru K., Matthews C., Maucsil E.,  
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,  
 RA Mesirov J., Mihalev A., Mihova T., Mikkelson T., Menga V., Moru K.,  
 RA Moses J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,  
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
 RA Norbu N., O'donnell P., Okawa O., O'leary S., Omotosho B.,  
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,  
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
 RA Rutman M., Schupbach R., Seaman C., Settupalli S., Sharpe T.,  
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,  
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuanga P.,  
 RA Tenzing P., Testaye S., Theodore J., Thoultsang Y., Topham K.,  
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,  
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
 RA Zimmer A., Zody M., Lander E.;  
 RT "The genome sequence of Ustilago maydis.";  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AACP0100040; EAK81699.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1220 AA; 130516 MW; 588850F6AC5C65C CRC64;  
 Query Match 91.4%; Score 32; DB 2; Length 1220;  
 Best Local Similarity 85.7%; Pred. No. 3.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVSRLY 7  
 DB 1082 KLSRLY 1088  
 ID HAT1\_YEAST STANDARD; PRT; 374 AA.  
 AC Q12341; O6Q515;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Histone acetyltransferase type B catalytic subunit (EC 2.3.1.48).  
 GN Name=HAT1; OrderedLocusNames=YPL001W; ORFNames=LPA16W, YP8132.12;  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, PARTIAL PROTEIN SEQUENCE, AND CHARACTERIZATION.  
 RX MEDLINE=97011141; PubMed=8858151; DOI=10.1016/S0092-8674(00)81325-2;  
 RA Parthun M.R., Widom J., Gottschling D.E.;  
 RT "The major cytoplasmic histone acetyltransferase in yeast: links to  
 RL chromatin replication and histone metabolism.";  
 RL Cell 87:85-94(1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=7559580; DOI=10.1074/jbc.270.42.24674;  
 RA Kleff S., Andrusis E.D., Anderson C.W., Sternglanz R.;

```

RT "Identification of a gene encoding a yeast histone H4
RT acetyltransferase.";
RL J. Biol. Chem. 270:24674-24677(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Alberman K., Allen E., Ansoorge W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth U., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,
RA Huntcke-Smith S., Hyman R.W., Johnston M., Kaiman S., Kiehn K.,
RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Mueller-Auer S., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Petel F.X., Pohl T.M., Purnelle B., Rajandream M.A., Rehmman S.,
RA Rieger M., Riles L., Roberts D., Schaefer M., Scharfe M., Scherens B.,
RA Schramm S., Schroeder M., Sidcu A.-M., Tettelin H., Urrestarazu L.A.,
RA Ushinsky S., Vierendeels F., Viessers S., Voss H., Walsh S.V.,
RA Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.-W.,
RA Zollner A., Vo D.H., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:103-105(1997).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX STRAIN=S288c;
RA Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley P.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA LaBaer J.;
RT "Creation of the YLEX clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombinational cloning system.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-320.
RX MEDLINE=9839469; PubMed=9727486; DOI=10.1016/S0092-8674(00)81584-6;
RA Duttall R.N., Tafrov S.T., Sternglanz R., Ramakrishnan V.;
RT "Structure of the histone acetyltransferase Hat1: a paradigm for the
RT GCN5-related N-acetyltransferase superfamily.";
RL Cell 94:427-438(1998).
CC -1- FUNCTION: Acetylates the lysine at residue 12 of free histone H4
CC but does not modify histone H4 when packaged in chromatin. HAT1
CC has intrinsic substrate specificity that modifies lysine in
CC recognition sequence GXKXG.
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + histone = CoA + acetylhistone.
CC -1- SUBUNIT: Oligomer (>200 kDa) of HAT1 and HAT2 subunits.
CC -1- INTERACTION:
CC P39984:HAT2; NDEXP=1; InAct=EBI-8176, EBI-8185;
CC P53861:INL30C; NDEXP=1; InAct=EBI-8176, EBI-29191;
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, also detected in nuclear
CC extracts.
CC -1- SIMILARITY: To S.pombe SPAC139.06.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; Z48493; CAA88385.1; -; Genomic DNA.
CC EMBL; Z71255; CAA95040.1; -; Genomic DNA.
CC EMBL; U33335; AAB68104.1; -; Genomic DNA.
CC EMBL; AY558042; AAS56368.1; -; Genomic DNA.
CC PIR; A57583; A57583.
CC PDB; 1BOB; X-ray; @=1-320.
CC IntAct; Q12341; -.
CC GeneOnline; 143983; -.
CC Ensembl; YPL001W; Saccharomyces cerevisiae.
CC SGD; S000005922; HAT1.

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DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0000123; C:histone acetyltransferase complex; IPI.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004406; F:H3/H4 histone acetyltransferase activity; IMP.
DR GO; GO:0006348; P:chromatin silencing at telomere; IMP.
DR GO; GO:0016573; P:histone acetylation; IDA.
KW 3D-structure; Acyltransferase; Complete proteome;
KW Direct protein sequencing; Nuclear protein; Transferase.
FT COMPLETAS 314 317 Poly-Leu.
FT CONFLICT 87 87 L -> V (in Ref. 4).
FT HELIX 8 10
FT STRAND 12 14
FT HELIX 15 18
FT STRAND 19 24
FT STRAND 28 31
FT HELIX 37 40
FT TURN 41 44
FT STRAND 45 47
FT STRAND 49 50
FT STRAND 53 59
FT TURN 60 62
FT STRAND 65 70
FT STRAND 73 74
FT TURN 78 79
FT HELIX 83 88
FT TURN 89 90
FT TURN 93 94
FT STRAND 97 98
FT HELIX 101 114
FT TURN 117 120
FT STRAND 122 129
FT TURN 130 131
FT STRAND 132 139
FT HELIX 144 153
FT TURN 154 154
FT HELIX 155 160
FT TURN 162 163
FT TURN 169 170
FT TURN 172 173
FT STRAND 174 181
FT TURN 182 184
FT STRAND 187 196
FT STRAND 213 222
FT HELIX 224 226
FT TURN 231 245
FT TURN 247 248
FT STRAND 249 254
FT HELIX 259 275
FT TURN 276 277
FT HELIX 278 281
FT TURN 282 283
FT TURN 285 286
FT HELIX 290 300
FT TURN 301 301
FT STRAND 302 302
FT HELIX 304 317
FT TURN 318 318
SQ SEQUENCE 374 AA; 43873 MW; 8DECA134274413E6 CRC64;

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Query Match 88.6%; Score 31; DB 1; Length 374;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
 Db 326 KVSRLY 332

RESULT 9  
 Q9AWB2\_SOYBN  
 ID Q9AWB2\_SOYBN PRELIMINARY; PRT; 573 AA.  
 AC Q9AWB2;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)

```
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ferredoxin:sulfite reductase precursor (Fragment).
GN Name=sir;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Keaton M.A., Cannon G.C., Heinhorst S.;
RT "cDNA sequence for soybean ferredoxin:sulfite reductase.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY017473; AAG59996.1; -; mRNA.
DR HSSP: P17846; 4AOP.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR006066; Nlr_Si.
DR InterPro: IPR006067; Nlr_Sir_4Fe4S.
DR InterPro: IPR005117; Nlr_Sir_beta_fer.
DR InterPro: IPR011787; Sir.
DR Pfam: PF01077; Nlr_Sir; 1.
DR Pfam: PF03460; Nlr_Sir_ferr; 2.
DR PRINTS: PR00397; SIROHAM.
DR TIGRFAMs: TIGR02042; sir; 1.
DR PROSITE: PS00365; Nlr_Sir; 1.
KW Signal.
FT SIGNAL. 1 55 Potential.
FT CHAIN 56 >573 ferredoxin:sulfite reductase.
FT NON_TER 573
SQ SEQUENCE 573 AA; 63821 MW; FD02A907B746B2D9 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 573;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7
DB 135 KVSNNQLY 141

RESULT 10
ID Q75NZO_PEA PRELIMINARY; PRT; 685 AA.
AC Q75NZO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Sulfite reductase precursor.
GN Name=sir;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sekine K., Sato N.;
RT "Cloning of pea sulfite reductase.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB168112; BAB12837.1; -; mRNA.
DR HSSP: P17846; 1AOP.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR006066; Nlr_Si.
DR InterPro: IPR006067; Nlr_Sir_4Fe4S.
DR InterPro: IPR005117; Nlr_Sir_beta_fer.
DR InterPro: IPR011787; Sir.
DR Pfam: PF01077; Nlr_Sir; 2.
DR Pfam: PF03460; Nlr_Sir_ferr; 2.
DR PRINTS: PR00397; SIROHAM.
DR TIGRFAMs: TIGR02042; sir; 1.
DR PROSITE: PS00365; Nlr_Sir; 1.
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```
KW Transit peptide.
FT TRANSIT 1 51 Potential.
FT CHAIN 52 685 sulfite reductase.
SQ SEQUENCE 685 AA; 76839 MW; 170660B32867D40 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 685;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7
DB 133 KVSNNQLY 139

RESULT 11
CXH48 ASPSC
ID CXH48 ASPSC STANDARD; PRT; 64 AA.
AC P19004;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cytotoxin homolog S4C8.
OS Aspidelaps scutatus (Shield-nose snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Aspidelaps.
OX NCBI_TaxID=8607;
RN [1]
RP PROTEIN SEQUENCE, AND LETHAL DOSE.
RC TISSUE=venom;
RX MEDLINE=88185648; PubMed=3356299; DOI=10.1016/0020-711X(88)90361-8;
RA Joubert F.J.;
RT "Snake venom toxins -- II. The primary structures of cytotoxin
RT homologues S9C2 and S4C8 from Aspidelaps scutatus (shield or shield-
RT nose snake) venom.";
RL Int. J. Biochem. 20:337-345(1988).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -|- TOXIC DOSE: LD(50) is 9.4 mg/kg by intravenous injection.
CC -|- SIMILARITY: Belongs to the snake toxin family. Orphan group XIII
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR: J50299; JS0299.
DR HSSP: P07525; 1CHV.
DR InterPro: IPR003572; Cytotoxin.
DR Pfam: PF00087; Toxin_1_1.
DR PRINTS: PR00282; CYTOTOXIN.
DR PRODOM: PD000206; Snake toxin; 1.
DR PROSITE: PS00272; SNAKE_TOXIN; 1.
KW Cardiotoxin; Direct protein sequencing; Multigene family; Toxin.
FT DISULFID 3 22 By similarity.
FT DISULFID 15 40 By similarity.
FT DISULFID 44 55 By similarity.
FT DISULFID 56 62 By similarity.
SQ SEQUENCE 64 AA; 7317 MW; 2AC8FEE8B6EE092 CRC64;

Query Match 85.7%; Score 30; DB 1; Length 64;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7
DB 24 KVSNNRMV 30

RESULT 12
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DR TIGR: GSD31172; -.
DR InterPro: IPR008312; UCP028301.
DR Pfam: PF05591; DUF770; 1.
DR PIRSF: PIRSF028301; UCP028301; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 161 AA; 18185 MW; 29EE10B908B58BFF CRC64;

Query Match      85.7%; Score 30; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNRLY 7
Db 77 VSNRLY 82
|||||

RESULT 14
Q4U9D3_THEAN
ID Q4U9D3_THEAN PRELIMINARY; PRT; 189 AA.
AC Q4U9D3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames-TA08960;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OC NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A.; Renaud H.; Murphy L.; Harris D.A.; Quail M.A.; Berriman M.;
RA Hall N.; Barrell B.G.;
RT "The chromosome 3 genome sequence of Theileria annulata.";
EL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940353; CAI76570.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 189 AA; 21158 MW; 41DA80AA475E3237 CRC64;

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Query Match      85.7%; Score 30; DB 2; Length 189;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY    1 KVSNRLY 7
      |::|||
DB    13 KIENRLY 19

RESULT 15
YGL5_BACST
ID_   YGL5_BACST          STANDARD;          PRT;       216 AA.
AC    P32815;
DT    01-OCT-1993 (Rel. 27, Created)
DT    01-OCT-1993 (Rel. 27, Last sequence update)
DT    13-SEP-2005 (Rel. 49, Last annotation update)
DE    Hypothetical protein in gldA 3'-region (ORF5) (Fragment).
OS    Bacillus stearothermophilus.
OC    Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
NCBI  taxID=1422;
RN    [1]
RP    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC    STRAIN=var. Non-diataticus;
RX    MEDLINE=92184120; PubMed=139360; DOI=10.1016/0378-1119(92)90438-U;
RA    Mallender P.R., Pritchard A., Moir A.;
RT    "Cloning and characterization of a gene from Bacillus
RT    stearothermophilus var. non-diataticus encoding a glycerol
RT    dehydrogenase."
RL    Gene 110:9-16(1992).
CC    -!- SIMILARITY: Contains 2 4Fe-4S type ferredoxin domains.
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 CC removed.

CC -----  
 CC EMBL; M65289; AAA22480.1; -; Genomic\_DNA.

DR PIR; PQ0299; PQ0299.

DR InterPro; IPR001450; 4Fe4S\_Fe\_S\_bd.

DR InterPro; IPR011989; ARM-like.

DR InterPro; IPR004155; PBS\_lyase\_HEAT.

DR Pfam; PF00037; Fer4; 1.

DR Pfam; PF03130; HEAT\_PBS; 2.

DR PROSITE; PS00198; 4Fe4S\_FERREDOXIN; 1.

KW 4Fe-4S; Hypothetical protein; Iron; Iron-sulfur; Metal-binding.

FT METAL 27 27 Iron-sulfur 1 (4Fe-4S) (Potential).

FT METAL 30 30 Iron-sulfur 1 (4Fe-4S) (Potential).

FT METAL 33 33 Iron-sulfur 1 (4Fe-4S) (Potential).

FT METAL 37 37 Iron-sulfur 2 (Potential).

FT METAL 79 79 Iron-sulfur 2 (Potential).

FT METAL 82 82 Iron-sulfur 2 (Potential).

FT METAL 86 86 Iron-sulfur 1 (4Fe-4S) (Potential).

FT NON\_TER 1

SQ SEQUENCE 216 AA; 24210 MW; 0A95D704B2CA0695 CRC64;

Query Match 85.7%; Score 30; DB 1; Length 216;

Best Local Similarity 71.4%; Pred. No. 1.8e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSRLY 7

Db : ||||

71 KIGNRLY 77

Search completed: December 30, 2005, 13:33:23

Job time : 66 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 15.6935 Seconds  
(without alignments)  
36.877 Million cell updates/sec

Title: US-10-735-916A-4  
Perfect score: 35  
Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	31	88.6	113	2	US-09-232-290-20
2	31	88.6	687	2	US-09-720-524-4
3	31	88.6	687	2	US-10-757-114-4
4	30	85.7	323	2	US-09-328-352-5170
5	30	85.7	365	2	US-09-230-586A-25
6	30	85.7	388	2	US-09-134-001C-3820
7	30	85.7	463	1	US-08-426-428-2
8	30	85.7	463	2	US-08-871-314-2
9	30	85.7	463	2	US-09-886-319A-73
10	30	85.7	463	2	US-09-919-039-154
11	30	85.7	463	2	US-09-949-016-6132
12	30	85.7	474	2	US-09-949-016-7306
13	30	85.7	3025	6	5223423-3
14	29	82.9	267	1	US-08-667-809B-2
15	29	82.9	274	1	US-08-307-499-27
16	29	82.9	274	2	US-08-239-268-27
17	29	82.9	375	1	US-08-121-714-8
18	29	82.9	375	1	US-08-477-108A-8
19	29	82.9	375	1	US-08-477-112-8
20	29	82.9	375	4	PCT-US93-08322-8
21	29	82.9	378	2	US-09-543-681A-4604
22	29	82.9	379	1	US-08-121-714-4
23	29	82.9	379	1	US-08-477-108A-4
24	29	82.9	379	1	US-08-477-112-4
25	29	82.9	379	2	US-10-094-944-9
26	29	82.9	379	4	PCT-US93-08322-4
27	29	82.9	540	2	US-09-248-796A-15935

28	28	80.0	56	2	US-09-513-999C-6825	Sequence 6825, Ap
29	28	80.0	100	2	US-09-840-459-26	Sequence 26, Appl
30	28	80.0	100	2	US-09-497-625A-26	Sequence 26, Appl
31	28	80.0	343	2	US-09-489-039A-10330	Sequence 10330, A
32	28	80.0	352	2	US-09-816-028A-21	Sequence 21, Appl
33	28	80.0	352	2	US-10-303-162-21	Sequence 21, Appl
34	28	80.0	352	2	US-10-303-134-21	Sequence 21, Appl
35	28	80.0	352	2	US-10-303-118-21	Sequence 21, Appl
36	28	80.0	352	2	US-10-303-128-21	Sequence 21, Appl
37	28	80.0	395	2	US-09-252-991A-30497	Sequence 30497, A
38	28	80.0	443	2	US-09-248-796A-19547	Sequence 19547, A
39	28	80.0	496	2	US-09-248-796A-18957	Sequence 18957, A
40	28	80.0	621	2	US-09-059-522-1	Sequence 1, Appli
41	28	80.0	621	2	US-09-382-027-1	Sequence 1, Appli
42	28	80.0	658	2	US-09-248-796A-17674	Sequence 17674, A
43	28	80.0	1287	2	US-09-252-991A-29606	Sequence 29606, A
44	27	77.1	138	2	US-09-489-039A-9722	Sequence 9722, Ap
45	27	77.1	166	2	US-08-916-576B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-232-290-20  
; Sequence 20, Application US/09232290A  
; Patent No. 6815540  
; GENERAL INFORMATION:  
; APPLICANT: NIEBA, LARS  
; APPLICANT: HONEGER, ANNEMARIE  
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH INCREASED SOLUBILITY  
; FILE REFERENCE: MORPHO/7  
; CURRENT APPLICATION NUMBER: US/09/232,290A  
; CURRENT FILING DATE: 1999-01-15  
; EARLIER APPLICATION NUMBER: PCT/EP96/02230  
; EARLIER FILING DATE: 1996-05-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Murine  
US-09-232-290-20

Query Match 88.6%; Score 31; DB 2; Length 113;  
Best Local Similarity 85.7%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KVSNNLY 7  
DB 55 KVSNNRY 61

RESULT 2  
US-09-720-524-4  
; Sequence 4, Application US/09720524  
; Patent No. 6720172  
; GENERAL INFORMATION:  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins  
; FILE REFERENCE: BB-1167-D  
; CURRENT APPLICATION NUMBER: US/09/720,524  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 60/092,833  
; PRIOR FILING DATE: 1998-07-14  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 4  
; LENGTH: 687  
; TYPE: PRT  
; ORGANISM: Glycine max

US-09-720-524-4

Query Match 88.6%; Score 31; DB 2; Length 687;  
Best Local Similarity 85.7%; Pred. No. 97;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
|:|:|:|:  
Db 135 KVSNNQLY 141

RESULT 3

US-10-757-114-4

; Sequence 4, Application US/10757114

; Patent No. 6939710

; GENERAL INFORMATION:

; APPLICANT: E. I. du Pont de Nemours and Company

; TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins

; FILE REFERENCE: BB-1167-D

; CURRENT APPLICATION NUMBER: US/10/757,114

; CURRENT FILING DATE: 2004-01-14

; PRIOR APPLICATION NUMBER: US/09/720,524

; PRIOR FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 60/092,833

; PRIOR FILING DATE: 1998-07-14

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 4

; LENGTH: 687

; TYPE: PRT

; ORGANISM: Glycine max

US-10-757-114-4

Query Match

88.6%; Score 31; DB 2; Length 687;

Best Local Similarity 85.7%; Pred. No. 97;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7

|:|:|:|:  
Db 135 KVSNNQLY 141

RESULT 4

US-09-328-352-5170

; Sequence 5170, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: GTC99-03PA

; CURRENT FILING DATE: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 5170

; LENGTH: 323

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-5170

Query Match

85.7%; Score 30; DB 2; Length 323;

Best Local Similarity 71.4%; Pred. No. 75;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7

|:|:|:|:  
Db 241 KVSNNRIY 247

RESULT 5

US-09-290-586A-25

; Sequence 25, Application US/09290586A

; Patent No. 6800473

; GENERAL INFORMATION:

; APPLICANT: SANTAMARIA, Ignacio

; APPLICANT: VELASCO, Gloria

; APPLICANT: CAZORLA, Maite

; APPLICANT: FUEYO, Antonio

; APPLICANT: CAMPO, Elias

; APPLICANT: LOPEZ-OTIN, Carlos

; APPLICANT: AOKI, Takanori

; APPLICANT: IWATA, Kazushi

; TITLE OF INVENTION: NOVEL HUMAN CATHEPSIN L2 PROTEIN, GENE ENCODING SAID

; FILE REFERENCE: 99-410A/WMC/01332

; CURRENT APPLICATION NUMBER: US/09/290,586A

; CURRENT FILING DATE: 1999-04-13

; PRIOR APPLICATION NUMBER: JP 10-172147

; PRIOR FILING DATE: 1998-06-05

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 25

; LENGTH: 365

; TYPE: PRT

; ORGANISM: Human

US-09-290-586A-25

Query Match

85.7%; Score 30; DB 2; Length 365;

Best Local Similarity 85.7%; Pred. No. 85;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7

|:|:|:|:  
Db 65 KVSNNRLY 71

RESULT 6

US-09-134-001C-3820

; Sequence 3820, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: GTC-007

; CURRENT FILING DATE: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3820

; LENGTH: 388

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3820

Query Match

85.7%; Score 30; DB 2; Length 388;

Best Local Similarity 71.4%; Pred. No. 91;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7

|:|:|:|:  
Db 243 KIGNRLY 249

RESULT 7

US-08-426-428-2

; Sequence 2, Application US/08426428

; Patent No. 5637462

; GENERAL INFORMATION:

; APPLICANT: Coleman, Roger

; APPLICANT: Braxton, Scott M.

; APPLICANT: Seilhamer, Jeffrey J.

; TITLE OF INVENTION: NEW CATHEPSIN C HOMOLOG

[illegible]

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; SEQ ID NO 154
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 014284CD1
US-09-919-039-154

Query Match      85.7%; Score 30; DB 2; Length 463;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
Db 162 KYSRLY 168

RESULT 11
US-09-949-016-6132
; Sequence 6132, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6132
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6132

Query Match      85.7%; Score 30; DB 2; Length 463;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
Db 162 KYSRLY 168

RESULT 12
US-09-949-016-7306
; Sequence 7306, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7306
; LENGTH: 474
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7306

Query Match      85.7%; Score 30; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
Db 173 KYSRLY 179

RESULT 13
5223423-3
; Patent No. 5223423
; APPLICANT: FRANCHINI, GENOVEPPA,WONG-STAAAL, FLOSSIE;
; GALLO, ROBERT
; TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
; HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/331,212
; FILING DATE: 03-31-1989
; SEQ ID NO:3:
; LENGTH: 3025
5223423-3

Query Match      85.7%; Score 30; DB 6; Length 3025;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNRLY 7
Db 2030 VSNRLY 2035

RESULT 14
US-08-667-809B-2
; Sequence 2, Application US/08667809B
; Patent No. 5986174
; GENERAL INFORMATION:
; APPLICANT: Barbour, Eric
; APPLICANT: Baszczyński, Chris
; APPLICANT: Rosichan, Jeffrey L.
; APPLICANT: Horowitz, Jeanine
; TITLE OF INVENTION: MAIZE PROMOTER SEQUENCE FOR LEAF- AND
; TITLE OF INVENTION: STALK-PREFERRED GENE EXPRESSION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,809B
; FILING DATE: 21-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 2:
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SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-667-809B-2

Query Match 82.9%; Score 29; DB 1; Length 267;  
Best Local Similarity 71.4%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
|:|||||  
Db 18 KISRLH 24

RESULT 15  
US-08-307-499-27  
; Sequence 27, Application US/08307499  
; Patent No. 5651972  
; GENERAL INFORMATION:  
; APPLICANT: Moyer, Richard W.  
; APPLICANT: Vi uela, Eladio  
; APPLICANT: Gibbs, E.P.J.  
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a  
; TITLE OF INVENTION: Live Vaccine Vector  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: U.S.A.  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,499  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: US 07/908,241  
; APPLICATION NUMBER: US 07/908,241  
; FILING DATE: 1-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/908,630  
; FILING DATE: 29-JUN-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/342,212  
; FILING DATE: 21-APR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 274 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-307-499-27

Query Match 82.9%; Score 29; DB 1; Length 274;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
|:|||||  
Db 229 RVNRLY 235

Search completed: December 30, 2005, 13:37:17  
Job time : 16.6935 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 52.0484 Seconds  
(without alignments)  
56.194 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNRLY 7

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	35	100.0	112	US-10-735-916A-54	Sequence 54, Appl
3	35	100.0	112	US-10-735-916A-61	Sequence 61, Appl
4	35	100.0	112	US-10-735-916A-65	Sequence 65, Appl
5	35	100.0	122	US-10-735-916A-49	Sequence 49, Appl
6	35	100.0	131	US-10-735-916A-63	Sequence 63, Appl
7	35	100.0	131	US-10-735-916A-67	Sequence 67, Appl
8	32	91.4	214	US-10-425-115-303579	Sequence 303579,
9	31	88.6	92	US-10-425-115-264792	Sequence 264792,
10	31	88.6	223	US-10-424-599-283409	Sequence 283409,
11	31	88.6	687	US-10-424-599-283410	Sequence 283410,
12	31	88.6	687	US-10-757-114-4	Sequence 4, Appli
13	30	85.7	71	US-10-424-599-225929	Sequence 225929,
14	30	85.7	176	US-10-739-930-6956	Sequence 6956, Ap
15	30	85.7	223	US-10-425-115-336315	Sequence 336315,
16	30	85.7	269	US-10-437-963-134241	Sequence 134241,
17	30	85.7	388	US-10-724-972A-6036	Sequence 6036, Ap
18	30	85.7	419	US-10-480-988-16	Sequence 16, Appl
19	30	85.7	439	US-10-297-509-1	Sequence 1, Appli
20	30	85.7	463	US-09-886-319A-73	Sequence 73, Appl
21	30	85.7	463	US-09-974-298-66	Sequence 66, Appl
22	30	85.7	463	US-09-919-039-154	Sequence 154, App
23	30	85.7	463	US-10-204-752-29	Sequence 29, Appl
24	30	85.7	463	US-10-376-564-73	Sequence 73, Appl
25	30	85.7	463	US-10-287-436A-393	Sequence 393, App
26	30	85.7	463	US-10-287-436A-1093	Sequence 1093, App
27	30	85.7	463	US-10-631-467-642	Sequence 642, App

ALIGNMENTS

RESULT 1

US-10-735-916A-4  
; Sequence 4, Application US/10735916A

; Publication No. US20050084906A1

; GENERAL INFORMATION:

; APPLICANT: GOETTSCH, Liliane

; APPLICANT: CORVAIA, Nathalie

; APPLICANT: LEGER, Olivier

; APPLICANT: DUFLOS, Alain

; APPLICANT: BECK, Alain

; APPLICANT: HAEUM, Jean-Francois

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 017753-183

; CURRENT APPLICATION NUMBER: US/10/735,916A

; PRIOR FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 03/08 538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 02/00 653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 02/00 654

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 02/05 753

; PRIOR FILING DATE: 2002-05-07

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-735-916A-4

Query Match 100.0%; Score 35; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7

Db 1 KVSNNRLY 7

RESULT 2

US-10-735-916A-54

; Sequence 54, Application US/10735916A

; Publication No. US20050084906A1

; GENERAL INFORMATION:

; APPLICANT: GOETTSCH, Liliane

; APPLICANT: CORVAIA, Nathalie

; APPLICANT: LEGER, Olivier

; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; PUBLICATION NO. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 54  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-54

Query Match 100.0%; Score 35; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7  
| | | | |  
Db 55 KVSRLY 61

RESULT 3  
US-10-735-916A-61  
; Sequence 61, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 61  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-735-916A-61

Query Match 100.0%; Score 35; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7  
| | | | |

Db 55 KVSRLY 61  
RESULT 4  
US-10-735-916A-65  
; Sequence 65, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 65  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-735-916A-65

Query Match 100.0%; Score 35; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7  
| | | | |  
Db 55 KVSRLY 61

RESULT 5  
US-10-735-916A-49  
; Sequence 49, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 49



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; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-49

Query Match      100.0%; Score 35; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNNLY 7
       |||||
Db      65 KVSNNLY 71

RESULT 6
US-10-735-916A-63
; Sequence 63, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFIOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: PCT/FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 63
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-63

Query Match      100.0%; Score 35; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNNLY 7
       |||||
Db      74 KVSNNLY 80

RESULT 8
US-10-425-115-303579
; Sequence 303579, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 303579
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_39938C.1.pep
US-10-425-115-303579

Query Match      91.4%; Score 32; DB 4; Length 214;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNNLY 7
       |||||
Db      116 KVSNNLY 122

RESULT 9
US-10-425-115-264792
; Sequence 264792, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 264792
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; LENGTH: 92
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(92)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_17309C.1.pgp
US-10-425-115-264792

Query Match      88.6%; Score 31; DB 4; Length 92;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
   :|||:
Db 85 KISNKL 91

RESULT 10
US-10-424-599-283409
; Sequence 283409, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 283409
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(223)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97941C.1.pgp
US-10-424-599-283409

Query Match      88.6%; Score 31; DB 4; Length 223;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
   :|||:
Db 136 KVSQNL 142

RESULT 11
US-10-424-599-283410
; Sequence 283410, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 283410
; LENGTH: 687
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97942C.1.pgp
US-10-424-599-283410

Query Match      88.6%; Score 31; DB 4; Length 687;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
   :|||:
Db 135 KVSQNL 141

RESULT 12
US-10-757-114-4
; Sequence 4, Application US/10757114
; Publication No. US20040137496A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
; FILE REFERENCE: BB-1167-D
; CURRENT APPLICATION NUMBER: US/10/757,114
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US/09/720,524
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/092,833
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_46044C.1.pgp
US-10-757-114-4

Query Match      88.6%; Score 31; DB 4; Length 687;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
   :|||:
Db 135 KVSQNL 141

RESULT 13
US-10-424-599-225929
; Sequence 225929, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 225929
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_46044C.1.pgp
US-10-424-599-225929

Query Match      85.7%; Score 30; DB 4; Length 71;
Best Local Similarity 71.4%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KVSRLY 7  
|:|:|:|  
Db 32 KISRLY 38

RESULT 14

US-10-739-930-6956  
; Sequence 6956, Application US/10739930  
; Publication No. US20040216190A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 6956  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Brassica napus  
; FEATURE:  
; OTHER INFORMATION: Clone ID: BRANA-23APR03-C27607\_1.p  
US-10-739-930-6956

Query Match 85.7%; Score 30; DB 5; Length 176;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
|:|:|:|  
Db 47 KISRLY 53

RESULT 15

US-10-425-115-336315  
; Sequence 336315, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 336315  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_69828C.1.pep  
US-10-425-115-336315

Query Match 85.7%; Score 30; DB 4; Length 223;  
Best Local Similarity 85.7%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
|:|:|:|  
Db 188 KISRLH 194

Search completed: December 30, 2005, 14:14:51  
Job time : 53.0484 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 2.59677 Seconds  
(without alignments)  
20.187 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNRLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_New.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	7	US-11-012-353-4	Sequence 4, Appli
2	35	100.0	112	US-11-012-353-54	Sequence 54, Appl
3	35	100.0	112	US-11-012-353-61	Sequence 61, Appl
4	35	100.0	112	US-11-012-353-65	Sequence 65, Appl
5	35	100.0	122	US-11-012-353-49	Sequence 49, Appl
6	35	100.0	131	US-11-012-353-63	Sequence 63, Appl
7	35	100.0	131	US-11-012-353-67	Sequence 67, Appl
8	30	85.7	488	US-10-821-234-1000	Sequence 1000, Ap
9	28	80.0	232	US-10-467-657-4338	Sequence 4338, Ap
10	27	77.1	168	US-11-108-172-631	Sequence 631, Appl
11	27	77.1	483	US-11-113-775A-1	Sequence 1, Appli
12	27	77.1	483	US-11-113-775A-2	Sequence 2, Appli
13	27	77.1	483	US-11-113-799-1	Sequence 1, Appli
14	27	77.1	483	US-11-113-799-2	Sequence 2, Appli
15	27	77.1	485	US-10-630-203-12	Sequence 12, Appl
16	27	77.1	485	US-11-113-775A-3	Sequence 3, Appli
17	27	77.1	485	US-11-113-799-3	Sequence 3, Appli
18	27	77.1	1032	US-11-014-367-3	Sequence 3, Appli
19	26	74.3	99	US-10-467-657-4402	Sequence 4402, Ap
20	26	74.3	425	US-11-096-276-2	Sequence 2, Appli
21	26	74.3	439	US-11-082-389-80	Sequence 80, Appl
22	26	74.3	495	US-10-510-386-188	Sequence 188, App
23	26	74.3	496	US-10-793-626-1030	Sequence 1030, Ap
24	26	74.3	513	US-10-878-556A-112	Sequence 112, App
25	26	74.3	564	US-11-082-389-78	Sequence 78, Appl

26	74.3	724	6	US-10-793-626-968	Sequence 968, App
27	71.4	45	6	US-10-957-887B-238	Sequence 238, App
28	71.4	45	6	US-10-957-887B-242	Sequence 242, App
29	71.4	211	6	US-10-467-657-2142	Sequence 2142, Ap
30	71.4	311	6	US-10-793-626-1248	Sequence 1248, Ap
31	68.6	7	6	US-10-932-334-5	Sequence 2, Appli
32	68.6	7	7	US-11-125-837-2	Sequence 5, Appli
33	68.6	7	7	US-11-125-837-14	Sequence 14, Appl
34	68.6	7	7	US-11-105-708-18	Sequence 18, Appl
35	68.6	43	6	US-10-957-887B-67	Sequence 67, Appl
36	68.6	100	6	US-10-932-334-56	Sequence 56, Appl
37	68.6	100	7	US-11-054-669-75	Sequence 75, Appl
38	68.6	100	7	US-11-084-554-107	Sequence 107, App
39	68.6	100	7	US-11-084-554-118	Sequence 118, App
40	68.6	112	6	US-10-502-145-15	Sequence 15, Appl
41	68.6	112	6	US-10-502-145-19	Sequence 19, Appl
42	68.6	112	6	US-10-502-145-23	Sequence 23, Appl
43	68.6	112	6	US-10-507-662-39	Sequence 39, Appl
44	68.6	112	7	US-11-012-353-55	Sequence 55, Appl
45	68.6	112	7	US-11-012-353-56	Sequence 56, Appl

## ALIGNMENTS

### RESULT 1

US-11-012-353-4  
; Sequence 4, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: Patent in Ver. 3.3  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-4

Query Match 100.0%; Score 35; DB 7; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
| | | | |  
Db 1 KVSNNRLY 7

### RESULT 2

US-11-012-353-54  
; Sequence 54, Application US/11012353

```
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-54

Query Match      100.0%; Score 35; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 55 KVSNNRLY 61

RESULT 3
US-11-012-353-61
; Sequence 61, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 61
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-65

Query Match      100.0%; Score 35; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 55 KVSNNRLY 61

RESULT 4
US-11-012-353-65
; Sequence 65, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 65
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-65

Query Match      100.0%; Score 35; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 55 KVSNNRLY 61

RESULT 5
US-11-012-353-49
; Sequence 49, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; SEQ ID NO 61
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; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 65
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-65

Query Match      100.0%; Score 35; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 55 KVSNNRLY 61

RESULT 5
US-11-012-353-49
; Sequence 49, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; SEQ ID NO 61
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;; CURRENT APPLICATION NUMBER: US/11/012,353  
;; CURRENT FILING DATE: 2004-12-16  
;; PRIOR APPLICATION NUMBER: 10/735,916  
;; PRIOR FILING DATE: 2003-12-16  
;; PRIOR APPLICATION NUMBER: FR 0308538  
;; PRIOR FILING DATE: 2003-07-11  
;; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
;; PRIOR FILING DATE: 2003-01-20  
;; PRIOR APPLICATION NUMBER: FR 0205753  
;; PRIOR FILING DATE: 2002-05-07  
;; PRIOR APPLICATION NUMBER: FR 0200653  
;; PRIOR FILING DATE: 2002-01-18  
;; PRIOR APPLICATION NUMBER: FR 0200654  
;; PRIOR FILING DATE: 2002-01-18  
;; NUMBER OF SEQ ID NOS: 162  
;; SOFTWARE: PatentIn Ver. 3.3  
;; SEQ ID NO 49  
;; LENGTH: 122  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-11-012-353-49

Query Match 100.0%; Score 35; DB 7; Length 122;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNLY 7  
|||||||  
DB 65 KVSNNLY 71

RESULT 6  
US-11-012-353-63  
;; Sequence 63, Application US/11012353  
;; Publication No. US20050249730A1  
;; GENERAL INFORMATION:  
;; APPLICANT: GOETSCH, LILIANE  
;; APPLICANT: CORVAIA, NATHALIE  
;; APPLICANT: DUFLOS, ALAIN  
;; APPLICANT: HABUW, JEAN-FRANCOIS  
;; APPLICANT: LEGER, OLIVIER  
;; APPLICANT: BECK, ALAIN  
;; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
;; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
;; FILE REFERENCE: 017753-198  
;; CURRENT APPLICATION NUMBER: US/11/012,353  
;; CURRENT FILING DATE: 2004-12-16  
;; PRIOR APPLICATION NUMBER: 10/735,916  
;; PRIOR FILING DATE: 2003-12-16  
;; PRIOR APPLICATION NUMBER: FR 0308538  
;; PRIOR FILING DATE: 2003-07-11  
;; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
;; PRIOR FILING DATE: 2003-01-20  
;; PRIOR APPLICATION NUMBER: FR 0205753  
;; PRIOR FILING DATE: 2002-05-07  
;; PRIOR APPLICATION NUMBER: FR 0200653  
;; PRIOR FILING DATE: 2002-01-18  
;; PRIOR APPLICATION NUMBER: FR 0200654  
;; NUMBER OF SEQ ID NOS: 162  
;; SOFTWARE: PatentIn Ver. 3.3  
;; SEQ ID NO 63  
;; LENGTH: 131  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-012-353-63

Query Match 100.0%; Score 35; DB 7; Length 131;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNLY 7  
|||||||

DB 74 KVSNNLY 80  
RESULT 7  
US-11-012-353-67  
;; Sequence 67, Application US/11012353  
;; Publication No. US20050249730A1  
;; GENERAL INFORMATION:  
;; APPLICANT: GOETSCH, LILIANE  
;; APPLICANT: CORVAIA, NATHALIE  
;; APPLICANT: DUFLOS, ALAIN  
;; APPLICANT: HABUW, JEAN-FRANCOIS  
;; APPLICANT: LEGER, OLIVIER  
;; APPLICANT: BECK, ALAIN  
;; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
;; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
;; FILE REFERENCE: 017753-198  
;; CURRENT APPLICATION NUMBER: US/11/012,353  
;; CURRENT FILING DATE: 2004-12-16  
;; PRIOR APPLICATION NUMBER: 10/735,916  
;; PRIOR FILING DATE: 2003-12-16  
;; PRIOR APPLICATION NUMBER: FR 0308538  
;; PRIOR FILING DATE: 2003-07-11  
;; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
;; PRIOR FILING DATE: 2003-01-20  
;; PRIOR APPLICATION NUMBER: FR 0205753  
;; PRIOR FILING DATE: 2002-05-07  
;; PRIOR APPLICATION NUMBER: FR 0200653  
;; PRIOR FILING DATE: 2002-01-18  
;; PRIOR APPLICATION NUMBER: FR 0200654  
;; NUMBER OF SEQ ID NOS: 162  
;; SOFTWARE: PatentIn Ver. 3.3  
;; SEQ ID NO 67  
;; LENGTH: 131  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-012-353-67

Query Match 100.0%; Score 35; DB 7; Length 131;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNLY 7  
|||||||  
DB 74 KVSNNLY 80

RESULT 8  
US-10-821-234-1000  
;; Sequence 1000, Application US/10821234  
;; Publication No. US20050255114A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Labat, Ivan  
;; APPLICANT: Stache-Crain, Birgit  
;; APPLICANT: Andarmani, Susan  
;; APPLICANT: Tang, Y. Tom  
;; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
;; FILE REFERENCE: 821A  
;; CURRENT APPLICATION NUMBER: US/10/821,234  
;; CURRENT FILING DATE: 2004-04-07  
;; PRIOR APPLICATION NUMBER: US 60/462,047  
;; PRIOR FILING DATE: 2003-04-07  
;; NUMBER OF SEQ ID NOS: 1704  
;; SOFTWARE: pt\_seq\_genes Version 1.0  
;; SEQ ID NO 1000  
;; LENGTH: 488  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-821-234-1000

Query Match 85.7%; Score 30; DB 6; Length 488;  
Best Local Similarity 85.7%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
| | | | |  
Db 187 KYSNNRLY 193

## RESULT 9

US-10-467-657-4338  
; Sequence 4338, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 4338  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-4338

Query Match 80.0%; Score 28; DB 6; Length 232;  
Best Local Similarity 71.4%; Pred. No. 16;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
: | | | | |  
Db 211 RVNNRLY 217

## RESULT 10

US-11-108-172-631  
; Sequence 631, Application US/11108172  
; Publication No. US20050260177A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Jiang, Yuchu  
; APPLICANT: Smith, Carole L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Clapper, Jonathan D.  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedwick Thomas S.  
; APPLICANT: Carter, Darick  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.471C15  
; CURRENT APPLICATION NUMBER: US/11/108,172  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 10/025,380  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: US 09/922,217  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 09/833,263  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 09/649,811

; PRIOR FILING DATE: 2000-08-28  
; PRIOR APPLICATION NUMBER: US 09/609,448  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 09/575,251  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 09/519,444  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: US 09/504,629  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: US 09/480,321  
; PRIOR FILING DATE: 2000-01-10  
; PRIOR APPLICATION NUMBER: US 09/476,296  
; PRIOR FILING DATE: 1999-12-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 631  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-108-172-631

Query Match 77.1%; Score 27; DB 7; Length 168;  
Best Local Similarity 71.4%; Pred. No. 19;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
: | | | | |  
Db 137 RYSNNRLY 143

## RESULT 11

US-11-113-775A-1  
; Sequence 1, Application US/11113775A  
; Publication No. US20050261158A1  
; GENERAL INFORMATION:  
; APPLICANT: Kottwitz, Beatrix  
; APPLICANT: Pegelow, Ulrich  
; TITLE OF INVENTION: DETERGENT WITH RINSE SURFACTANT AND A SPECIAL ALPHA-AMYLASE  
; FILE REFERENCE: HENK-0124  
; CURRENT APPLICATION NUMBER: US/11/113,775A  
; CURRENT FILING DATE: 2005-04-25  
; PRIOR APPLICATION NUMBER: DE 102004020430.6  
; PRIOR FILING DATE: 2004-04-27  
; PRIOR APPLICATION NUMBER: DE 102004048591.7  
; PRIOR FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-11-113-775A-1

Query Match 77.1%; Score 27; DB 7; Length 483;  
Best Local Similarity 57.1%; Pred. No. 59;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
| : | | | | |  
Db 172 KLNNNRLY 178

## RESULT 12

US-11-113-775A-2  
; Sequence 2, Application US/11113775A  
; Publication No. US20050261158A1  
; GENERAL INFORMATION:  
; APPLICANT: Kottwitz, Beatrix  
; APPLICANT: Pegelow, Ulrich  
; TITLE OF INVENTION: DETERGENT WITH RINSE SURFACTANT AND A SPECIAL ALPHA-AMYLASE  
; FILE REFERENCE: HENK-0124  
; CURRENT APPLICATION NUMBER: US/11/113,775A



; CURRENT FILING DATE: 2005-04-25  
; PRIOR APPLICATION NUMBER: DE 102004020430.6  
; PRIOR FILING DATE: 2004-04-27  
; PRIOR APPLICATION NUMBER: DE 102004048591.7  
; PRIOR FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-11-113-775A-2

Query Match 77.1%; Score 27; DB 7; Length 483;  
Best Local Similarity 57.1%; Pred. No. 59;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
|:|:|:|  
Db 172 KLNRIY 178

## RESULT 13

US-11-113-799-1  
; Sequence 1, Application US/11113799  
; Publication No. US20050261156A1  
; GENERAL INFORMATION:  
; APPLICANT: Kottwitz, Beatriz  
; APPLICANT: Pegelow, Ulrich  
; TITLE OF INVENTION: DETERGENT WITH SULFO-POLYMER RINSE AID AND A SPECIAL  
; FILE REFERENCE: HENK-0123 / H 06113  
; CURRENT APPLICATION NUMBER: US/11/113,799  
; CURRENT FILING DATE: 2005-04-25  
; PRIOR APPLICATION NUMBER: DE 102004020431.4  
; PRIOR FILING DATE: 2004-04-27  
; PRIOR APPLICATION NUMBER: DE 102004048590.9  
; PRIOR FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Variant of Seq. ID No. 3  
US-11-113-799-1

Query Match 77.1%; Score 27; DB 7; Length 483;  
Best Local Similarity 57.1%; Pred. No. 59;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
|:|:|:|  
Db 172 KLNRIY 178

## RESULT 14

US-11-113-799-2  
; Sequence 2, Application US/11113799  
; Publication No. US20050261156A1  
; GENERAL INFORMATION:  
; APPLICANT: Kottwitz, Beatriz  
; APPLICANT: Pegelow, Ulrich  
; TITLE OF INVENTION: DETERGENT WITH SULFO-POLYMER RINSE AID AND A SPECIAL  
; FILE REFERENCE: HENK-0123 / H 06113  
; CURRENT APPLICATION NUMBER: US/11/113,799  
; CURRENT FILING DATE: 2005-04-25  
; PRIOR APPLICATION NUMBER: DE 102004020431.4  
; PRIOR FILING DATE: 2004-04-27  
; PRIOR APPLICATION NUMBER: DE 102004048590.9  
; PRIOR FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Variant of Seq. ID No. 3  
US-11-113-799-2

Query Match 77.1%; Score 27; DB 7; Length 483;  
Best Local Similarity 57.1%; Pred. No. 59;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
|:|:|:|  
Db 172 KLNRIY 178

## RESULT 15

US-10-630-203-12  
; Sequence 12, Application US/10630203  
; Publication No. US20050250663A1  
; GENERAL INFORMATION:  
; APPLICANT: Novozymes A/S  
; APPLICANT: Thisted, Thomas  
; APPLICANT: Kjaerulff, Soren  
; APPLICANT: Andersen, Carsten  
; APPLICANT: Fugleang, Claus Crone  
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties  
; FILE REFERENCE: 10062.200-US  
; CURRENT APPLICATION NUMBER: US/10/630,203  
; CURRENT FILING DATE: 2003-07-29  
; PRIOR APPLICATION NUMBER: US/09/918,543  
; PRIOR FILING DATE: 2001-07-31  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-10-630-203-12

Query Match 77.1%; Score 27; DB 6; Length 485;  
Best Local Similarity 57.1%; Pred. No. 60;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7  
|:|:|:|  
Db 172 KLNRIY 178

Search completed: December 30, 2005, 14:15:20  
Job time : 2.59677 secs

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OM protein - protein search, using sw model  
Run on: December 30, 2005, 14:26:51 ; Search time 193 Seconds  
(without alignments)  
16.807 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 49830

Minimum DB seq length: 7  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	7 ADJ76838	Adj76838 CDR seque
2	35	100.0	7	9 ADZ67008	Adz67008 Murine in
3	27	77.1	7	7 ADD94240	Add94240 Mouse HUI
4	26	74.3	7	6 ABP72121	Abp72121 Mouse FGF
5	26	74.3	7	7 ADD28189	Add28189 Mouse lec
6	26	74.3	7	7 ADD94239	Add94239 Mouse HUI
7	26	74.3	7	7 ADE36487	Ade36487 Mouse ant
8	26	74.3	7	7 ADL35323	Adl35323 Murine an
9	26	74.3	7	8 ADR68225	Adr68225 Murine 26
10	24	68.6	7	2 AAR75492	Aar75492 Mouse ant
11	24	68.6	7	2 AAW31748	Aaw31748 CDRL2 reg
12	24	68.6	7	2 AAW70921	Aaw70921 CDR2 of t
13	24	68.6	7	2 AAW70927	Aaw70927 CDR2 of t
14	24	68.6	7	2 AAW71895	Aaw71895 Anti-huma
15	24	68.6	7	3 AAY80282	Aay80282 Humanised
16	24	68.6	7	3 AAB12906	Aab12906 Anti-huma
17	24	68.6	7	3 AAB21365	Aab21365 Mouse ant
18	24	68.6	7	4 AAU07735	Aau07735 Human lig
19	24	68.6	7	4 AAG67671	Aag67671 Complemen
20	24	68.6	7	4 AAB97199	Aab97199 Murine an
21	24	68.6	7	5 ABP62375	Abp62375 Human imm
22	24	68.6	7	5 AAU70350	Aau70350 Mouse Kap
23	24	68.6	7	6 ABP58277	Abp58277 Murine mo
24	24	68.6	7	6 ABR40266	Abr40266 Murine pe

25	24	68.6	7	6 ABR39455	Ab39455 Anti-Abet
26	24	68.6	7	6 ABU08302	Abu08302 Mouse ant
27	24	68.6	7	6 ABR39783	Ab39783 Anti-Abet
28	24	68.6	7	6 AAG79999	Aag79999 Humanised
29	24	68.6	7	7 ADC03152	Adc03152 Colon spe
30	24	68.6	7	7 ADE27681	Ade27681 Mouse ant
31	24	68.6	7	7 ADD94149	Add94149 Mouse HUI
32	24	68.6	7	7 ADE94056	Ade94056 Anti-Abet
33	24	68.6	7	7 ADH61993	Adh61993 Mouse ant
34	24	68.6	7	8 ADH17765	Adh17765 Murine an
35	24	68.6	7	8 ADL35322	Adl35322 Human CD4
36	24	68.6	7	8 ADM61704	Adm61704 Humanised
37	24	68.6	7	8 ADM78082	Adm78082 Human SJB
38	24	68.6	7	8 ADM78106	Adm78106 Human SJB
39	24	68.6	7	8 ADM78124	Adm78124 Human SJB
40	24	68.6	7	8 ADM78130	Adm78130 Human SJB
41	24	68.6	7	8 ADP84868	Adp84868 Complemen
42	24	68.6	7	8 ADR19272	Adr19272 Glycosyla
43	24	68.6	7	8 ADS87340	Ads87340 Humanised
44	24	68.6	7	8 ADR68224	Adr68224 Murine 26
45	24	68.6	7	8 ADR68226	Adr68226 Murine 26

ALIGNMENTS

RESULT 1  
ADJ76838  
ID ADJ76838 standard; peptide; 7 AA.  
XX  
AC ADJ76838;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE CDR sequence for anti-IGF-1R antibody.  
XX  
KW cytostatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX  
OS Mus musculus.  
XX  
PN WO2003059951-A2.  
XX  
PD 24-JUL-2003.  
XX  
PF 20-JAN-2003; 2003WO-FR000178.  
XX  
PR 18-JAN-2002; 2002FR-00000653.  
PR 18-JAN-2002; 2002FR-00000654.  
PR 07-MAY-2002; 2002FR-00005753.  
XX  
PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
PI Goetsch L, Corvaia N, Leger O;  
XX  
DR WPI; 2003-569653/53.  
DR N-PSDB; ADJ76837.  
XX  
PT New antibodies that bind to human insulin-like growth factor receptor,  
XX useful for treatment, prevention and diagnosis of cancers.  
XX  
PS Claim 1; SEQ ID NO 4; 164pp; French.  
XX  
CC The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 35; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
 |||||  
 Db 1 KVSNNRLY 7

RESULT 2

ID ADZ67008  
 XX ADZ67008 standard; peptide; 7 AA.

AC ADZ67008;

XX 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:4.

KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

OS US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFLO/) DUFLOS A.

PA (HAEU/) HAEUW J.

PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

DR N-PSDB; ADZ67007.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

PT antibody or its functional fragment, being capable of binding human IGF-

PT IR and specifically inhibiting tyrosine kinase activity of receptor,

PT useful for treating cancer.

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-1R and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-1R and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-1R and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-1R and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 35; DB 9; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
 |||||  
 Db 1 KVSNNRLY 7

RESULT 3

ADD94240

ID ADD94240 standard; peptide; 7 AA.

XX ADD94240;

XX 29-JAN-2004 (first entry)

XX Mouse HUI77 mutant light chain CDR amino acid sequence SeqID125.

XX grafted antibody; complementarity determining region; CDR; light CDR;  
 KW heavy CDR; cryptic collagen epitope; solid tumour;  
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
 KW collagen agonist; collagen antagonist; cancer metastasis;  
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;  
 KW mutant; mutein.

XX Synthetic.

OS Mus musculus.

XX WO2003046204-A2.

XX 05-JUN-2003.

XX 26-NOV-2002; 2002WO-US038147.

XX 26-NOV-2001; 2001US-00995529.

XX 06-DEC-2001; 2001US-00011250.

PA (CELL-) CELL MATRIX INC.  
 XX Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;  
 XX WPI; 2003-513649/48.  
 XX  
 XX New cryptic collagen antibody with one or more complementarity  
 PT determining regions, useful for diagnosing and treating disorders  
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
 XX  
 XX Claim 24; SEQ ID NO 125; 232pp; English.  
 XX  
 XX This invention relates to a novel grafted antibody or its functional  
 CC fragment comprising one or more complementarity determining regions  
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
 CC acid (aa) substitution where the antibody has specific binding activity  
 CC for a cryptic collagen epitope. The growth of all solid tumours requires  
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
 CC to limiting tumour growth. The invention may allow development of  
 CC therapeutics with a cytostatic activity as a collagen agonist or  
 CC antagonist. The invention is useful for diagnosing and treating disorders  
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
 CC present sequence is the amino acid sequence of a mutant mouse anti-  
 CC cryptic collagen site antibody HUI77 variable region light chain CDR  
 CC which may be used during the creation of an antibody of the invention.  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 77.1%; Score 27; DB 7; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KVSNNRLY 7  
 DB 1 KVSNNRPF 7  
 RESULT 4  
 ID ABP72121 standard; peptide; 7 AA.  
 XX  
 AC ABP72121;  
 XX  
 XX 03-JUN-2003 (first entry)  
 DT  
 XX Mouse FGF-8 related protein CDR2 SEQ ID 9.  
 DE  
 XX Mouse; humanised; antibody; fibroblast growth factor 8; FGF8; cytostatic;  
 KW cancer; prostate; breast; ovarian; testicular; CDR2.  
 XX  
 XX Mus musculus.  
 OS  
 XX WO2003002608-A1.  
 PN  
 XX 09-JAN-2003.  
 PD  
 XX 28-JUN-2002; 2002WO-JP006591.  
 PF  
 XX 28-JUN-2001; 2001JP-00196176.  
 PR  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Shitara K, Nakamura K, Hirota M, Shimada N;  
 PI  
 XX WPI; 2003-239169/23.  
 DR  
 XX Humanised antibodies and antibody fragments reacting with fibroblast  
 PT growth factor 8 useful for the treatment and diagnosis of cancer.  
 XX  
 XX Claim 3; Page 69; 86pp; Japanese.  
 PS  
 XX The invention relates to novel humanised antibodies and antibody  
 CC fragments which react with fibroblast growth factor 8 (FGF8) and inhibit

CC its biological functions. The polypeptides of the invention have  
 CC cytostatic activity. The antibody is useful for the treatment of cancer,  
 CC including prostate, breast, ovarian and testicular cancer. The present  
 CC sequence is used in the exemplification of the invention  
 XX  
 XX Sequence 7 AA;  
 Query Match 74.3%; Score 26; DB 6; Length 7;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVSNNRL 6  
 DB 1 KVSNNRI 6  
 RESULT 5  
 ID ADD28189 standard; peptide; 7 AA.  
 XX  
 AC ADD28189;  
 XX  
 XX 15-JAN-2004 (first entry)  
 DT  
 XX Mouse lectin tolerance related peptide SEQ ID NO:22.  
 DE  
 XX mouse; antibody; lectin; sugar; N-acetylglucosamine;  
 KW Fc gamma receptor IIa; cytostatic; antiallergic; immunomodulator;  
 KW cardiant; virucide; antibacterial; tumour; allergy; inflammation;  
 KW autoimmune disease; circulatory system; viral infection;  
 KW bacterial infection.  
 XX  
 OS Mus musculus.  
 XX  
 XX WO2003084570-A1.  
 PN  
 XX 16-OCT-2003.  
 PD  
 XX 09-APR-2003; 2003WO-JP004505.  
 PF  
 XX 09-APR-2002; 2002JP-00106951.  
 PR  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Nakamura K, Shitara K, Hatanaka S, Niwa R, Okazaki A;  
 PI  
 XX WPI; 2003-812677/76.  
 DR  
 XX Drugs containing antibody compositions produced by cells tolerant to  
 PT lectin recognizing specific sugar-chain structure, appropriate for  
 PT patients suffering from Fc gammaRIIa polymorphism e.g. in treating  
 PT tumors.  
 XX  
 XX Example 3; SEQ ID NO 22; 214pp; Japanese.  
 XX  
 XX The invention relates to a novel drug containing as the active ingredient  
 CC an antibody composition produced by cells tolerant to a lectin  
 CC recognising a sugar-chain structure in which an alpha-bond is formed  
 CC between the 6-position of N-acetylglucosamine at the reducing end of an N  
 CC -glycoside bond-type complex sugar chain and the 1-position of fucose,  
 CC which has affinity to human Fc gamma receptor IIa. A drug of the  
 CC invention has cytostatic, antiallergic, immunomodulator, cardiant,  
 CC virucide, and antibacterial activity. The drugs are useful in screening  
 CC and treating patients not suitable for drugs not derived from these  
 CC cells, particularly as diagnostics, preventives or remedies for diseases  
 CC accompanying tumour, allergy or inflammation, autoimmune diseases,  
 CC diseases of the circulatory system, and viral or bacterial infections.  
 CC The present sequence is used in the exemplification of the invention.  
 XX  
 XX Sequence 7 AA;  
 Query Match 74.3%; Score 26; DB 7; Length 7;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;

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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVS NRL 6
Db 1 KVS NRI 6

RESULT 6
ADD94239
ID ADD94239 standard; peptide; 7 AA.
AC ADD94239;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse HUI77 mutant light chain CDR amino acid sequence SeqID124.
XX
KW grafted antibody; complementarity determining region; CDR; light CDR;
KW heavy CDR; cryptic collagen epitope; solid tumour;
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW collagen agonist; collagen antagonist; cancer metastasis;
KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
KW mutant; mutein.
XX
OS Synthetic.
OS Mus musculus.
XX
PN WO2003046204-A2.
XX
PD 05-JUN-2003.
XX
PF 26-NOV-2002; 2002WO-US038147.
XX
PR 26-NOV-2001; 2001US-0095529.
XX
PR 06-DEC-2001; 2001US-00011250.
XX
PA (CELL-) CELL MATRIX INC.
XX
PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX
DR WPI; 2003-513649/48.
XX
PT New cryptic collagen antibody with one or more complementarity
PT determining regions, useful for diagnosing and treating disorders
PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX
PS Claim 24; SEQ ID NO 124; 232pp; English.
XX
CC This invention relates to a novel grafted antibody or its functional
CC fragment comprising one or more complementarity determining regions
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
CC acid (aa) substitution where the antibody has specific binding activity
CC for a cryptic collagen epitope. The growth of all solid tumours requires
CC new blood vessel growth, angiogenesis, inhibition of which is an approach
CC to limiting tumour growth. The invention may allow development of
CC therapeutics with a cytostatic activity as a collagen agonist or
CC antagonist. The invention is useful for diagnosing and treating disorders
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
CC present sequence is the amino acid sequence of a mutant mouse anti-
CC cryptic collagen site antibody HUI77 variable region light chain CDR
CC which may be used during the creation of an antibody of the invention.
XX
SQ Sequence 7 AA;

Query Match 74.3%; Score 26; DB 7; Length 7;
Best Local Similarity 71.4%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVS NRL 7
Db 1 KVS NRI 7

```

```

RESULT 7
ADE36487
ID ADE36487 standard; peptide; 7 AA.
XX
AC ADE36487;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse anti-FGF-8 antibody-related peptide #5.
XX
KW arthritis; anti-FGF-8; sic fibroblast growth factor;
KW cartilage protection agent; joint destruction inhibitor;
KW synovial proliferation inhibitor; mouse; murine.
XX
OS Mus musculus.
XX
PN WO2003057251-A1.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-JP013650.
XX
PR 28-DEC-2001; 2001JP-00400677.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Tamura T, Uchii M, Suda T, Miki I, Tanaka A;
XX
DR WPI; 2003-587078/55.
XX
PT Treatment and prevention of arthritis comprising the use of anti-FGF-8
PT (sic fibroblast growth factor) antibody.
XX
PS Claim 11; SEQ ID NO 11; 193pp; Japanese.
XX
CC The invention comprises a method for treating and preventing arthritis,
CC the method involves the use of anti-FGF-8 (sic fibroblast growth factor)
CC antibody. The antibody and method of the invention is useful for: the
CC detection, treatment and prevention of arthritis; as a cartilage
CC protection agent; as a joint destruction inhibitor; and as a synovial
CC proliferation inhibitor. The present amino acid sequence represents a
CC mouse peptide that was used in an example of the invention.
XX
SQ Sequence 7 AA;

Query Match 74.3%; Score 26; DB 7; Length 7;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVS NRL 6
Db 1 KVS NRI 6

RESULT 8
ADL35323
ID ADL35323 standard; peptide; 7 AA.
XX
AC ADL35323;
XX
DT 20-MAY-2004 (first entry)
XX
DE Murine anti-Fc gamma receptor IIIa antibody-related peptide - SEQ 80.
XX
KW antibody binding; Fc gamma receptor IIIa; Fc region sugar chain;
KW cytostatic; anti-allergic; anti-inflammatory; immunosuppressive;
KW vasotropic; virucide; cancer; allergy; inflammatory; autoimmune;
KW circulatory; viral infection; murine; mouse.
XX
OS Mus musculus.
XX
PN WO2003085119-A1.
XX

```

PD 16-OCT-2003.  
 XX 09-APR-2003; 2003WO-JP004504.  
 XX 09-APR-2002; 2002JP-00106950.  
 PR (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Nakamura K, Shitara K;  
 PI WPI; 2003-812729/76.  
 XX Method of enhancing the binding activity of antibody to Fc-gamma receptor  
 PT IIIa for production of antibodies with high cytotoxicity as cancer,  
 PT allergic, viral and other disease therapeutic agents.  
 XX Example 14; SEQ ID NO 80; 296pp; Japanese.  
 XX The invention relates to a novel method for enhancing the binding  
 CC activity of an antibody to the Fc-gamma receptor IIIa by increasing the  
 CC proportion of N-glycoside bond type complex sugar chains attached to the  
 CC Fc region of the antibody which do not have the 1-position of fucose  
 CC bound to the 6-position of N-acetylglucosamine at the reducing end of the  
 CC sugar chain. The method of the invention has cytostatic, antiallergic,  
 CC antiinflammatory, immunosuppressive, vasotropic and virucide applications  
 CC and may be useful for generating antibodies to be used in the treatment,  
 CC prevention and diagnosis of diseases including cancer, allergies,  
 CC inflammatory disorders, autoimmune diseases, circulatory disorders and  
 CC viral infections. The current sequence is that of an anti-Fc-gamma  
 CC receptor IIIa antibody-related peptide of the invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 74.3%; Score 26; DB 7; Length 7;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 KVSNNRL 6  
 Db 1 KVSNNRI 6  
 RESULT 9  
 ADR68225  
 ID ADR68225 standard; peptide; 7 AA.  
 XX  
 AC ADR68225;  
 XX 18-NOV-2004 (first entry)  
 DT Murine 266 antibody light chain CDR2 variant #2.  
 XX antibody; neuroprotective; nootropic; antibody therapy; antigen-binding;  
 XX light chain; heavy chain; human; amyloid-beta peptide;  
 KW complementarity determining region; Alzheimer's disease; murine;  
 KW humanised antibody.  
 XX  
 OS Mus sp.  
 XX WO2004071408-A2.  
 XX 26-AUG-2004.  
 PD 06-FEB-2004; 2004WO-US002004.  
 XX 10-FEB-2003; 2003US-0446380P.  
 PR (MOLE-) APPLIED MOLECULAR EVOLUTION INC.  
 PA Davies J, Tang Y, Watkins JD;  
 XX WPI; 2004-625759/60.  
 DR  
 XX

PT New humanized antibody or its antigen-binding portion that specifically  
 PT binds human amyloid-beta peptide, useful in the manufacture of a  
 PT medicament for treating Alzheimer's disease.  
 XX Claim 1; SEQ ID NO 24; 58pp; English.  
 XX The invention relates to an antibody, or its antigen-binding portion,  
 CC comprising a light chain and a heavy chain that specifically binds human  
 CC amyloid-beta (A-beta) peptide. The new antibody or its antigen-binding  
 CC portion that specifically binds human A-beta comprises a light chain and a  
 CC heavy chain. The light chain comprises a light chain: complementarity  
 CC determining region 1 (CDR1) comprising amino acid sequences ADR68208-  
 CC ADR68223; CDR2 comprising amino acid sequences ADR68229-ADR68237. The heavy chain  
 CC comprises a heavy chain: CDR1 comprising amino acid sequences ADR68238-  
 CC ADR68239; CDR2 comprising amino acid sequences ADR68240-ADR68269; and  
 CC CDR3 comprising amino acid sequences ADR68270-ADR68277, provided that the  
 CC antibody does not comprise: a light chain CDR1 comprising the sequence  
 CC ADR68208; a light chain CDR2 comprising the sequence ADR68224; a light  
 CC chain CDR3 comprising the sequence ADR68229; a heavy CDR1 comprising the  
 CC sequence ADR68238; a heavy CDR2 comprising the sequence ADR68240; or a  
 CC heavy CDR3 comprising the sequence ADR68270. The antibody is useful in  
 CC the manufacture of a medicament for treating Alzheimer's disease. This  
 CC sequence corresponds to an example of the CDR2 from the murine 266  
 CC antibody light chain used to generate the humanised antibody of the  
 CC invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 74.3%; Score 26; DB 8; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 KVSNNRL 7  
 Db 1 KVSNNRF 7  
 RESULT 10  
 AAR75492  
 ID AAR75492 standard; peptide; 7 AA.  
 XX  
 AC AAR75492;  
 XX 07-FEB-1996 (first entry)  
 DT Mouse antibody variable region CDR2 peptide #5.  
 XX  
 DE Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;  
 XX antibody; immunotolerance; animal; variegated display library; CDR;  
 KW variable region; antigen; immunorecessive; cell surface marker; foetal;  
 KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;  
 KW familial hypercholesterolaemia; binding affinity;  
 KW complementarity determining region.  
 XX  
 OS Synthetic.  
 XX WO9515982-A2.  
 XX 15-JUN-1995.  
 PD 08-DEC-1994; 94WO-US014106.  
 XX 08-DEC-1993; 93US-00164022.  
 PR 06-DEC-1994; 94US-00350400.  
 XX (GENZ ) GENZYME CORP.  
 PA Barsomian G, Copeland DP, Hillhouse D, Johnson T;  
 XX WPI; 1995-224291/29.  
 DR  
 XX Generating new antibodies specific for immunorecessive epitopes - by  
 PT

PT selection from variegated V gene library cloned from immuno:tolerance  
 PT derived antibody repertoire, useful in diagnosis, purificn. and therapy,  
 PT e.g. of cancer.

XX Claim 75; Page 96; 109pp; English.

XX Peptides AAR75462-92 are examples of complementarity determining regions  
 CC (CDRs) used to generate antibodies against immunorecessive antigens. The  
 CC CDRs are derived from the heavy and light chain variable regions of the  
 CC antibodies FB3-2 (AAQ92500-1), F4-7 (AAQ92502-3) and H3-3 (AAQ92504-5).  
 CC The peptides AAR75488-92 represent CDR2 from the variable regions of the  
 CC above antibodies, used to generate a single variable region. The CDR  
 CC sequences were isolated from a variegated display library (VDL) of  
 CC variable regions derived from a repertoire of antibodies from an  
 CC immunocolerised animal. The VDL is generated by PCR amplifying the  
 CC variable regions from the antibody coding sequences using the primers  
 CC AAQ74153-74. The constructed antibodies are generated against an  
 CC immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or  
 CC stem cell, which can differentiate between variant or related forms of  
 CC the antigen. The antibodies generated can be used in the diagnosis, e.g.  
 CC detection of the immunorecessive antigen, or in therapy e.g. of cancer,  
 CC Alzheimer's disease or familial hypercholesterolaemia. The method of  
 CC production of the antibody allows rapid and sensitive isolation of  
 CC antibodies that would be difficult to isolate by standard methods. The  
 CC antibodies produced have greater binding affinity than those produced by  
 CC combinatorial/hybridoma methods

XX Sequence 7 AA;

Query Match 68.6%; Score 24; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5  
 |||||  
 Db 1 KVSNR 5

RESULT 11

AAW31748  
 ID AAW31748 standard; peptide; 7 AA.

XX AAW31748;

XX 15-APR-1998 (first entry)

XX CDRL2 region of L chain subunit of Fas specific antibody.

XX Fas; antibody; human; immunoglobulin; variable region; rheumatism;  
 KW autoimmune disease; rheumatoid arthritis; therapy; CDR; light chain;  
 KW complementarity determining region.

XX Synthetic.

XX EP799891-A1.

XX 08-OCT-1997.

XX 27-MAR-1997; 97EP-00302415.

XX 01-APR-1996; 96JP-00078570.

XX (SANY ) SANKYO CO LTD.

XX Serizawa N, Ichikawa K, Nakahara K, Yonehara S;

XX WPI; 1997-482673/45.

XX Anti-Fas recombinant antibodies - useful for treating auto-immune  
 PT diseases, especially rheumatoid arthritis.

XX Claim 10; Page 28; 72pp; English.

XX

CC This sequence represents a fragment of the protein of the invention. The  
 CC protein of the invention is a recombinant protein (A), that comprises at  
 CC least one region corresponding to an immunoglobulin (Ig) variable region  
 CC which enables the protein to recognise and specifically bind to an  
 CC antigen, preferably human Fas, and has substantially no more  
 CC immunogenicity in a human patient than a human antibody. The proteins are  
 CC useful for treating autoimmune diseases, especially rheumatism  
 CC (rheumatoid arthritis). (A) is based on a murine monoclonal antibody. As  
 CC the protein lacks the constant region, it has substantially no more  
 CC immunogenicity in the human patient than a human antibody

XX Sequence 7 AA;

Query Match 68.6%; Score 24; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5  
 |||||  
 Db 1 KVSNR 5

RESULT 12

AAW70921  
 ID AAW70921 standard; peptide; 7 AA.

XX AAW70921;

XX 14-OCT-1998 (first entry)

XX CDR2 of the light chain of monoclonal antibody RV-138.

XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
 KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;  
 KW viral infection; inhibit; fusion; protection; transcription;  
 KW antiviral agent; prophylaxis; diagnosis; infection; contamination.

XX Synthetic.

XX Mus sp.

XX FR2758331-A1.

XX 17-JUL-1998.

XX 14-JAN-1997; 97FR-00000300.

XX 14-JAN-1997; 97FR-00000300.

XX (UYBO-) UNIV BOURGOGNE.

XX WPI; 1998-390320/34.

XX New peptide(s) recognising viral epitope with tropism to mucosa - useful  
 PT for, e.g. diagnosing, preventing and treating viral infection(s).

XX Claim 12; Page 29; 51pp; French.

XX AAW70905-46 represent peptide sequences that can recognise, by antigen-  
 CC antibody type reactions, at least 1 epitope of a pathogenic virus having  
 CC tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR  
 CC regions of monoclonal antibodies specific for respiratory syncytial virus  
 CC (RSV). AAW70917-28 are analogous to CDR regions of monoclonal antibodies  
 CC specific for site III or IV of the VP6 protein of rota virus (RV). The  
 CC peptides can neutralise viral infections and may also inhibit fusion  
 CC between infected and uninfected cells or cells and viruses. They provide  
 CC passive or active protection and/or inhibit transcription of the virus,  
 CC so are useful as antiviral agents or for prophylaxis, in human or  
 CC veterinary medicine. The peptides can be labelled and used to diagnose  
 CC infection or contamination by the virus. The peptides are particularly  
 CC directed against RSV or RS but may also be used against papilloma, adeno,  
 CC entero, polio, influenza or immune deficiency viruses

XX Sequence 7 AA;

XX



```

Query Match      68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNR 5
      |||||
DB      1 KVSNR 5

RESULT 13
AAW70927
ID AAW70927 standard; peptide; 7 AA.
XX
AC AAW70927;
XX
XX
DT 14-OCT-1998 (first entry)
XX
DE CDR2 of the light chain of monoclonal antibody RV-133.
XX
KW Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
KW respiratory syncytial virus; RSV; VP6 protein; monoclonal antibody;
KW viral infection; inhibit; fusion; protection; transcription;
KW antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX
OS Synthetic.
OS Mus sp.
XX
XX
PN FR2758331-A1.
XX
PD 17-JUL-1998.
XX
PF 14-JAN-1997; 97FR-00000300.
XX
PR 14-JAN-1997; 97FR-00000300.
XX
PA (UYBO-) UNIV BOURGOGNE.
XX
XX
DR WPI; 1998-390320/34.
XX
PT New peptide(s) recognising viral epitope with tropism to mucosa - useful
PT for, e.g. diagnosing, preventing and treating viral infection(s).
XX
PS Claim 12; Page 31; 51pp; French.
XX
CC AAW70905-46 represent peptide sequences that can recognise, by antigen-
CC antibody type reactions, at least 1 epitope of a pathogenic virus having
CC tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR
CC regions of monoclonal antibodies specific for respiratory syncytial virus
CC (RSV). AAW70917-28 are analogous to CDR regions of monoclonal antibodies
CC specific for site III or IV of the VP6 protein of rota virus (RV). The
CC peptides can neutralise viral infections and may also inhibit fusion
CC between infected and uninfected cells or cells and viruses. They provide
CC passive or active protection and/or inhibit transcription of the virus,
CC so are useful as antiviral agents or for prophylaxis, in human or
CC veterinary medicine. The peptides can be labelled and used to diagnose
CC infection or contamination by the virus. The peptides are particularly
CC directed against RSV or RS but may also be used against papilloma, adeno,
CC entero, polio, influenza or immune deficiency viruses
XX
SQ Sequence 7 AA;

Query Match      68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNR 5
      |||||
DB      1 KVSNR 5

RESULT 14
AAW71895
ID AAW71895 standard; peptide; 7 AA.
XX
AC AAW71895;
XX
DT 18-JAN-1999 (first entry)
XX
DE Anti-human Fas monoclonal antibody CH11 light chain CDR2.
XX
KW Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
KW autoimmune disease; rheumatoid arthritis; therapy; human; mouse;
KW antibody engineering; complementarity determining region; CDR.
XX
OS Mus musculus.
XX
PN EP866131-A2.
XX
PD 23-SEP-1998.
XX
PF 20-MAR-1998; 98EP-00302113.
XX
PR 21-MAR-1997; 97JP-00067938.
XX
PA (SANY ) SANKYO CO LTD.
XX
PI Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;
XX
DR WPI; 1998-482965/42.
XX
PT Production of anti-Fas protein humanised antibodies - for use in inducing
PT apoptosis on Fas expressing cells in the treatment of autoimmune
PT diseases, especially rheumatoid arthritis.
XX
XX
PS Example 4; Page 53; 187pp; English.
XX
CC This peptide comprises complementarity determining region 2 (CDR2) of the
CC light chain variable region (see AAW71889) of the mouse anti-human Fas
CC monoclonal antibody CH11. CDR1 (see AAW71894) and CDR3 (see AAW71896)
CC have also been identified. The invention relates to novel humanised
CC antibodies comprising humanised light and heavy chains (see AAW71876-81)
CC of CH11. These humanised anti-human Fas antibodies are capable of
CC inducing apoptosis in cells expressing Fas (e.g. synovialocytes) and are
CC useful in the treatment of autoimmune disease and chronic rheumatoid
CC arthritis
XX
SQ Sequence 7 AA;

Query Match      68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNR 5
      |||||
DB      1 KVSNR 5

RESULT 15
AAW80282
ID AAW80282 standard; peptide; 7 AA.
XX
AC AAW80282;
XX
DT 30-MAY-2000 (first entry)
XX
DE Humanised anti-Fas antibody light chain CDR2 peptide SEQ ID NO:6.
XX
KW Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease;
KW diagnosis; CDR; complementarity determining region; apoptosis;
KW immunosuppressive.
XX
OS Homo sapiens.
OS Mus sp.
XX
PN JP2000014383-A.

```

XX 18-JAN-2000.  
PD  
XX  
XX 03-JUL-1998; 98JP-00204318.  
PF  
XX  
XX 03-JUL-1998; 98JP-00204318.  
PR  
XX  
XX (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
PA  
XX  
XX WPI; 2000-199626/18.  
DR  
XX  
XX Novel recombinant antibody used for treating and diagnosing autoimmune  
PT diseases - is humanized anti-fas antibody which controls and induces  
PT apoptosis in cells expressing fas antigen.  
XX  
XX  
XX Claim 5; Page 12; 25pp; Japanese.  
PS  
XX  
XX The present invention describes a recombinant antibody (A) which binds to  
CC fas antigen, and controls and induces apoptosis in cells which expressed  
CC fas antigen. The complementarity determining regions (CDR) of (A) contain  
CC amino acid sequences obtained from a mammal other than human, other  
CC regions contain amino acid sequences from human and they partly contain  
CC modified amino acids. (A) has immunosuppressive activity. (A) is used for  
CC treating and/or diagnosing autoimmune diseases. The present sequence  
CC represents a specifically claimed light chain CDR2 of (A)  
XX  
SQ Sequence 7 AA;  
Query Match 68.6%; Score 24; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;  
QY 1 KVSNR 5  
Db 1 KVSNR 5  
|||||

Search completed: December 30, 2005, 14:47:21  
Job time : 186 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 14:40:17 ; Search time 36 Seconds  
(without alignments)  
18.709 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 141

Minimum DB seq length: 7

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:.\*  
1: Piri:.\*  
2: Pir2:.\*  
3: Pir3:.\*  
4: Pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	37.1	7	2 A38081	amine oxidase (cop
2	11	31.4	7	2 S42620	aggreccan - bovine
3	11	31.4	7	2 A11483	aspartate transami
4	10	28.6	7	2 S17976	glucose isomerase
5	9	25.7	7	1 NYPG7	hypothalamic hepta
6	9	25.7	7	2 S19630	ribosomal protein
7	9	25.7	7	2 PQ0663	membrane protein -
8	9	25.7	7	2 A28709	phosphonoacetaldeh
9	9	25.7	7	2 PN0150	omega-gliadine 1'
10	9	25.7	7	2 S78024	ribosomal protein
11	9	25.7	7	2 PH0932	T-cell receptor be
12	9	25.7	7	2 A28340	myomodulin - Calif
13	9	25.7	7	2 ECMUCR	catch-relaxing pep
14	8	22.9	7	2 A60139	fatty-acid synthase
15	8	22.9	7	2 B39127	phosphotransferase
16	8	22.9	7	2 I40504	hypothetical prote
17	8	22.9	7	2 PT0520	T-cell receptor be
18	8	22.9	7	2 PT0521	T-cell receptor be
19	8	22.9	7	2 S45311	microcin C7 - Esch
20	7	20.0	7	1 A61324	dermorphin - Rohde
21	7	20.0	7	2 S71870	glutathione transf
22	7	20.0	7	2 S71867	glutathione transf
23	7	20.0	7	2 A60224	Met-enkephalin-Arg
24	7	20.0	7	2 S36662	dermorphin (lys-7)
25	7	20.0	7	2 S21230	dermorphin (Trp-4)
26	7	20.0	7	2 PH1602	Ig H chain V-D-J r
27	7	20.0	7	2 E33932	Ig mu chain D regi
28	7	20.0	7	2 PT0663	T-cell receptor be
29	7	20.0	7	2 PT0567	T-cell receptor be

30 7 20.0 7 2 PT0671 T-cell receptor be  
31 7 20.0 7 2 A58718 carnocin UI49 - Ca  
32 7 20.0 7 2 PC2370 probable H+-transp  
33 7 20.0 7 2 PC2132 FMRamide-related  
34 7 20.0 7 2 I56695 hypothetical L2 pr  
35 6 17.1 7 1 XEYDGD galactose oxidase  
36 6 17.1 7 2 JN0859 peptidyl-dipeptida  
37 6 17.1 7 2 PH1408 Ig heavy chain V r  
38 6 17.1 7 2 S16364 opacity protein P.  
39 6 17.1 7 2 S16365 opacity protein P.  
40 6 17.1 7 2 S38516 mabinlin II chain  
41 6 17.1 7 2 A34818 vicilin 72K chain  
42 6 17.1 7 2 H33098 180K exoantigen -  
43 6 17.1 7 2 A34026 acetylcholinestera  
44 6 17.1 7 2 I50210 gene C-rel protein  
45 6 17.1 7 2 C56793 platelet glycoprot

#### ALIGNMENTS

##### RESULT 1

A38081  
amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (*Pichia angusta*) (fragment)  
C;Species: *Pichia angusta*  
C;Date: 31-Dec-1993 #sequence\_revision 03-Feb-1994 #text\_change 20-Apr-2000  
C;Accession: A38081  
R;Ma, D.; Janes, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Klinman, J.P.  
J. Biol. Chem. 267, 7979-7982, 1992  
A;Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine  
A;Reference number: A38081; MUID:92235001; PMID:1569055  
A;Accession: A38081  
A;Molecule type: protein  
A;Residues: 1-7 <MUA>  
A;Cross-references: UNIPARC:UPI000017CA48  
C;Keywords: copper; oxidoreductase; quinoprotein; topaquinone  
F;4/Modified site: topaquinone (Tyr) #status experimental

Query Match 37.1%; Score 13; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSNRLY 7  
| : |  
DB 1 VANYEY 6

##### RESULT 2

S42620  
aggreccan - bovine (fragment)  
C;Species: *Bos primigenius taurus* (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C;Accession: S42620  
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.  
Matrix Biol. 14, 171-179, 1994  
A;Title: Aggreccan in bovine tendon.  
A;Reference number: S42620; MUID:94340214; PMID:7520336  
A;Accession: S42620  
A;Molecule type: protein  
A;Residues: 1-7 <VOG>  
A;Cross-references: UNIPARC:UPI000017C497  
A;Experimental source: flexor tendon  
C;Keywords: cartilage

Query Match 31.4%; Score 11; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSNR 5  
| : |  
DB 4 VSPR 7

```
RESULT 3
A11483
A:Alternate names: aspartate aminotransferase - sheep (fragment)
A:Alternate names: aspartate aminotransferase, mitochondrial
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
C:Accession: A11483
R:Campos-Cavieles, M.; Milstein, C.P.
Biochem. J. 147, 275-281, 1975
A:Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitoch
A:Reference number: A11483; MUID:76039441; PMID:1180894
A:Accession: A11483
A:Molecule type: protein
A:Residues: 1-7 <CAM>
A:Cross-references: UNIPARC:UPI000017C59C
A:Experimental source: liver
C:Keywords: aminotransferase, mitochondrion; phosphoprotein; pyridoxal phosphate
F:2/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LY 7
||
DB 6 LY 7

RESULT 4
S17976
Glucose isomerase - Thermoanaerobacterium saccharolyticum (fragment)
C:Species: Thermoanaerobacterium saccharolyticum
C:Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 09-Jul-2004
C:Accession: S17976
R:Lee, C.; Zeikus, J.G.
Biochem. J. 273, 565-571, 1991
A:Title: Purification and characterization of thermostable glucose isomerase from Clostr
A:Reference number: S15119; MUID:91144536; PMID:1996956
A:Accession: S17976
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-7 <LEE>
A:Cross-references: UNIPROT:P30435; UNIPARC:UPI0000173053
A:Note: the sequence from page 568 is inconsistent with that from page 565 in having 6-G
A:Note: the source is designated as Thermoanaerobacter strain B6A

Query Match 28.6%; Score 10; DB 2; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 NRLY 7
||
DB 2 NKIF 5

RESULT 5
NYPG7
hypothalamic heptapeptide - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A01417
R:Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong,
Horm. Metab. Res. 13, 228-232, 1981
A:Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasi
A:Reference number: A01417; MUID:81213960; PMID:6263778
A:Accession: A01417
A:Molecule type: protein
A:Residues: 1-7 <CHA>
A:Cross-references: UNIPROT:P01153; UNIPARC:UPI000012CFC6
C:Superfamily: hypothalamic heptapeptide
C:Keywords: hypothalamus

Query Match 25.7%; Score 9; DB 1; Length 7;
```

```
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LY 7
||
DB 2 IY 3

RESULT 6
S19630
ribosomal protein L30 - Streptomyces griseus (fragment)
C:Species: Streptomyces griseus
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Oct-2004
C:Accession: S19630
R:Ochi, K.
Int. J. Syst. Bacteriol. 42, 144-150, 1992
A:Title: Electrophoretic heterogeneity of ribosomal protein At-L30 among actinomycete ge
A:Reference number: S19630; MUID:92144363; PMID:1736962
A:Accession: S19630
A:Molecule type: protein
A:Residues: 1-7 <OCH>
A:Cross-references: UNIPARC:UPI0000177352
A:Experimental source: strain IFO 13189
C:Superfamily: Ribosomal protein L30p
C:Keywords: protein biosynthesis; ribosome

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVS 3
||
DB 4 KIT 6

RESULT 7
PQ0663
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C:Species: porcine epidemic diarrhea virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C:Accession: PQ0663
R:Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1795-1804, 1993
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
A:Reference number: JQ2191; MUID:93389433; PMID:8397280
A:Accession: PQ0663
A:Molecule type: mRNA
A:Residues: 1-7 <BRI>
A:Cross-references: UNIPARC:UPI0000170FAC; GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID:
C:Comment: This virus is coronavirus related to human coronavirus 229E.
C:Keywords: membrane protein

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KV 2
||
DB 2 KV 3

RESULT 8
A28709
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C:Species: Bacillus cereus
C:Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C:Accession: A28709
R:Olson, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A:Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence
A:Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence
A:Reference number: A28709; MUID:88241058; PMID:3132206
```

A;Accession: A28709

A;Status: Preliminary

A;Molecule type: protein

A;Residues: 1-7 <OLS>

A;Cross-references: UNIPARC:UPI000017AC8C

Query Match 25.7%; Score 9; DB 2; Length 7;

Best Local Similarity 25.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSN 4

Db 2 KIDH 5

#### RESULT 9

PN0150

omega-gliadine 1' - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PN0150

R;Odintsova, T.I.; Egorov, T.A.

Biokhimiia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0150

A;Molecule type: protein

A;Residues: 1-7 <ODI>

A;Cross-references: UNIPARC:UPI000017B0D2

A;Experimental source: strain K-907

Query Match 25.7%; Score 9; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SNRL 6

Db 1 SRQL 4

#### RESULT 10

S78024

ribosomal protein Yml21, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)

C;Species: Saccharomyces cerevisiae

C;Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 14-Nov-1997

C;Accession: S78024

R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma

Eur. J. Biochem. 245, 449-456, 1997

A;Title: Identification and characterization of the genes for mitochondrial ribosomal pr

A;Reference number: S78018; MUID:97296414; PMID:9151978

A;Accession: S78024

A;Molecule type: protein

A;Residues: 1-7 <KIT>

A;Cross-references: UNIPARC:UPI000017B33C

C;Genetics:

A;Genome: nuclear

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 25.7%; Score 9; DB 2; Length 7;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSNRL 6

Db 2 LXNLL 6

#### RESULT 11

PH0932

T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0932

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0932

A;Molecule type: mRNA

A;Residues: 1-7 <GOL>

A;Cross-references: UNIPARC:UPI000017C9E4

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 25.7%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RL 6

Db 6 RL 7

#### RESULT 12

A28340

myomodulin - California sea hare

C;Species: Aplysia californica (California sea hare)

C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004

C;Accession: A28340

R;Cropper, E.C.; Tenenbaum, R.; Kolkas, M.A.G.; Kupfermann, I.; Weiss, K.R.

Proc. Natl. Acad. Sci. U.S.A. 84, 5483-5486, 1987

A;Title: Myomodulin: A bioactive neuropeptide present in an identified cholinergic bucc

A;Reference number: A28340; MUID:87261010; PMID:3474664

A;Accession: A28340

A;Molecule type: protein

A;Residues: 1-7 <CRO>

A;Cross-references: UNIPROT:PI5513; UNIPARC:UPI000017BD99

Query Match 25.7%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RL 6

Db 6 RL 7

#### RESULT 13

ECMOCR

catch-relaxing peptide - blue mussel

N;Alternate names: CARP

C;Species: Mytilus edulis (blue mussel)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004

C;Accession: A29342

R;Hirata, T.; Kubota, I.; Takabatake, I.; Kawahara, A.; Shimamoto, N.; Muneoka, Y.

Brain Res. 422, 374-376, 1987

A;Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.

A;Reference number: A29342; MUID:88052022; PMID:3676797

A;Accession: A29342

A;Molecule type: protein

A;Residues: 1-7 <HIR>

A;Cross-references: UNIPROT:PI0420; UNIPARC:UPI0000126FB4

C;Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxa

C;Keywords: amidated carboxyl end; hormone; retractor muscle

F;7/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.7%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RL 6

Db 6 RL 7

#### RESULT 14

A60139  
 fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 26-May-2000  
 C:Accession: A60139  
 R:Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.  
 Biochim. Biophys. Acta 828, 380-382, 1985  
 A:Title: Amino acid sequence around the reactive serine residue of the thioesterase domain  
 A:Reference number: A60139; MUID:85175165; PMID:3921056  
 A:Accession: A60139  
 A:Molecule type: protein  
 A:Residues: 1-7 <HAR>  
 A:Cross-references: UNIPARC:UPI00001753A5  
 C:Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homologue  
 C:Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enzyme  
 P:5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental

Query Match 22.9%; Score 8; DB 2; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSNRLY 7  
 Db 1 VAGSY 6

RESULT 15  
 B39127  
 phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)  
 C:Species: Escherichia coli  
 C:Date: 27-Nov-1991 #sequence\_revision 27-Nov-1991 #text\_change 08-Oct-1999  
 C:Accession: B39127  
 R:Hardesty, C.; Ferran, C.; DiRienzo, J.M.  
 J. Bacteriol. 173, 449-456, 1991  
 A:Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sc  
 rin.  
 A:Reference number: A39127; MUID:91100329; PMID:1846143  
 A:Accession: B39127  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-7 <HAR>  
 A:Cross-references: UNIPARC:UPI0000170D6E; GB:M38416; NID:9155142; PIDN:AAA98418.1; PID:  
 C:Keywords: phosphotransferase

Query Match 22.9%; Score 8; DB 2; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVS 3  
 Db 5 QIS 7

Search completed: December 30, 2005, 14:52:02  
 Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:27:11 ; Search time 227 Seconds  
(without alignments)  
21.756 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNRLY 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 107

Minimum DB seq length: 7

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	42.9	7	2	O50556 ACTAC
2	12	34.3	7	2	Q65578 9ALPH
3	11	31.4	7	1	ALL7 CYDPO
4	11	31.4	7	1	FAR1_PROCL
5	11	31.4	7	1	UN06 PINPS
6	11	31.4	7	2	Q9YI09 ADE04
7	11	31.4	7	2	Q9YI00 ADE07
8	11	31.4	7	2	Q9YVE3 ADE07
9	11	31.4	7	2	Q9YQ10 SCORO
10	11	31.4	7	2	Q99182 9SMEG
11	10	28.6	7	2	F83492 BIOCC
12	10	28.6	7	2	Q95945 YEAST
13	9	25.7	7	1	CARP MYTED
14	9	25.7	7	1	E105_LITRU
15	9	25.7	7	1	HY7_FIG
16	9	25.7	7	2	P92210 AGRCR
17	9	25.7	7	2	P92214 9POAL
18	9	25.7	7	2	P92218 9POAL
19	9	25.7	7	2	P92221 BROIN
20	9	25.7	7	2	P92226 CRIDE
21	9	25.7	7	2	P92372 9FOAL
22	9	25.7	7	2	P92381 9FOAL
23	9	25.7	7	2	P92385 HORWA
24	9	25.7	7	2	P92387 9POAL
25	9	25.7	7	2	P92390 HETAPI
26	9	25.7	7	2	P92393 HORVU
27	9	25.7	7	2	P92403 LOPEL
28	9	25.7	7	2	P92421 PSAFR
29	9	25.7	7	2	P92425 PSEPI
30	9	25.7	7	2	P92427 PERICTYON
31	9	25.7	7	2	P92430 AEGTIA

32	9	25.7	7	2	P92440 THIBE
33	9	25.7	7	2	P92442 TARC
34	9	25.7	7	2	Q47029 ENTCL
35	9	25.7	7	2	Q8GL04 BORBU
36	9	25.7	7	2	Q8GL12 BORBU
37	9	25.7	7	2	P70804 AZOVI
38	8	22.9	7	1	IPYR CANAL
39	8	22.9	7	1	UF04 MOUSE
40	8	22.9	7	2	Q15903 HUMAN
41	8	22.9	7	2	Q47505 ECOLI
42	8	22.9	7	2	O55184 RAT
43	8	22.9	7	2	Q63480 RAT
44	7	20.0	7	1	ALL2 CARMA
45	7	20.0	7	1	ALL3 CARMA

P92440	thinopyrum
P92442	taeniatheru
Q47029	enterobacte
Q8GL04	borrelia bu
Q8GL12	borrelia bu
P70804	azotobacter
P83777	candida alb
P83642	mus musculu
Q15903	homo sapien
Q47505	escherichia
O55184	rattus norv
Q63480	rattus norv
P81805	carcinus ma
P81806	carcinus ma

#### ALIGNMENTS

##### RESULT 1

O50556 ACTAC  
ID O50556 ACTAC PRELIMINARY; PRT; 7 AA.

AC O50556;

DT 01-JUN-1998 (T-EMBLrel. 06, Created)

DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)

DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)

DE GlyA (Fragment).

GN Name=glyA;

OS Actinobacillus actinomycetemcomitans (Haemophilus

actinomycetemcomitans).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Actinobacillus.

OX NCBI\_TaxID=714;

RN [1]

RP NUCLEOTIDE SEQUENCES.

RC STRAIN=ATCC 33384;

RX MEDLINE=96355846; PubMed=8751884;

RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,

RA Craig E.;

RT "cis Elements and trans factors are both important in strain-specific

regulation of the leukotoxin gene in Actinobacillus

actinomycetemcomitans";

RL Infect. Immun. 64:3451-3460(1996).

DR ENBL; US1862; AAB88721.1; -; Genomic\_DNA.

FT NON TER 1 1

SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 42.9%; Score 15; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NRL 6

Db 1 NRL 3

##### RESULT 2

Q65578 9ALPH  
ID Q65578 9ALPH PRELIMINARY; PRT; 7 AA.

AC Q65578;

DT 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein (fragment).

OS Bovine herpesvirus 1.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicellovirus.

OX NCBI\_TaxID=10320;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Cooper;

RX MEDLINE=95313343; PubMed=7793062;

RA Vicek C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,

RA Letchworth G.J., Schwyz M.;  
 RT "Nucleotide sequence analysis of a 30-kb region of the bovine  
 RT herpesvirus 1 genome which exhibits a colinear gene arrangement with  
 RT the UL21 to UL4 genes of herpes simplex virus.";  
 RL Virology 210:100-108(1995).  
 DR EMBL; 248053; CAA88130.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 758 MW; 6DD33455B1F1B1C0 CRC64;  
 Query Match 34.3%; Score 12; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SNR 5  
 Db 4 SNK 6  
 RESULT 3  
 ALL7\_CYDPO STANDARD; PRT; 7 AA.  
 ID ALL7\_CYDPO  
 AC P82158;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Cydiastatin-7.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysa;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829; DOI=10.1016/S0196-9781(97)00188-5;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: Belongs to the allatostatin family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 873 MW; 672879CAB8569350 CRC64;  
 Query Match 31.4%; Score 11; DB 1; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 2.2e+06;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 RLY 7  
 Db 1 KMY 3  
 RESULT 4  
 FARI\_PROCL STANDARD; PRT; 7 AA.  
 ID FARI\_PROCL  
 AC P38459;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cardioexcitatory FMRamide homolog NF1.  
 OS Procamburus clarkii (Red swamp crayfish).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

OC Astacoidea; Cambaridae; Procamburus.  
 OX NCBI\_TaxID=6728;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=93248032; PubMed=8387183; DOI=10.1016/0196-9781(93)90021-8;  
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
 RT "Isolation of two FMRamide-related peptides from crayfish pericardial  
 RT organs.";  
 RL Peptides 14:137-143(1993).  
 CC -|- FUNCTION: Increases the rate and amplitude of spontaneous  
 CC contractions of semi-isolated hearts. Increases the amplitude of  
 CC excitatory postsynaptic potentials in abdominal extensor muscle.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;  
 Query Match 31.4%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 NR 5  
 Db 1 NR 2  
 RESULT 5  
 UN06\_PINPS STANDARD; PRT; 7 AA.  
 ID UN06\_PINPS  
 AC P81675;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Unknown protein from 2D-PAGE of needles (N141) (Fragment).  
 OS Pinus pinaster (Maritime pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RX DOI=10.1002/(SICI)1522-2683(19990101)20:4<1098::AID-ELPS1098>3.3.CO;2-Q;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Flomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 6.6, its MW is: 25 kDa.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 KW Direct protein sequencing.  
 FT NON\_TER 1  
 FT NON\_TER 7  
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;  
 Query Match 31.4%; Score 11; DB 1; Length 7;



Best Local Similarity 100.0%; Pred. No. 2.2e+06; Mismatches 0; Indels 0; Gaps 0;

QY 6 LY 7  
DB 1 LY 2

RESULT 6  
Q9YIQ9\_ADE04  
ID Q9YIQ9\_ADE04 PRELIMINARY; PRT; 7 AA.  
AC Q9YIQ9;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE PVI core protein (Fragment).  
GN Name=pVI;  
OS Human adenovirus 4 (HAdV-4).  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=28280;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2-G T95-873;  
RX MEDLINE=99175282; PubMed=10074533;  
RA Crawford-Mikszta L.K.; Nang R.N.; Schnurr D.P.;  
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease."  
RL J. Clin. Microbiol. 37:1107-1112(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2-G T95-873;  
RA Crawford-Mikszta L.K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF065064; AAD03659.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 RLY 7  
DB 5 RCY 7

RESULT 7  
Q9YI09\_ADE07  
ID Q9YI09\_ADE07 PRELIMINARY; PRT; 7 AA.  
AC Q9YI09;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE PVI core protein (Fragment).  
GN Name=pVI;  
OS Human adenovirus type 7a.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=85755;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Kn T96-0620;  
RX MEDLINE=99175282; PubMed=10074533;  
RA Crawford-Mikszta L.K.; Nang R.N.; Schnurr D.P.;  
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease."  
RL J. Clin. Microbiol. 37:1107-1112(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Kn T96-0620;  
RA Crawford-Mikszta L.K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF065068; AAD03668.1; -; Genomic\_DNA.  
FT NON\_TER 1 1

SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 RLY 7  
DB 5 RCY 7

RESULT 8  
Q9YVE3\_ADE07  
ID Q9YVE3\_ADE07 PRELIMINARY; PRT; 7 AA.  
AC Q9YVE3;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PVI core protein (Fragment).  
GN Name=pVI;  
OS Human adenovirus 7 (HAdV-7).  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=10519;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Gomen;  
RX MEDLINE=99175282; PubMed=10074533;  
RA Crawford-Mikszta L.K.; Nang R.N.; Schnurr D.P.;  
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease."  
RL J. Clin. Microbiol. 37:1107-1112(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Gomen;  
RA Crawford-Mikszta L.K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF065065; AAD03662.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 RLY 7  
DB 5 RCY 7

RESULT 9  
Q9YQ10\_9COCO  
ID Q9YQ10\_9COCO PRELIMINARY; PRT; 7 AA.  
AC Q9YQ10;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical fusion protein.  
OS Transmissible gastroenteritis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; Group 1 species.  
OX NCBI\_TaxID=11149;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=88078100; PubMed=2825819; DOI=10.1016/0300-9084(87)90178-7;  
RA Raeschaert D., Gelfi J., Laude H.;  
RT "Enteric coronavirus TGEV: partial sequence of the genomic RNA, its organization and expression."  
RL J. Clin. Microbiol. 37:591-600(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=95159435; PubMed=7856095;  
RA Eleouet J., Raeschaert D., Lambert P., Levy L., Laude H.;  
RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1

```

RT of transmissible gastroenteritis virus.";
RL Virology 206:817-822(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99099045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Piana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes.";
RL J. Virol. 73:1535-1545(1999).
DR EMBL; AJ011482; CAA09625.1; -; Genomic_RNA.
KW Hypothetical protein.
SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LY 7
DB 2 LY 3

RESULT 10
O99182_9SMEG
ID O99182_9SMEG PRELIMINARY; PRT; 7 AA.
AC O99182;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN Name=COI;
OS Gnatholebias zonatus.
OG Mitochondrion.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
OX NCBI_TaxID=135316;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20072928; PubMed=10603257; DOI=10.1006/mpev.1999.0656;
RA Murphy W.J., Thomerson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT sequences.";
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002591; AAD01074.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LY 7
DB 2 LY 3

RESULT 11
P83492_BIOOC
ID P83492_BIOOC PRELIMINARY; PRT; 7 AA.
AC P83492;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).
OS Bionectria ochroleuca (Gliocladium roseum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.

```

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OX NCBI_TaxID=29856;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=Gr87;
RA Zhao M., Zhang K.;
RL Submitted (DSC-2002) to Swiss-Prot.
CC -!- FUNCTION: Acts as a serine protease.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR InterPro; IPR000209; Pept_S8_S53.
DR PROSITE; PS00136; SUBTILASE_ASF; PARTIAL.
DR PROSITE; PS00137; SUBTILASE_HIS; PARTIAL.
DR PROSITE; PS00138; SUBTILASE_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 688 MW; 776DD455A6C1ADB0 CRC64;

Query Match 28.6%; Score 10; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SN 4
DB 4 SN 5

RESULT 12
Q95945_YEAST
ID Q95945_YEAST PRELIMINARY; PRT; 7 AA.
AC Q95945;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inside intron 5 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=D273-10B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system. Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24066.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 28.6%; Score 10; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVS 3
DB 5 KLS 7

RESULT 13
CARP_MYED
ID CARP_MYED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Catch-relaxing peptide (CARP).

```

OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.  
RN NCBI\_TaxID=6550;  
[1]  
PROTEIN SEQUENCE.  
RX MEDLINE=88052022; PubMed=3676797;  
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,  
RA Muneoka Y.;  
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";  
RL Brain Res. 422:374-376(1987).  
CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)  
CC and inhibitory (relaxation) effects on the anterior byssus  
CC retractor muscle.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC PIR; A29342; ECMUCR.  
DR Amidation; Direct protein sequencing; Hormone.  
KW Leucine amide.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;  
  
Query Match 25.7%; Score 9; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RL 6  
Db 6 RL 7  
  
RESULT 14  
EI05 LITRU STANDARD; PRT; 7 AA.  
ID P82101;  
AC P82101;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SRP-2005 (Rel. 48, Last annotation update)  
DE Electrin-5.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylinae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
PROTEIN SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin glands.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC Amidation; Amphibian defense peptide; Direct protein sequencing.  
KW MOD RES 7  
FT Alanine amide.  
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;  
  
Query Match 25.7%; Score 9; DB 1; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.2e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LY 7  
Db 1 IY 2  
  
RESULT 15  
HY7 PIG STANDARD; PRT; 7 AA.  
ID HY7 PIG  
AC P01153;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Hypothalamic heptapeptide.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
PROTEIN SEQUENCE, AND SYNTHESIS.  
RX MEDLINE=81213980; PubMed=6263778;  
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,  
RA Saifran M., Kong A., Hamilton J.W., Conn D.V., Schally A.V.;  
RT "Isolation, structure and synthesis of a heptapeptide with in vitro  
RT ACTH-releasing activity from porcine hypothalamus.";  
RL Horm. Metab. Res. 13:228-232(1981).  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC PIR; A01417; NYPG7.  
DR Direct protein sequencing.  
KW SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;  
  
Query Match 25.7%; Score 9; DB 1; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.2e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 LY 7  
Db 2 IY 3  
  
Search completed: December 30, 2005, 14:51:14  
Job time : 229 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:44:07 ; Search time 45 Seconds  
(without alignments)  
12.861 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 17689

Minimum DB seq length: 7

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*
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- 4: /cgn2\_6/prodata/1/iaa/PTUS COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	68.6	7	1	US-08-053-171-28
2	24	68.6	7	1	US-08-560-558B-30
3	24	68.6	7	2	US-09-217-268B-30
4	24	68.6	7	2	US-09-563-222C-30
5	24	68.6	7	2	US-09-914-695-22
6	24	68.6	7	2	US-09-518-737-9
7	21	60.0	7	1	US-08-244-626-6
8	20	57.1	7	2	US-10-226-795-29
9	19	54.3	7	2	US-09-563-222C-9
10	19	54.3	7	2	US-09-254-180C-5
11	19	54.3	7	2	US-09-724-409-4
12	19	54.3	7	2	US-09-724-530-4
13	19	54.3	7	2	US-09-623-548A-654
14	19	54.3	7	2	US-09-657-276-654
15	19	54.3	7	2	US-09-328-296-4
16	18	51.4	7	2	US-09-128-572-47
17	18	51.4	7	2	US-09-782-385A-47
18	17	48.6	7	1	US-08-672-610A-23
19	17	48.6	7	1	US-08-790-912-8
20	17	48.6	7	2	US-09-187-859-2663
21	17	48.6	7	2	US-09-187-859-2693
22	17	48.6	7	2	US-09-187-859-3177
23	17	48.6	7	2	US-09-187-859-3267
24	17	48.6	7	2	US-09-839-542B-2663
25	17	48.6	7	2	US-09-839-542B-2693
26	17	48.6	7	2	US-09-839-542B-3177
27	17	48.6	7	2	US-09-839-542B-3267

28	17	48.6	7	2	US-09-535-852-521	Sequence 521, App
29	17	48.6	7	2	US-09-535-852-611	Sequence 611, App
30	17	48.6	7	2	US-09-206-786A-23	Sequence 23, Appl
31	17	48.6	7	2	US-09-936-588-129	Sequence 129, App
32	17	48.6	7	2	US-10-006-869-2663	Sequence 2663, Ap
33	17	48.6	7	2	US-10-006-869-2693	Sequence 2693, Ap
34	17	48.6	7	2	US-10-006-869-3177	Sequence 3177, Ap
35	17	48.6	7	2	US-10-006-869-3267	Sequence 3267, Ap
36	16	45.7	7	1	US-08-153-799-11	Sequence 11, Appl
37	16	45.7	7	1	US-08-793-490-7	Sequence 7, Appli
38	16	45.7	7	2	US-09-128-572-45	Sequence 45, Appl
39	16	45.7	7	2	US-09-326-718-5	Sequence 5, Appli
40	16	45.7	7	2	US-09-336-093-11	Sequence 11, Appl
41	16	45.7	7	2	US-08-952-445-8	Sequence 8, Appli
42	16	45.7	7	2	US-09-461-325-321	Sequence 321, App
43	16	45.7	7	2	US-08-135-319A-21	Sequence 21, Appl
44	16	45.7	7	2	US-09-557-465D-11	Sequence 11, Appl
45	16	45.7	7	2	US-10-012-542-321	Sequence 321, App

ALIGNMENTS

RESULT 1  
US-08-053-171-28  
; Sequence 28, Application US/08053171  
; Patent No. 5562903  
; GENERAL INFORMATION:  
; APPLICANT: Co, Loibner  
; TITLE OF INVENTION: Antibody Derivatives  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM: Floppy disk  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,171  
; FILING DATE: 22-APR-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-54-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..7  
; OTHER INFORMATION: /note= "Second  
; OTHER INFORMATION: complementarity-determining region (CDR2) of  
; OTHER INFORMATION: BR55-2 antibody light chain"  
; US-08-053-171-28

Query Match 68.6%; Score 24; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 2
US-08-560-558E-30
; Sequence 30, Application US/08560558E
; Patent No. 5891996
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Humanized and chimeric monoclonal
; TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
; TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
; STREET: P.O. Box 2250
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: United States of America
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS95
; SOFTWARE: WordPerfect 5.1/5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,558E
; FILING DATE: No. 5891996ember 17, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turner, Allen C.
; REGISTRATION NUMBER: 33,041
; REFERENCE/DOCKET NUMBER: 2720US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 532-1922
; TELEFAX: (801) 531-9168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-560-558E-30

Query Match 68.6%; Score 24; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 3
US-09-217-268B-30
; Sequence 30, Application US/09217268B
; Patent No. 6506883
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
; FILE REFERENCE: 2720.IUS
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 7
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; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-30

Query Match 68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 4
US-09-563-222C-30
; Sequence 30, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-30

Query Match 68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 5
US-09-914-695-22
; Sequence 22, Application US/09914695
; Patent No. 6706487
; GENERAL INFORMATION:
; APPLICANT: Abdel-Meguid, Sherin
; APPLICANT: Ho, Yen Sen
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Taylor, Alexander H.
; TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
; FILE REFERENCE: P50897
; CURRENT APPLICATION NUMBER: US/09/914,695
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/07349
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,299
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
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US-09-914-695-22

Query Match 68.6%; Score 24; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNR 5  
Db 1 KVSNR 5

## RESULT 6

US-09-518-737-9  
; Sequence 9, Application US/09518737  
; Patent No. 6709833  
; GENERAL INFORMATION:  
; APPLICANT: FUKUI, YASUHIRO  
; APPLICANT: NAGATA, SATOSHI  
; APPLICANT: SHIRAI, RYUICHI  
; APPLICANT: SAITO, NAOKI  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING  
; FILE REFERENCE: 1965/49618  
; CURRENT APPLICATION NUMBER: US/09/518,737  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: JP 1999-250209  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-518-737-9

Query Match 68.6%; Score 24; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNR 5  
Db 1 KVSNR 5

## RESULT 7

US-08-244-626-6  
; Sequence 6, Application US/08244626  
; Patent No. 5502167  
; GENERAL INFORMATION:  
; APPLICANT: Waldmann, Herman  
; APPLICANT: Walsh, Louise  
; APPLICANT: Crowe, James Scott  
; APPLICANT: Lewis, Alan Peter  
; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.  
; STREET: 555 Thirteenth Street, N. W.  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/244,626  
; FILING DATE: July 15, 1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB92/02251  
; FILING DATE: December 4, 1992  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ernst, Barbara G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1808-153A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-244-626-6

Query Match 60.0%; Score 21; DB 1; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNR 5  
Db 1 KVSNR 5

## RESULT 8

US-10-226-795-29  
; Sequence 29, Application US/10226795  
; Patent No. 6875433  
; GENERAL INFORMATION:  
; APPLICANT: HART, MARY KATE  
; APPLICANT: WILSON, JULIE  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING  
; FILE REFERENCE: ARMY 166  
; CURRENT APPLICATION NUMBER: US/10/226,795  
; CURRENT FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic light  
; OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence  
US-10-226-795-29

Query Match 57.1%; Score 20; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNR 5  
Db 1 KASNR 5

## RESULT 9

US-09-563-222C-9  
; Sequence 9, Application US/09563222C  
; Patent No. 6696620  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/09/563,222C  
; CURRENT FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-563-222C-9

Query Match 54.3%; Score 19; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNR 5  
|||  
Db 2 VSNR 5

RESULT 10  
US-09-254-180C-5  
; Sequence 5, Application US/09254180C  
; Patent No. 677540  
; GENERAL INFORMATION:  
; APPLICANT: OKUMURA, Ko  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: USHIO, Yoshitaka  
; APPLICANT: HIGUCHI, Hirofumi  
; APPLICANT: NAKATA, Motomi  
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or  
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand  
; FILE REFERENCE: 050006-0055  
; CURRENT APPLICATION NUMBER: US/09/254,180C  
; CURRENT FILING DATE: 1999-04-15  
; PRIOR APPLICATION NUMBER: PCT/JP97/02983  
; PRIOR FILING DATE: 1997-08-27  
; PRIOR APPLICATION NUMBER: 271546/1996  
; PRIOR FILING DATE: 1996-09-20  
; PRIOR APPLICATION NUMBER: 231472/1996  
; PRIOR FILING DATE: 1996-09-02  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-254-180C-5

Query Match 54.3%; Score 19; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNR 5  
|||  
Db 2 VSNR 5

RESULT 11  
US-09-724-409-4  
; Sequence 4, Application US/09724409  
; Patent No. 6838261  
; GENERAL INFORMATION:  
; APPLICANT: Siegall, Clay  
; APPLICANT: Wahl, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005  
; CURRENT APPLICATION NUMBER: US/09/724,409  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/328,296  
; PRIOR FILING DATE: 1999-06-08

; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-724-409-4

Query Match 54.3%; Score 19; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNR 5  
|||  
Db 2 VSNR 5

RESULT 12  
US-09-724-530-4  
; Sequence 4, Application US/09724530  
; Patent No. 6843989  
; GENERAL INFORMATION:  
; APPLICANT: Siegall, Clay  
; APPLICANT: Wahl, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005  
; CURRENT APPLICATION NUMBER: US/09/724,530  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/328,296  
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-724-530-4

Query Match 54.3%; Score 19; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNR 5  
|||  
Db 2 VSNR 5

RESULT 13  
US-09-623-548A-654  
; Sequence 654, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617



; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 654  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-654

Query Match 54.3%; Score 19; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRLY 7  
||:|  
Db 1 NRVY 4

## RESULT 14

US-09-657-276-654  
; Sequence 654, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 654  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-654

Query Match 54.3%; Score 19; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRLY 7  
||:|  
Db 1 NRVY 4

## RESULT 15

US-09-328-296-4  
; Sequence 4, Application US/09328296  
; Patent No. 6946129  
; GENERAL INFORMATION:  
; APPLICANT: Siegall, Clay  
; APPLICANT: Wahl, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005

; CURRENT APPLICATION NUMBER: US/09/328,296  
; CURRENT FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-328-296-4

Query Match 54.3%; Score 19; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSNR 5  
||||  
Db 2 VSNR 5

Search completed: December 30, 2005, 14:52:47  
Job time : 46 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 14:51:25 ; Search time 159 Seconds  
(without alignments)  
18.395 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNRLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 28819

Minimum DB seq length: 7

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	5	US-10-735-916A-4
2	27	77.1	7	3	US-09-995-529-125
3	27	77.1	7	3	US-09-995-529-125
4	26	74.3	7	3	US-09-995-529-124
5	26	74.3	7	3	US-09-995-529-124
6	26	74.3	7	4	US-10-434-469-11
7	26	74.3	7	5	US-10-482-105-9
8	26	74.3	7	5	US-10-409-611-80
9	26	74.3	7	5	US-10-409-608A-22
10	26	74.3	7	5	US-10-500-207A-11
11	24	68.6	7	3	US-09-217-268B-30
12	24	68.6	7	3	US-09-796-744-9
13	24	68.6	7	3	US-09-518-737-9
14	24	68.6	7	3	US-09-563-222-30
15	24	68.6	7	3	US-09-995-529-34
16	24	68.6	7	3	US-09-995-529-34
17	24	68.6	7	4	US-10-231-452-6
18	24	68.6	7	4	US-10-226-435A-2
19	24	68.6	7	4	US-10-663-244-17
20	24	68.6	7	4	US-10-762-629-22
21	24	68.6	7	4	US-10-487-322-2
22	24	68.6	7	4	US-10-783-950-30
23	24	68.6	7	5	US-10-487-326-2
24	24	68.6	7	5	US-10-486-908-2
25	24	68.6	7	5	US-10-729-441-5
26	24	68.6	7	5	US-10-723-748-9
27	24	68.6	7	5	US-10-687-035-7

Sequence 6, Appli  
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Sequence 57, Appli  
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Sequence 5, Appli  
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Sequence 17, Appli  
Sequence 2, Appli  
Sequence 9, Appli  
Sequence 16, Appli  
Sequence 116, App  
Sequence 116, App  
Sequence 271, App  
Sequence 121, App  
Sequence 121, App  
Sequence 40, Appl  
Sequence 141, App  
Sequence 443, App

28 24 68.6 7 5 US-10-505-980-6  
29 24 68.6 7 5 US-10-512-527-2  
30 24 68.6 7 5 US-10-810-881A-57  
31 24 68.6 7 5 US-10-497-475-2  
32 24 68.6 7 5 US-10-897-406-5  
33 24 68.6 7 6 US-11-009-443-5  
34 24 68.6 7 6 US-11-009-443-17  
35 24 68.6 7 6 US-11-070-697-2  
36 24 68.6 7 6 US-11-094-718-9  
37 23 65.7 7 3 US-09-972-656-16  
38 23 65.7 7 5 US-10-877-773-116  
39 23 65.7 7 5 US-10-877-774-116  
40 23 65.7 7 5 US-10-946-647-271  
41 20 57.1 7 3 US-09-995-529-121  
42 20 57.1 7 3 US-09-995-529-121  
43 20 57.1 7 4 US-10-022-066-40  
44 20 57.1 7 4 US-10-022-066-141  
45 20 57.1 7 4 US-10-022-066-443

#### ALIGNMENTS

RESULT 1  
US-10-735-916A-4  
; Sequence 4, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-4

Query Match 100.0%; Score 35; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7  
Db 1 KVSNNRLY 7

RESULT 2  
US-09-995-529-125  
; Sequence 125, Application US/09995529  
; Publication No. US20030099655A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying

```
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-125
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Query Match 77.1%; Score 27; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KVSNNRLY 7
Db 1 KVSNNRFF 7
```

## RESULT 3

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US-09-995-529-125
; Sequence 125, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-125
```

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Query Match 77.1%; Score 27; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KVSNNRLY 7
Db 1 KVSNNRFF 7
```

## RESULT 4

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US-09-995-529-124
; Sequence 124, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 7
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-124
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Query Match 74.3%; Score 26; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KVSNNRLY 7
Db 1 KVSNNRFF 7
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## RESULT 5

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US-09-995-529-124
; Sequence 124, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-124
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Query Match 74.3%; Score 26; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KVSNNRLY 7
Db 1 KVSNNRFF 7
```

## RESULT 6

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US-10-434-469-11
; Sequence 11, Application US/10434469
; Publication No. US20040091480A1
; GENERAL INFORMATION:
; APPLICANT: Nobuo HANAI
; APPLICANT: Motoko YAMASAKI
; APPLICANT: Akiko FURUYA
; APPLICANT: Akira TANAKA
; APPLICANT: Kenya SHITARA
; APPLICANT: Naoki SHIWADA
; TITLE OF INVENTION: Anti-fibroblast growth factor-8 monoclonal antibod
; FILE REFERENCE: 249-310
; CURRENT APPLICATION NUMBER: US/10/434,469
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: JP 08-081754
; PRIOR FILING DATE: 1996-04-03
; PRIOR APPLICATION NUMBER: US 08/832,236
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: US 09/326,590
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: US 09/876,040
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-434-469-11

Query Match      74.3%; Score 26; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
Db 1 KVSURL 6
   |||||:
   |||||:

RESULT 7
US-10-482-105-9
; Sequence 9, Application US/10482105
; Publication No. US20040253234A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: Humanized anti-FGF-8 antibody and the antibody fragment thereof
; FILE REFERENCE: 11399W01
; CURRENT APPLICATION NUMBER: US/10/482,105
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: JP2001-196176
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-482-105-9

Query Match      74.3%; Score 26; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
Db 1 KVSURL 6
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RESULT 8
US-10-409-611-80
; Sequence 80, Application US/10409611
; Publication No. US20040259150A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Method of enhancing of binding activity of antibody composition b
; FILE REFERENCE: 249-303
; CURRENT APPLICATION NUMBER: US/10/409,611
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: P2002-106950
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-409-611-80

Query Match      74.3%; Score 26; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
Db 1 KVSURL 6
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RESULT 9
US-10-409-608A-22
; Sequence 22, Application US/10409608A
; Publication No. US20050031613A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Therapeutic agent for patients having human FcγRIIIa
; FILE REFERENCE: 249-304
; CURRENT APPLICATION NUMBER: US/10/409,608A
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 2002-106951
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-409-608A-22

Query Match      74.3%; Score 26; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
Db 1 KVSURL 6
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   |||||:

RESULT 10
US-10-500-207A-11
; Sequence 11, Application US/10500207A
; Publication No. US20050175608A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
; FILE REFERENCE: 1442
; CURRENT APPLICATION NUMBER: US/10/500,207A
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: JP2001-400677
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-500-207A-11

Query Match      74.3%; Score 26; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
Db 1 KVSURL 6
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   |||||:

RESULT 11
US-09-217-268B-30
; Sequence 30, Application US/09217268B
; Patent No. US20020065398A1
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epid
; FILE REFERENCE: 2720.1US
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-30

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 12
US-09-796-744-9
; Sequence 9, Application US/09796744
; Patent No. US20020098527A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: SHOJI, EMI
; APPLICANT: SAKURADA, MIKKIKO
; APPLICANT: FURUYA, AKIKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: NIWA, RINPEI
; APPLICANT: SHIBATA, KENJI
; APPLICANT: YAMASAKI, MOTOO
; TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF
; FILE REFERENCE: 249-170
; CURRENT APPLICATION NUMBER: US/09/796,744
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: JP 2000-59508
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 2000-401563
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-796-744-9

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 13
US-09-518-737-9
; Sequence 9, Application US/09518737
; Publication No. US20030008321A1
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIISA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOAKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03

US-09-518-737-9
; Sequence 34, Application US/0995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-34

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 14
US-09-563-222-30
; Sequence 30, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-30

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 15
US-09-995-529-34
; Sequence 34, Application US/0995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-34

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5
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Db 1 KYSNR 5

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OM protein - protein search, using sw model  
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(without alignments)  
4.368 Million cell updates/sec

Title: US-10-735-916A-4  
Perfect score: 35  
Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 1076

Minimum DB seq length: 7  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New.\*  
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4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pap.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pap.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	35	100.0	7	7 US-11-012-353-4	Sequence 4, Appli
2	24	68.6	7	6 US-10-932-334-5	Sequence 5, Appli
3	24	68.6	7	7 US-11-125-837-2	Sequence 2, Appli
4	24	68.6	7	7 US-11-125-837-14	Sequence 14, Appli
5	24	68.6	7	7 US-11-105-708-18	Sequence 18, Appli
6	21	60.0	7	7 US-11-009-939-19	Sequence 19, Appli
7	19	54.3	7	7 US-11-102-743-4	Sequence 4, Appli
8	17	48.6	7	6 US-10-485-788A-334	Sequence 334, Appl
9	17	48.6	7	7 US-11-096-706-34	Sequence 34, Appli
10	17	48.6	7	7 US-11-096-706-56	Sequence 56, Appli
11	17	48.6	7	7 US-11-096-706-62	Sequence 62, Appli
12	17	48.6	7	7 US-11-096-706-168	Sequence 168, App
13	17	48.6	7	7 US-11-096-706-191	Sequence 191, App
14	17	48.6	7	7 US-11-096-706-194	Sequence 194, App
15	17	48.6	7	7 US-11-096-706-200	Sequence 200, App
16	16	45.7	7	7 US-11-062-186-27	Sequence 27, Appl
17	15	42.9	7	6 US-10-467-657-9189	Sequence 9189, Ap
18	15	42.9	7	7 US-11-096-706-29	Sequence 29, Appl
19	15	42.9	7	7 US-11-096-706-76	Sequence 76, Appli
20	15	42.9	7	7 US-11-096-706-193	Sequence 193, App
21	15	42.9	7	7 US-11-096-706-202	Sequence 202, App
22	15	42.9	7	7 US-11-096-706-204	Sequence 204, App
23	15	42.9	7	7 US-11-093-274-13	Sequence 13, Appli
24	15	42.9	7	7 US-11-093-274-14	Sequence 14, Appli
25	15	42.9	7	7 US-11-093-274-15	Sequence 15, Appli

26	14	40.0	7	6 US-10-997-066-34	Sequence 34, Appli
27	14	40.0	7	6 US-10-842-877A-4	Sequence 4, Appli
28	14	40.0	7	6 US-10-485-788A-284	Sequence 284, App
29	14	40.0	7	7 US-11-096-706-40	Sequence 40, Appli
30	14	40.0	7	7 US-11-096-706-46	Sequence 46, Appli
31	14	40.0	7	7 US-11-096-706-150	Sequence 150, App
32	14	40.0	7	7 US-11-069-834-12	Sequence 12, Appli
33	13	37.1	7	6 US-10-726-554-10	Sequence 10, Appli
34	13	37.1	7	6 US-10-999-866-56	Sequence 56, Appli
35	13	37.1	7	6 US-10-842-877A-2	Sequence 2, Appli
36	13	37.1	7	6 US-10-842-877A-13	Sequence 13, Appli
37	13	37.1	7	6 US-10-842-877A-17	Sequence 17, Appli
38	13	37.1	7	6 US-10-842-877A-18	Sequence 18, Appli
39	13	37.1	7	6 US-10-485-788A-164	Sequence 164, App
40	13	37.1	7	6 US-10-485-788A-274	Sequence 274, App
41	13	37.1	7	7 US-11-096-706-58	Sequence 58, Appli
42	13	37.1	7	7 US-11-096-706-175	Sequence 175, App
43	12	34.3	7	6 US-10-516-768-37	Sequence 37, Appli
44	12	34.3	7	6 US-10-997-759-11	Sequence 11, Appli
45	12	34.3	7	6 US-10-467-657-9107	Sequence 9107, Ap

ALIGNMENTS

RESULT 1  
US-11-012-353-4  
; Sequence 4, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETTSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; PRIOR FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn ver. 3.3  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-4

Query Match 100.0%; Score 35; DB 7; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7  
|  
|  
|  
|  
|  
|  
|  
Db 1 KVSNNLY 7

RESULT 2  
US-10-932-334-5  
; Sequence 5, Application US/10932334

; Publication No. US20050249728A1  
; GENERAL INFORMATION:  
; APPLICANT: ImmunoGen, Inc.  
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY  
; FILE REFERENCE: A8689  
; CURRENT APPLICATION NUMBER: US/10/932,334  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US/10/729,441  
; PRIOR FILING DATE: 2003-12-08  
; PRIOR APPLICATION NUMBER: 10/170,390  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antibody light chain complementarity determining region  
US-10-932-334-5

Query Match 68.6%; Score 24; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5  
Db 1 KVSNR 5

## RESULT 3

US-11-125-837-2  
; Sequence 2, Application US/11125837  
; Publication No. US20050266003A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Rong-Hwa  
; APPLICANT: Chang, Chung Nan  
; APPLICANT: Chen, Pei-Jiun  
; APPLICANT: Huang, Chiu-Chen  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: 13062-011001  
; CURRENT APPLICATION NUMBER: US/11/125,837  
; CURRENT FILING DATE: 2005-05-10  
; PRIOR APPLICATION NUMBER: US 60/569,892  
; PRIOR FILING DATE: 2004-05-10  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-125-837-2

Query Match 68.6%; Score 24; DB 7; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5  
Db 1 KVSNR 5

## RESULT 4

US-11-125-837-14  
; Sequence 14, Application US/11125837  
; Publication No. US20050266003A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Rong-Hwa  
; APPLICANT: Chang, Chung Nan  
; APPLICANT: Chen, Pei-Jiun  
; APPLICANT: Huang, Chiu-Chen  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: 13062-011001

; CURRENT APPLICATION NUMBER: US/11/125,837  
; CURRENT FILING DATE: 2005-05-10  
; PRIOR APPLICATION NUMBER: US 60/569,892  
; PRIOR FILING DATE: 2004-05-10  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-125-837-14

Query Match 68.6%; Score 24; DB 7; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5  
Db 1 KVSNR 5

## RESULT 5

US-11-105-708-18  
; Sequence 18, Application US/11105708  
; Publication No. US20050281821A1  
; GENERAL INFORMATION:  
; APPLICANT: Pernasetti, Flavia  
; APPLICANT: Freimark, Bruce  
; APPLICANT: Van Epps, Dennis  
; APPLICANT: Brooke, Peter C  
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition  
; FILE REFERENCE: 30797-704.501  
; CURRENT APPLICATION NUMBER: US/11/105,708  
; CURRENT FILING DATE: 2005-04-13  
; PRIOR APPLICATION NUMBER: 09/478,977  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: 60/152,496  
; PRIOR FILING DATE: 1999-09-02  
; PRIOR APPLICATION NUMBER: 60/143,534  
; PRIOR FILING DATE: 1999-09-02  
; PRIOR APPLICATION NUMBER: 60/114,878  
; PRIOR FILING DATE: 1999-01-06  
; PRIOR APPLICATION NUMBER: 60/114,877  
; PRIOR FILING DATE: 1999-01-06  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-105-708-18

Query Match 68.6%; Score 24; DB 7; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5  
Db 1 KVSNR 5

## RESULT 6

US-11-009-939-19  
; Sequence 19, Application US/11009939  
; Publication No. US2005026598A1  
; GENERAL INFORMATION:  
; APPLICANT: Elson, Greg Christopher Andrew  
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof  
; FILE REFERENCE: 23135-402  
; CURRENT APPLICATION NUMBER: US/11/009,939  
; CURRENT FILING DATE: 2005-12-10

; PRIOR APPLICATION NUMBER: 60/528,811  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,812  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,962  
; PRIOR FILING DATE: 2003-12-10  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-009-939-19

Query Match 60.0%; Score 21; DB 7; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.3e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNR 5  
DB 1 RVSNR 5

RESULT 7  
US-11-102-743-4  
; Sequence 4, Application US/11102743  
; Publication No. US20050266002A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegal, Clay  
; APPLICANT: Wahli, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005  
; CURRENT APPLICATION NUMBER: US/11/102,743  
; CURRENT FILING DATE: 2005-04-08  
; PRIOR APPLICATION NUMBER: US/09/328,296  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-102-743-4

Query Match 54.3%; Score 19; DB 7; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSNR 5  
DB 2 VSNR 5

RESULT 8  
US-10-485-788A-334  
; Sequence 334, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schweizer, Johannes  
; APPLICANT: Carlick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 334  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-788A-334

Query Match 48.6%; Score 17; DB 6; Length 7;  
Best Local Similarity 60.0%; Pred. No. 4.3e+04;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNRLY 7  
DB 2 SHQLY 6

RESULT 9  
US-11-096-706-34  
; Sequence 34, Application US/11096706  
; Publication No. US20050245476A1  
; GENERAL INFORMATION:  
; APPLICANT: Sangamo Biosciences, Inc.  
; APPLICANT: Collingwood, Trevor  
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins  
; FILE REFERENCE: 019496-008220US  
; CURRENT APPLICATION NUMBER: US/11/096,706  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 60/560,535  
; PRIOR FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 60/576,757  
; PRIOR FILING DATE: 2004-06-02  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 34  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition  
; OTHER INFORMATION: region)  
US-11-096-706-34

Query Match 48.6%; Score 17; DB 7; Length 7;  
Best Local Similarity 75.0%; Pred. No. 4.3e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNRL 6  
DB 3 SNRI 6

RESULT 10  
US-11-096-706-56  
; Sequence 56, Application US/11096706  
; Publication No. US20050245476A1  
; GENERAL INFORMATION:  
; APPLICANT: Sangamo Biosciences, Inc.  
; APPLICANT: Collingwood, Trevor  
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins  
; FILE REFERENCE: 019496-008220US  
; CURRENT APPLICATION NUMBER: US/11/096,706  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 60/560,535  
; PRIOR FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 60/576,757  
; PRIOR FILING DATE: 2004-06-02  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 56  
; LENGTH: 7

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; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-56

Query Match      48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNRL 6
Db      3 SNRI 6

RESULT 11
US-11-096-706-62
; Sequence 62, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-62

Query Match      48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNRL 6
Db      3 SNRI 6

RESULT 12
US-11-096-706-168
; Sequence 168, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 168
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding
; OTHER INFORMATION: domain)
US-11-096-706-168

Query Match      48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNRL 6
Db      3 SNRI 6

RESULT 13
US-11-096-706-191
; Sequence 191, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding
; OTHER INFORMATION: domain)
US-11-096-706-191

Query Match      48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNRL 6
Db      3 SNRI 6

RESULT 14
US-11-096-706-194
; Sequence 194, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 194
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding
; OTHER INFORMATION: domain)
US-11-096-706-194
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Query Match 48.6%; Score 17; DB 7; Length 7;  
Best Local Similarity 75.0%; Pred. No. 4.3e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNRL 6  
|||:  
Db 3 SNRI 6

## RESULT 15

US-11-096-706-200  
; Sequence 200, Application US/11096706  
; Publication No. US20050245476A1  
; GENERAL INFORMATION:  
; APPLICANT: Sangamo Biosciences, Inc.  
; APPLICANT: Collingwood, Trevor  
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins  
; FILE REFERENCE: 019496-008220US  
; CURRENT APPLICATION NUMBER: US/11/096,706  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 60/560,535  
; PRIOR FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 60/576,757  
; PRIOR FILING DATE: 2004-06-02  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 200  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding  
; OTHER INFORMATION: domain)  
US-11-096-706-200

Query Match 48.6%; Score 17; DB 7; Length 7;  
Best Local Similarity 75.0%; Pred. No. 4.3e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNRL 6  
|||:  
Db 3 SNRI 6

Search completed: December 30, 2005, 15:05:35  
Job time : 16 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

QM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 20.1774 Seconds  
(without alignments)  
36.877 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPVWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep:\*
  - 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*
  - 3: /cgn2\_6/ptodata/1/iaa/H COMB.pep:\*
  - 4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep:\*
  - 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep:\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	112	1	US-08-752-844-15
2	56	100.0	112	1	US-08-591-196-15
3	56	100.0	112	2	US-03-293-533-15
4	56	100.0	149	1	US-08-752-844-2
5	56	100.0	149	1	US-08-591-196-2
6	56	100.0	149	2	US-09-192-838B-2
7	56	100.0	149	2	US-03-293-533-2
8	56	100.0	149	2	US-03-324-191-2
9	56	100.0	263	1	US-08-752-844-66
10	56	100.0	263	2	US-03-293-533-66
11	53	94.6	9	1	US-07-977-696C-72
12	53	94.6	9	1	US-08-129-930B-72
13	53	94.6	9	2	US-08-976-288A-72
14	53	94.6	9	2	US-09-947-839B-72
15	53	94.6	131	1	US-07-977-696C-11
16	53	94.6	131	1	US-08-129-930B-11
17	53	94.6	131	2	US-08-976-288A-11
18	53	94.6	131	2	US-09-947-839B-11
19	47	83.9	9	1	US-07-977-696C-34
20	47	83.9	9	1	US-08-129-930B-34
21	47	83.9	9	1	US-08-560-558B-31
22	47	83.9	9	2	US-08-134-346A-21
23	47	83.9	9	2	US-08-976-288A-34
24	47	83.9	9	2	US-09-217-268B-31
25	47	83.9	9	2	US-09-947-839B-34
26	47	83.9	110	2	US-10-114-716A-42
27	47	83.9	113	1	US-08-497-312-18

Sequence 15, Appl  
Sequence 27, Appl  
Sequence 21, Appl  
Sequence 35, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 95, Appl  
Sequence 50, Appl  
Sequence 190, Appl  
Sequence 12, Appl  
Sequence 14, Appl  
Sequence 29, Appl  
Sequence 15, Appl  
Sequence 48, Appl  
Sequence 50, Appl  
Sequence 3, Appl  
Sequence 19, Appl

US-09-232-290-15  
US-08-560-558B-27  
US-09-217-268B-27  
US-09-217-268B-35  
US-08-497-312-14  
US-08-129-930B-95  
US-08-134-346A-50  
US-08-976-288A-95  
US-09-726-219A-190  
US-09-196-522-190  
US-09-646-028-12  
US-09-646-028-14  
US-08-053-171-29  
US-08-053-171-15  
US-08-331-398A-48  
US-08-331-398A-50  
US-08-077-252B-3  
US-08-859-649-19

#### ALIGNMENTS

RESULT 1  
US-08-752-844-15  
; Sequence 15, Application US/08752844  
; Patent No. 5935821  
; GENERAL INFORMATION:  
; APPLICANT: Chatterjee, Malaya  
; APPLICANT: Foon, Kenneth A.  
; APPLICANT: Chatterjee, Sunil K.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,844  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 30414-20002.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-752-844-15

Query Match 100.0%; Score 56; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVWT 9

|||||

Db 94 FQSHVPWT 102

## RESULT 2

US-08-591-196-15  
; Sequence 15, Application US/08591196  
; Patent No. 5977316  
; GENERAL INFORMATION:  
; APPLICANT: Chatterjee, Malaya  
; APPLICANT: Foon, Kenneth A.  
; APPLICANT: Chatterjee, Sunil K.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA

ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/591,196  
; FILING DATE: 16-JAN-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 30414-20002.20  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-591-196-15

Query Match 100.0%; Score 56; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9

Db 94 FQSHVPWT 102

## RESULT 3

US-09-293-533-15  
; Sequence 15, Application US/09293533  
; Patent No. 6509016  
; GENERAL INFORMATION:  
; APPLICANT: Chatterjee, Malaya  
; APPLICANT: Foon, Kenneth A.  
; APPLICANT: Chatterjee, Sunil K.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA

ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/293,533  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,844  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 30414-20002.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-293-533-15

Query Match 100.0%; Score 56; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9

Db 94 FQSHVPWT 102

## RESULT 4

US-08-752-844-2  
; Sequence 2, Application US/08752844  
; Patent No. 5935821  
; GENERAL INFORMATION:  
; APPLICANT: Chatterjee, Malaya  
; APPLICANT: Foon, Kenneth A.  
; APPLICANT: Chatterjee, Sunil K.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA

ZIP: 94304-1018

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,844  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 30414-20002.21  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792

Query Match 100.0%; Score 56; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-752-844-2

Query Match 100.0%; Score 56; DB 1; Length 149;  
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
DB 113 FQSHVPWT 121

RESULT 5  
US-08-591-196-2  
Sequence 2, Application US/08591196  
Patent No. 5977316  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Foon, Kenneth A.  
APPLICANT: Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,196  
FILING DATE: 16-JAN-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Schiff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-591-196-2

Query Match 100.0%; Score 56; DB 1; Length 149;  
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
DB 113 FQSHVPWT 121

RESULT 6  
US-09-192-838B-2  
Sequence 2, Application US/09192838B

Patent No. 6355244  
GENERAL INFORMATION:  
APPLICANT: FOON, Kenneth A.  
APPLICANT: CHATTERJEE, Malaya  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS  
FILE REFERENCE: 304142000500  
CURRENT APPLICATION NUMBER: US/09/192,838B  
CURRENT FILING DATE: 1998-11-16  
PRIOR APPLICATION NUMBER: 60/065,774  
PRIOR FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 2  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Mus Musculus  
US-09-192-838B-2

Query Match 100.0%; Score 56; DB 2; Length 149;  
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
DB 113 FQSHVPWT 121

RESULT 7  
US-09-293-533-2  
Sequence 2, Application US/09293533  
Patent No. 6509016  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Foon, Kenneth A.  
APPLICANT: Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,533  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,844  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Schiff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-293-533-2

Query Match 100.0%; Score 56; DB 2; Length 149;  
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
DB 113 FQSHVPWT 121

## RESULT 8

US-09-324-191-2  
; Sequence 2, Application US/09324191  
; Patent No. 6562798  
; GENERAL INFORMATION:  
; APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION  
; APPLICANT: CHATTERJEE, Malaya  
; APPLICANT: FOON, Kenneth A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS  
; FILE REFERENCE: 304142000540  
; CURRENT APPLICATION NUMBER: US/09/324,191  
; CURRENT FILING DATE: 1999-06-02  
; EARLIER APPLICATION NUMBER: 60/065,774  
; EARLIER FILING DATE: 1997-11-17  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-09-324-191-2

Query Match 100.0%; Score 56; DB 2; Length 149;  
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
DB 113 FQSHVPWT 121

## RESULT 9

US-08-752-844-66  
; Sequence 66, Application US/08752844  
; Patent No. 5935821  
; GENERAL INFORMATION:  
; APPLICANT: Chatterjee, Malaya  
; APPLICANT: Foon, Kenneth A.  
; APPLICANT: Chatterjee, Sunil K.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/752,844  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,844  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 30414-20002.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792  
TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 263 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-752-844-66

Query Match 100.0%; Score 56; DB 1; Length 263;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
DB 245 FQSHVPWT 253

## RESULT 10

US-09-293-533-66  
; Sequence 66, Application US/09293533  
; Patent No. 6509016  
; GENERAL INFORMATION:  
; APPLICANT: Chatterjee, Malaya  
; APPLICANT: Foon, Kenneth A.  
; APPLICANT: Chatterjee, Sunil K.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/293,533  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,844  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 30414-20002.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 263 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-293-533-66

Query Match 100.0%; Score 56; DB 2; Length 263;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
DB 245 FQSHVPWT 253

RESULT 11  
US-07-977-696C-72  
; Sequence 72, Application US/07977696C  
; Patent No. 5792852  
; GENERAL INFORMATION:  
; APPLICANT: do Couto Dr., Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides with Specificity  
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination  
; TITLE OF INVENTION: and Therapeutic Methods.  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/977,696C  
; FILING DATE: 11-16-92  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel Ph.D., Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: P66 38227  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 748-6868  
; TELEFAX: (510) 748-6688  
; TELEX: n.a.  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-977-696C-72  
Query Match 94.6%; Score 53; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FQGSHPWT 9  
Db 1 FQGTHVPWT 9  
RESULT 12  
US-08-129-930B-72  
; Sequence 72, Application US/08129930B  
; Patent No. 5804187  
; GENERAL INFORMATION:  
; APPLICANT: do Couto Dr., Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides with Broad  
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
; TITLE OF INVENTION: Diagnostic Vaccination and  
; TITLE OF INVENTION: Therapeutic Methods  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: V. AMZEL & ASSOC.  
; STREET: 2055 No. 5804187th Broadway, Suite 201  
; CITY: Walnut Creek

STATE: California  
COUNTRY: USA  
ZIP: 94596  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/129,930B  
FILING DATE: September 30, 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Ph.D., Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: CRFCC-008A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 521-1333  
TELEFAX: (510) 521-3541  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-129-930B-72  
Query Match 94.6%; Score 53; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FQGSHPWT 9  
Db 1 FQGTHVPWT 9  
RESULT 13  
US-08-976-288A-72  
; Sequence 72, Application US/08976288A  
; Patent No. 6315997  
; GENERAL INFORMATION:  
; APPLICANT: do Couto Dr., Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides With Broad  
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
; TITLE OF INVENTION: Diagnostic Vaccination and  
; TITLE OF INVENTION: Therapeutic Methods  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder & Poplawski  
; STREET: 444 South Flower St., 19th Floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/976,288A  
; FILING DATE: No. 6315997ember 21, 1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/129,930  
; FILING DATE: September 30, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/977,696  
; FILING DATE: No. 6315997ember 16, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Viviana Amzel Ph.D.  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P6639938  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 622-7700  
TELEFAX: (213) 489-4210  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-976-288A-72

Query Match 94.6%; Score 53; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
|||:||||  
DB 1 FQGTHVPWT 9

RESULT 14  
US-09-947-839B-72  
; Sequence 72, Application US/09947839B  
; Patent No. 6936706  
; GENERAL INFORMATION:  
; APPLICANT: do Couto, Fernando J.R.  
; Ceriani Dr., Roberto L.  
; Peterson Dr., Jerry A.  
; Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides with Specificity  
; for Carcinomas and Kit and Diagnostic Vaccination  
; and Therapeutic Methods.  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: V. Amzel & Assoc.  
; STREET: P.O.Box 159  
; CITY: Gladwyne  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19035

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/09/947,839B  
FILING DATE: 06-Sep-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: CRFC-083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-649-0609  
TELEFAX: 240-359-0299  
TELEX: n.a.

INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-09-947-839B-72

Query Match 94.6%; Score 53; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FQGSHPVPT 9  
|||:||||  
DB 1 FQGTHVPWT 9

RESULT 15  
US-07-977-696C-11  
; Sequence 11, Application US/07977696C  
; Patent No. 5792852  
; GENERAL INFORMATION:  
; APPLICANT: do Couto, Fernando J.R.  
; Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides with Specificity  
; for Carcinomas and Kit and Diagnostic Vaccination  
; and Therapeutic Methods.  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/07/977,696C  
FILING DATE: 11-16-92  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Ph.D., Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P66 38227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 748-6868  
TELEFAX: (510) 748-6868  
TELEX: n.a.

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-977-696C-11

Query Match 94.6%; Score 53; DB 1; Length 131;  
Best Local Similarity 88.9%; Pred. No. 0.035;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
|||:||||  
DB 113 FQGTHVPWT 121

Search completed: December 30, 2005, 13:37:17  
Job time : 20.1774 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 79.9839 Seconds  
(without alignments)  
49.440 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQSHVPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	5	ABP52345 Fv region
2	56	100.0	9	7	ADD94151 Mouse HUI
3	56	100.0	9	7	ADJ76840 CDR seque
4	56	100.0	9	9	ADZ67010 Murine in
5	56	100.0	109	5	ABP52310 Fv region
6	56	100.0	112	2	RAY49217 Light cha
7	56	100.0	112	2	RAY25397 WO9932630
8	56	100.0	112	5	AAE15711 Mouse mon
9	56	100.0	112	5	AAE15713 Mouse mon
10	56	100.0	112	5	AAE15704 Mouse mon
11	56	100.0	112	5	AAE15712 Mouse mon
12	56	100.0	112	6	ADA14777 Peptide f
13	56	100.0	112	7	ADC35319 Anti-idio
14	56	100.0	112	7	ADD94125 Mouse HUI
15	56	100.0	112	7	ADJ76888 Anti-IGF-
16	56	100.0	112	7	ADJ76890 Anti-IGF-
17	56	100.0	112	7	ADJ76899 Anti-IGF-
18	56	100.0	112	7	ADJ76895 Anti-IGF-
19	56	100.0	112	7	ADJ80422 Murine an
20	56	100.0	112	7	ADJ80420 Hybrid hu
21	56	100.0	112	7	ADJ80419 Hybrid hu
22	56	100.0	112	7	ADJ80421 Hybrid hu
23	56	100.0	112	9	ADZ67058 Murine im
24	56	100.0	112	9	ADZ67069 Human ant

25	56	100.0	112	9	ADZ67060 Mouse ant
26	56	100.0	112	9	ADZ67065 Human ant
27	56	100.0	114	8	ADI26490 Human ECL
28	56	100.0	114	8	ADI26498 Human ECL
29	56	100.0	115	1	AAP81364 Light cha
30	56	100.0	115	1	AAP81366 Chimeric
31	56	100.0	115	1	AAP81366 Light cha
32	56	100.0	120	1	AAB62303 Chimeric
33	56	100.0	120	1	AAB62303 Anti-IGF-
34	56	100.0	122	7	ADJ76883 Murine im
35	56	100.0	122	7	ADZ67053 Anti-IGF-
36	56	100.0	131	7	ADJ76901 Anti-IGF-
37	56	100.0	131	7	ADJ76897 Anti-IGF-
38	56	100.0	131	9	ADZ67071 Human ant
39	56	100.0	131	9	ADZ67067 Human ant
40	56	100.0	149	2	AAW03199 Anti-idio
41	56	100.0	149	2	AAW03199 Mab 1A7 1
42	56	100.0	149	2	AAW03199 Anti-idio
43	56	100.0	149	2	AAW03199 Anti-idio
44	56	100.0	149	6	ADA14768 Monoclonal
45	56	100.0	149	7	ADC35310 Monoclonal
	56	100.0	249	1	AAP80154 Biosynthe

ALIGNMENTS

RESULT 1  
ABP52345  
ID ABP52345 standard; peptide; 9 AA.  
XX AC ABP52345;  
XX AC  
XX 17-OCT-2002 (first entry)  
XX Fv region SC100 antibody CDR-L3 amino acid sequence.  
XX Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;  
XX tumour; immune response; cancer; vaccine; antibody.  
XX Mus musculus.  
XX Synthetic.  
XX WO200258728-A2.  
XX 01-AUG-2002.  
XX 28-JAN-2002; 2002WO-GB000354.  
XX 26-JAN-2001; 2001GB-00002145.  
XX (SCAN-) SCANCEL LTD.  
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
XX Durrant LG, Parsons T, Robins A;  
XX WPI; 2002-608418/65.  
XX Use of polypeptides and nucleic acids encoding the polypeptides, in  
XX manufacturing medicament for stimulating a cytotoxic T cell response and  
XX for preventing or treating cancer, e.g. colorectal, lung, breast or  
XX ovarian cancer.  
XX Example 11; Page 46; 87pp; English.

The present invention describes the use of a polypeptide (I) in the manufacture of a medicament for stimulating a cytotoxic T cell response, where (I) comprises a first portion comprising the part of human FC that binds to CD64 and a second portion comprising one or more heterologous T cell epitopes. Also described is a method of stimulating a cytotoxic T cell response in a patient such as a mammal, preferably human, by administering (I) to the patient. (I) has cytostatic activity and can be used in vaccine production. (I) and the nucleic acid encoding (I) are useful in the manufacture of a medicament for stimulating cytotoxic T

CC	cell response. The medicament is useful for preventing and/or treating cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The medicament stimulates cytotoxic and helper T cell responses. The antibodies are useful as vaccines to stimulate helper and cytotoxic T cell responses. The polypeptides and nucleic acids are useful in optimising immunisation schedules for enhancing a protective immune response against cancer. The present sequence represents an Fv region SC100 antibody CDR-L3 amino acid sequence which is used in an example from the present invention
XX	
XX	
SQ	Sequence 9 AA;
	Query Match 100.0%; Score 56; DB 5; Length 9;
	Best Local Similarity 100.0%; Pred. No. 2e+06;
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FQGSHVPEWT 9 
DB	1 FQGSHVPEWT 9
RESULT 2	
ADD94151	ID ADD94151 standard; peptide; 9 AA.
XX	AC AC
XX	ADD94151;
DT	29-JAN-2004 (first entry)
XX	
DE	Mouse HUI77 light chain CDR3 partial amino acid sequence SeqID36.
XX	
KW	grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour;
KW	new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW	collagen agonist; collagen antagonist; cancer metastasis;
KW	anti-cryptic collagen; antibody; HUI77; variable region light chain;
KW	mouse; murine.
XX	
OS	Mus musculus.
XX	
PN	WO2003046204-A2.
XX	
PD	05-JUN-2003.
XX	
PX	26-NOV-2002; 2002WO-US038147.
PF	
XX	
PR	26-NOV-2001; 2001US-00995529.
PR	06-DEC-2001; 2001US-00011250.
XX	
PA	(CELL-) CELL MATRIX INC.
XX	
PI	Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX	
DR	WPI; 2003-513649/48.
DR	N-PSDE; ADD94150.
XX	
PT	New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
PT	
XX	
PS	Claim 25; SEQ ID NO 36; 232pp; English.
XX	
CC	This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the partial amino acid sequence of a mouse anti-

Best Local Similarity 100.0%; Pred. No. 2e+06; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9  
| | | | |  
Db 1 FQGSHPWT 9

RESULT 4  
ADZ67010  
ID ADZ67010 standard; peptide; 9 AA.

AC ADZ67010;  
XX  
DT 30-JUN-2005 (first entry)

XX Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:6.  
XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
KW musculoskeletal disease; respiratory disease; lung tumor;  
KW endocrine disease; gynecology and obstetrics; breast tumor;  
KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

OS Mus musculus.

XX US2005084906-A1.

PN 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFLOS A.

PA (HAEU/) HAEUW J.

PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

PI WPI; 2005-321968/33.

DR N-PSDB; ADZ67009.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.  
XX Claim 1; SEQ ID NO 6; 125pp; English.  
XX The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended

CC to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.

XX Sequence 9 AA;

QY Query Match 100.0%; Score 56; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9  
| | | | |  
Db 1 FQGSHPWT 9

RESULT 5  
ABP52310  
ID ABP52310 standard; peptide; 109 AA.

XX AC ABP52310;

XX 17-OCT-2002 (first entry)

DT Fv region SC100 antibody light chain related amino acid sequence #1.

XX Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;  
XX tumour; immune response; cancer; vaccine; antibody.

XX Mus musculus.

OS Synthetic.

XX WO200258728-A2.

XX 01-AUG-2002.

XX 28-JAN-2002; 2002WO-GB000354.

XX 26-JAN-2001; 2001GB-00002145.

XX (SCAN-) SCANCEL LTD.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Durrant LG, Parsons T, Robins A;

XX WPI; 2002-608418/65.

XX Use of polypeptides and nucleic acids encoding the polypeptides, in manufacturing medicament for stimulating a cytotoxic T cell response and for preventing or treating cancer, e.g. colorectal, lung, breast or ovarian cancer.

XX Example 11; Page 38; 87pp; English.

XX The present invention describes the use of a polypeptide (I) in the manufacture of a medicament for stimulating a cytotoxic T cell response, where (I) comprises a first portion comprising the part of human Fc that

CC binds to CD64 and a second portion comprising one or more heterologous T  
 CC cell epitopes. Also described is a method of stimulating a cytotoxic T  
 CC cell response in a patient such as a mammal, preferably human, by  
 CC administering (I) to the patient. (I) has cytostatic activity and can be  
 CC used in vaccine production. (I) and the nucleic acid encoding (I) are  
 CC useful in the manufacture of a medicament for stimulating cytotoxic T  
 CC cell response. The medicament is useful for preventing and/or treating  
 CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The  
 CC medicament stimulates cytotoxic and helper T cell responses. The  
 CC antibodies are useful as vaccines to stimulate helper and cytotoxic T  
 CC cell responses. The polypeptides and nucleic acids are useful in  
 CC optimising immunisation schedules for enhancing a protective immune  
 CC response against cancer. The present sequence represents an Fv region  
 CC SC100 antibody light chain related amino acid sequence which is used in  
 CC an example from the present invention

XX SQ Sequence 109 AA;

Query Match 100.0%; Score 56; DB 5; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 0.064;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWPT 9  
 Db 94 FQGSHPWPT 102  
 |||||

RESULT 6  
 AAY49217  
 ID AAY49217 standard; protein; 112 AA.  
 AC AAY49217;  
 DT 07-FEB-2000 (first entry)  
 XX Light chain variable region consensus sequence.  
 DE Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma;  
 KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;  
 KW tumor-associated antigen.  
 XX Synthetic.  
 OS US5977316-A.  
 PN 02-NOV-1999.  
 PD 16-JAN-1996; 96US-00591196.  
 PF 17-JAN-1995; 95US-00372676.  
 PR (KENT ) UNIV KENTUCKY.  
 PA Foon KA, Chatterjee SK, Chatterjee M;  
 PI WPI; 1996-354530/35.  
 DR Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)  
 PT - useful to treat or palliate a GD2-associated disease, e.g. melanoma and  
 PT glioma.  
 PS Disclosure; Fig 3C; 74pp; English.  
 XX The invention provides a monoclonal antibody (MAb) designated 1A7, which  
 CC elicits an anti-GD2 (tumor-associated antigen) immunological response in  
 CC humans. MAb 1A7 has defined light and heavy chain variable region  
 CC sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti  
 CC -GD2 immune response. The polypeptides can also be used for detecting or  
 CC purifying anti-GD2 antibody. The products can be used for treating GD2 -  
 CC associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue  
 CC carcinoma, and small cell carcinoma. They can be used for palliating the  
 CC disease or for reducing the risk of recurrence. The present sequence  
 CC represents the light chain variable region consensus sequence

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 56; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 0.066;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWPT 9  
 Db 94 FQGSHPWPT 102  
 |||||

RESULT 7  
 AAY25397  
 ID AAY25397 standard; protein; 112 AA.  
 AC AAY25397;  
 XX 07-SEP-1999 (first entry)  
 DT WO9932630 Seq ID 36.  
 DE Paraquat; antibody; light chain; herbicide; resistant; crop plant;  
 KW weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I;  
 KW free radical; lipid peroxidation; electron transport; photosystem II;  
 KW vacuole; cell surface; cytotoxic; sensitive.  
 XX Unidentified.  
 OS WO9932630-A1.  
 PN 01-JUL-1999.  
 PD 15-DEC-1998; 98WO-GB003760.  
 PF 19-DEC-1997; 97GB-00026955.  
 PR (ZENES ) ZENECA LTD.  
 PA Holt DC, Jones PG;  
 PI WPI; 1999-405173/34.  
 DR Herbicide binding proteins and related polynucleotides.  
 PT Disclosure; Page 44-45; 60pp; English.  
 PS This invention describes a novel herbicide binding protein which can  
 CC confer herbicide resistance activity. Crop plants, such as soybean,  
 CC cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower,  
 CC potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas,  
 CC barley, oat, turf grass, forage grass, sugar cane, pea, field bean, rice,  
 CC pine, poplar, apple, grape, citrus or nut plants, transformed with a  
 CC herbicide binding protein gene are resistant to the herbicide. Hence,  
 CC weeds can be selectively resistant in a field of the transformed crops.  
 CC The plants are substantially resistant or tolerant to herbicides, such as  
 CC paraquat or diquat, that inhibit photosynthesis by accepting electrons  
 CC from photosystem I thus generating free radicals which cause lipid  
 CC peroxidation or by blocking electron transport in photosystem II. The  
 CC herbicide binding proteins advantageously sequester the herbicide, e.g.  
 CC at the cell surface or in the vacuoles of a treated plant. Sequestration  
 CC at the cell surface prevents the entry of the herbicide into the cell so  
 CC that the herbicide cannot reach its intracellular target and exert any  
 CC significant cytotoxic effect. The herbicide binding protein inhibits the  
 CC mobility of the herbicide from the application site to the whole plant  
 CC preventing the herbicide reaching particularly sensitive organs.  
 CC Additionally, tolerant plants can be produced against herbicides that  
 CC have more than one target site

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 56; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 0.066;



Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9  
DB 94 FQGSHPWT 102

RESULT 8  
AAE15711  
ID AAE15711 standard; protein; 112 AA.  
AC AAE15711;  
XX 12-MAR-2002 (first entry)  
XX Mouse monoclonal antibody alpha 340 V<sub>k</sub> region variant, 340VKb.  
XX Mouse; humanised form; monoclonal antibody alpha 340; gene therapy;  
KW epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;  
KW gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;  
KW inhibitor; mutant; mutein; variant.  
XX Mus sp.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT Misc-difference 7 /note= "Wild type Thr substituted with Ser"  
FT Misc-difference 14 /note= "Wild type Ser substituted with Thr"  
FT Misc-difference 15 /note= "Wild type Leu substituted with Pro"  
FT Misc-difference 17 /note= "Wild type Asp substituted with Glu"  
FT Misc-difference 18 /note= "Wild type Gln substituted with Pro"  
FT Misc-difference 29 /note= "Wild type Ile substituted with Leu"  
FT Misc-difference 50 /note= "Wild type Lys substituted with Gln"  
FT Misc-difference 88 /note= "Wild type Leu substituted with Thr"  
FT Misc-difference 90 /note= "Wild type Ile substituted with Val"  
FT Misc-difference 109 /note= "Wild type Leu substituted with Val"  
FT Misc-difference 112 /note= "Wild type Asn substituted with Lys"  
XX WO200188138-A1.  
XX 22-NOV-2001.  
XX 21-MAY-2001; 2001WO-GB002226.  
XX 19-MAY-2000; 2000GB-00011981.  
XX 24-AUG-2000; 2000GB-00020794.  
XX (SCAN-) SCANCELL LTD.  
XX Ellis JRM, Durrant LG;  
XX WPI; 2002-062384/08.  
XX New humanized form of mouse monoclonal antibody 340 which binds to  
PT epidermal growth factor receptor and inhibits binding of growth factor.  
PT useful for treating colorectal, lung, breast, gastric and ovarian cancer.  
XX Example 2; Fig 7; 53pp; English.  
XX The present invention relates to a humanised form of the antibody 340 (a  
CC mouse monoclonal antibody which binds to epidermal growth factor (EGF)  
CC receptor and inhibits binding of EGF), obtainable from the cell line

CC deposited with the ECACC under accession number 97021428. The humanised  
CC form of the antibody 340 is useful in gene therapy, medicine and in the  
CC manufacture of a medicament for treatment or prophylaxis of cancer. The  
CC invention is useful for treating colorectal, lung, breast, gastric or  
CC ovarian cancers or also for preventing the recurrence of cancer after  
CC initial treatment or surgery. The invention is also useful for enhancing  
CC a protective immune response against cancer by optimised immunisation  
CC schedules. The humanised form of the antibody 340 has reduced  
CC immunogenicity but shows similar binding to cells expressing EGF  
CC receptor, as the original murine antibody and has increased ability to  
CC inhibit the growth of EGF receptor expressing cells. The invention is  
CC used as cell growth and apoptosis inhibitor. The present sequence is  
CC mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)  
CC region variant, 340VKb  
XX Sequence 112 AA;  
SQ Query Match 100.0%; Score 56; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FQGSHPWT 9  
DB 94 FQGSHPWT 102

RESULT 9  
AAE15713  
ID AAE15713 standard; protein; 112 AA.  
XX AAE15713;  
XX 12-MAR-2002 (first entry)  
XX Mouse monoclonal antibody alpha 340 V<sub>k</sub> region variant, 340VKd.  
XX Mouse; humanised form; monoclonal antibody alpha 340; gene therapy;  
KW epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;  
KW gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;  
KW inhibitor; mutant; mutein; variant.  
XX Mus sp.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT Misc-difference 7 /note= "Wild type Thr substituted with Ser"  
FT Misc-difference 14 /note= "Wild type Ser substituted with Thr"  
FT Misc-difference 15 /note= "Wild type Leu substituted with Pro"  
FT Misc-difference 17 /note= "Wild type Asp substituted with Glu"  
FT Misc-difference 18 /note= "Wild type Gln substituted with Pro"  
FT Misc-difference 50 /note= "Wild type Lys substituted with Val"  
FT Misc-difference 88 /note= "Wild type Leu substituted with Val"  
FT Misc-difference 109 /note= "Wild type Leu substituted with Val"  
FT Misc-difference 112 /note= "Wild type Asn substituted with Lys"  
XX WO200188138-A1.  
XX 22-NOV-2001.  
XX 21-MAY-2001; 2001WO-GB002226.  
XX 19-MAY-2000; 2000GB-00011981.  
XX 24-AUG-2000; 2000GB-00020794.  
XX

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PA (SCAN-) SCANCELL LTD.
XX
PI Ellis JRM, Durrant LG;
XX
XX WPI; 2002-062384/08.
DR
XX New humanized form of mouse monoclonal antibody 340 which binds to
PT epidermal growth factor receptor and inhibits binding of growth factor,
PT useful for treating colorectal, lung, breast, gastric and ovarian cancer.
XX
PS Example 2; Fig 7; 53pp; English.
XX
CC The present invention relates to a humanised form of the antibody 340 (a
CC mouse monoclonal antibody which binds to epidermal growth factor (EGF)
CC receptor and inhibits binding of EGF), obtainable from the cell line
CC deposited with the ECACC under accession number 97021428. The humanised
CC form of the antibody 340 is useful in gene therapy, medicine and in the
CC manufacture of a medicament for treatment or prophylaxis of cancer. The
CC invention is useful for treating colorectal, lung, breast, gastric or
CC ovarian cancers or also for preventing the recurrence of cancer after
CC initial treatment or surgery. The invention is also useful for enhancing
CC a protective immune response against cancer by optimised immunisation
CC schedules. The humanised form of the antibody 340 has reduced
CC immunogenicity but shows similar binding to cells expressing EGF
CC receptor, as the original murine antibody and has increased ability to
CC inhibit the growth of EGF receptor expressing cells. The invention is
CC used as cell growth and apoptosis inhibitor. The present sequence is
CC mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
CC region variant, 340VKd
XX
SQ Sequence 112 AA;
Query Match 100.0%; Score 56; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
DB 94 FQGSHPVPT 102

RESULT 10
AAE15704
ID AAE15704 standard; protein; 112 AA.
XX
XX AAE15704;
AC
DT 12-MAR-2002 (first entry)
XX
DE Mouse monoclonal antibody alpha 340 light chain variable (VK) region.
XX
KW Mouse; humanised form; monoclonal antibody alpha 340; gene therapy;
KW epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;
KW gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
KW inhibitor.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT 55..68
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT 95..102
FT /label= CDR3
FT /note= "Complementarity determining region 3"
XX
XX WO200189138-A1.
XX
XX 22-NOV-2001.
XX

PA 21-MAY-2001; 2001WO-GB002226.
XX
PR 19-MAY-2000; 2000GB-00011981.
PR 24-AUG-2000; 2000GB-00020794.
XX
PA (SCAN-) SCANCELL LTD.
XX
XX Ellis JRM, Durrant LG;
PI
XX WPI; 2002-062384/08.
DR
DR N-PSDB; AAD25247.
XX
XX New humanized form of mouse monoclonal antibody 340 which binds to
PT epidermal growth factor receptor and inhibits binding of growth factor,
PT useful for treating colorectal, lung, breast, gastric and ovarian cancer.
XX
PS Claim 6; Fig 2; 53pp; English.
XX
CC The present invention relates to a humanised form of the antibody 340 (a
CC mouse monoclonal antibody which binds to epidermal growth factor (EGF)
CC receptor and inhibits binding of EGF), obtainable from the cell line
CC deposited with the ECACC under accession number 97021428. The humanised
CC form of the antibody 340 is useful in gene therapy, medicine and in the
CC manufacture of a medicament for treatment or prophylaxis of cancer. The
CC invention is useful for treating colorectal, lung, breast, gastric or
CC ovarian cancers or also for preventing the recurrence of cancer after
CC initial treatment or surgery. The invention is also useful for enhancing
CC a protective immune response against cancer by optimised immunisation
CC schedules. The humanised form of the antibody 340 has reduced
CC immunogenicity but shows similar binding to cells expressing EGF
CC receptor, as the original murine antibody and has increased ability to
CC inhibit the growth of EGF receptor expressing cells. The invention is
CC used as cell growth and apoptosis inhibitor. The present sequence is
CC mouse monoclonal antibody alpha 340 light chain variable (VK) region
XX
SQ Sequence 112 AA;
Query Match 100.0%; Score 56; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
DB 94 FQGSHPVPT 102

RESULT 11
AAE15712
ID AAE15712 standard; protein; 112 AA.
XX
XX AAE15712;
AC
DT 12-MAR-2002 (first entry)
XX
DE Mouse monoclonal antibody alpha 340 Vk region variant, 340VKc.
XX
KW Mouse; humanised form; monoclonal antibody alpha 340; gene therapy;
KW epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;
KW gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
KW inhibitor; mutant; mutein; variant.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 7 /note= "Wild type Thr substituted with Ser"
FT Misc-difference 14 /note= "Wild type Ser substituted with Thr"
FT Misc-difference 15 /note= "Wild type Leu substituted with Pro"
FT Misc-difference 17 /note= "Wild type Asp substituted with Glu"
FT

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FT Misc-difference 18 /note= "Wild type Gln substituted with Pro"  
 FT Misc-difference 50 /note= "Wild type Lys substituted with Gln"  
 FT Misc-difference 88 /note= "Wild type Leu substituted with Thr"  
 FT Misc-difference 90 /note= "Wild type Ile substituted with Val"  
 FT Misc-difference 109 /note= "Wild type Leu substituted with Val"  
 FT Misc-difference 112 /note= "Wild type Asn substituted with Lys"  
 XX WO200188138-A1.  
 XX 22-NOV-2001.  
 XX 21-MAY-2001; 2001WO-GB002226.  
 XX 19-MAY-2000; 2000GB-00011981.  
 XX 24-AUG-2000; 2000GB-00020794.  
 XX (SCAN-) SCANCELL LTD.  
 XX Ellis JRM, Durrant LG;  
 XX WPI; 2002-062384/08.  
 XX New humanized form of mouse monoclonal antibody 340 which binds to  
 PT epidermal growth factor receptor and inhibits binding of growth factor,  
 PT useful for treating colorectal, lung, breast, gastric and ovarian cancer.  
 XX Example 2; Fig 7; 53pp; English.  
 XX The present invention relates to a humanised form of the antibody 340 (a  
 CC mouse monoclonal antibody which binds to epidermal growth factor (EGF)  
 CC receptor and inhibits binding of EGF), obtainable from the cell line  
 CC deposited with the ECACC under accession number 97021428. The humanised  
 CC form of the antibody 340 is useful in gene therapy, medicine and in the  
 CC manufacture of a medicament for treatment or prophylaxis of cancer. The  
 CC invention is useful for treating colorectal, lung, breast, gastric or  
 CC ovarian cancers or also for preventing the recurrence of cancer after  
 CC initial treatment or surgery. The invention is also useful for enhancing  
 CC a protective immune response against cancer by optimised immunisation  
 CC schedules. The humanised form of the antibody 340 has reduced  
 CC immunogenicity but shows similar binding to cells expressing EGF  
 CC receptor, as the original murine antibody and has increased ability to  
 CC inhibit the growth of EGF receptor expressing cells. The invention is  
 CC used as cell growth and apoptosis inhibitor. The present sequence is  
 CC mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)  
 CC region variant, 340VKC  
 XX Sequence 112 AA;  
 SQ Query Match 100.0%; Score 56; DB 5; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 0.066;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FQGSHPVPT 9  
 Db 94 FQGSHPVPT 102  
 RESULT 12  
 ADA14777  
 ID ADA14777 standard; peptide; 112 AA.  
 XX ADA14777;  
 AC ADA14777;  
 XX 06-NOV-2003 (first entry)  
 DT Peptide from antibody heavy chain resembling 1A7 #6.  
 DE  
 XX

KW heavy chain variable region; mouse; ganglioside GD2-associated tumour;  
 KW melanoma; antibody; anti-idiotypic; monoclonal antibody; 1A7;  
 KW neuroblastoma; glioma; sarcoma; small cell lung cancer.  
 OS Mus sp.  
 XX US6509016-B1.  
 XX 21-JAN-2003.  
 PD 15-APR-1999; 99US-00293533.  
 XX 17-JAN-1995; 95US-00372676.  
 PR 16-JAN-1996; 96US-00591196.  
 PR 21-NOV-1996; 96US-00752844.  
 XX (KENT) UNIV KENTUCKY.  
 XX Chatterjee M, Foon KA, Chatterjee SK;  
 PI WPI; 2003-401117/38.  
 DR Delaying recurrence and/or development of ganglioside GD2-associated  
 PT tumor in individual, by administering antibody containing light and heavy  
 PT chain variable region sequences contained in sequence of specified amino  
 PT acids.  
 XX Example 2; Fig 3; 82pp; English.  
 PS The invention relates to the recurrence and/or development of a  
 CC ganglioside GD2-associated tumour, e.g. melanoma, in an individual which  
 CC is delayed by administration of an antibody comprising light and heavy  
 CC chain variable region sequences of the anti-idiotypic monoclonal antibody  
 CC 1A7. The antibody is used for delaying recurrence and/or development of  
 CC GD2-associated tumour, e.g. melanoma, neuroblastoma, glioma, sarcoma, or  
 CC small cell lung cancer, in individual, and for treating individual with  
 CC GD2-associated tumour. The present sequence is a unique peptide region  
 CC from an antibody sequence resembling the anti-idiotypic antibody 1A7 heavy  
 CC chain.  
 XX Sequence 112 AA;  
 SQ Query Match 100.0%; Score 56; DB 6; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 0.066;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FQGSHPVPT 9  
 Db 94 FQGSHPVPT 102  
 RESULT 13  
 ADC35319  
 ID ADC35319 standard; protein; 112 AA.  
 XX ADC35319;  
 AC ADC35319;  
 XX 18-DEC-2003 (first entry)  
 DT Anti-idiotypic antibody VL region consensus sequence.  
 XX Mouse; monoclonal antibody; 1A7; anti-idiotypic antibody; ganglioside GD2;  
 KW cytostatic; melanoma; neuroblastoma; small cell lung cancer; tumour;  
 KW antibody; variable region; VH; VL; glioma; soft tissue sarcoma; vaccine.  
 XX Synthetic.  
 OS Mus sp.  
 XX US2003114398-A1.  
 PN 19-JUN-2003.  
 XX 21-MAY-2002; 2002US-00153401.  
 PF

XX 17-JAN-1995; 95US-00372676.  
 PR 16-JAN-1996; 96US-00591196.  
 PR 15-APR-1999; 99US-00293533.  
 XX (CHAT/) CHATTERJEE M.  
 PA (FOON/) FOON K A.  
 PA (CHAT/) CHATTERJEE S K.  
 XX Chatterjee M, Foon KA, Chatterjee SK;  
 PI WPI; 2003-810913/76.  
 XX Novel anti-idiotypic monoclonal antibody 1A7, that is capable of  
 PT recruiting a tumor-specific response against glycosphingolipid GD2,  
 PT useful for treating a GD2-associated disease e.g., melanoma, glioma, soft  
 PT tissue sarcoma.  
 XX Example 2; SEQ ID NO 15; 84pp; English.  
 XX The invention relates to a monoclonal antibody 1A7 (an anti-idiotypic  
 CC antibody eliciting an anti-GD2(ganglioside) response). Also included are  
 CC an antibody producing cell deposited under ATCC Accession No. HB-11786  
 CC (or its progeny), a polynucleotide comprising a sequence encoding a  
 CC polypeptide with immunological activity of 1A7 (where the polypeptide  
 CC comprises at least 5 consecutive amino acids from a variable region of  
 CC 1A7), an isolated polynucleotide comprising a region of at least 20  
 CC consecutive nucleotides that is capable of forming a stable duplex with a  
 CC polynucleotide encoding the light or heavy chain variable region of 1A7  
 CC under conditions where the region does not form a stable hybrid with a  
 CC polynucleotide consisting of a variable region encoding sequence  
 CC appearing as ABC35321 - ADC35370, a host cell comprising the  
 CC polynucleotide, a fusion polypeptide comprising 1A7, a humanised antibody  
 CC comprising 5 consecutive amino acids from the 1A7 variable regions and a  
 CC vaccine comprising the antibodies. The antibodies are useful for  
 CC eliciting an immune response in an individual, and for treating a GD2-  
 CC associated disease in an individual. The GD2-associated diseases is  
 CC chosen from melanoma, neuroblastoma, glioma, soft tissue sarcoma, and  
 CC small cell carcinoma. The individual has a clinically detectable tumour,  
 CC and the method is for palliating the GD2-associated disease. 1A7 is  
 CC preferably useful for treating a tumour that was previously detected in  
 CC the individual and has been treated and is clinically undetectable at the  
 CC time of the administering of 1A7, or for reducing the risk of recurrence  
 CC of a clinically detectable tumour. 1A7 and the humanised antibody are  
 CC useful for detecting the presence of an anti-GD2 antibody bound to a  
 CC tumour cell. The present sequence represents a consensus sequence for the  
 CC light or heavy chain variable region of monoclonal antibody 1A7.  
 XX Sequence 112 AA;  
 SQ Query Match 100.0%; Score 56; DB 7; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 0.066;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FQGSHPVPT 9  
 Db 94 FQGSHPVPT 102  
 RESULT 14  
 ADD94125  
 ID ADD94125 standard; protein; 112 AA.  
 AC ADD94125;  
 XX 29-JAN-2004 (first entry)  
 DT Mouse HUI77 variable region light chain partial amino acid sequence.  
 XX grafted antibody; complementarity determining region; CDR; light CDR;  
 KW heavy CDR; cryptic collagen epitope; solid tumour;  
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
 KW collagen agonist; collagen antagonist; cancer metastasis;

KW anti-cryptic collagen; antibody; HUI77; variable region light chain;  
 KW mouse; murine.  
 XX Mus musculus.  
 XX WO2003046204-A2.  
 XX 05-JUN-2003.  
 XX 26-NOV-2002; 2002WO-US038147.  
 XX 26-NOV-2001; 2001US-00995529.  
 PR 06-DEC-2001; 2001US-00011250.  
 XX (CELL-) CELL MATRIX INC.  
 PA Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;  
 PI WPI; 2003-513649/48.  
 DR N-PSDB; ADD94124.  
 XX New cryptic collagen antibody with one or more complementarity  
 PT determining regions, useful for diagnosing and treating disorders  
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
 XX Example 1; SEQ ID NO 10; 232pp; English.  
 XX This invention relates to a novel grafted antibody or its functional  
 CC fragment comprising one or more complementarity determining regions  
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
 CC acid (aa) substitution where the antibody has specific binding activity  
 CC for a cryptic collagen epitope. The growth of all solid tumours requires  
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
 CC to limiting tumour growth. The invention may allow development of  
 CC therapeutics with a cytostatic activity as a collagen agonist or  
 CC antagonist. The invention is useful for diagnosing and treating disorders  
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
 CC present sequence is the partial amino acid sequence of the mouse anti-  
 CC cryptic collagen site antibody HUI77 variable region light chain used  
 CC during the creation of the antibody of the invention.  
 XX Sequence 112 AA;  
 SQ Query Match 100.0%; Score 56; DB 7; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 0.066;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FQGSHPVPT 9  
 Db 94 FQGSHPVPT 102  
 RESULT 15  
 ADJ76888  
 ID ADJ76888 standard; protein; 112 AA.  
 XX ADJ76888;  
 AC ADJ76888;  
 XX 06-MAY-2004 (first entry)  
 DT Anti-IGF-IR related protein #5.  
 XX cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX Mus musculus.  
 OS WO2003059951-A2.  
 PN 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.  
PF 18-JAN-2002; 2002FR-00000653.  
XX 18-JAN-2002; 2002FR-00000654.  
PR 07-MAY-2002; 2002FR-00005753.  
XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
PA Goetsch L, Corvala N, Leger O;  
XX WPI; 2003-569653/53.  
XX New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.  
XX Disclosure; SEQ ID NO 54; 164pp; French.  
XX The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
CC hyperactivity of signal transduction pathways mediated by interaction of  
CC these receptors with their ligands. Especially they inhibit  
CC transformation of normal cells to tumor cells, inhibit growth and/or  
CC proliferation of tumor cells, so are useful against cancers of the  
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
CC protein sequence used to generate the Ab of the invention.  
XX SQ Sequence 112 AA;

Query Match 100.0%; Score 56; DB 7; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FQGSHPVPT 9  
Db 94 FQGSHPVPT 102

Search completed: December 30, 2005, 13:23:58  
Job time : 80.9839 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 12.7742 Seconds  
(without alignments)  
67.789 Million cell updates/sec

Title: US-10-735-916A-6  
Perfect score: 56  
Sequence: 1 FQSHVPWT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	103	2 PH1043	Ig light chain V r
2	53	94.6	121	2 S67944	Ig kappa chain BrE
3	47	83.9	102	2 S14590	Ig kappa chain V r
4	47	83.9	102	2 S14594	Ig kappa chain V r
5	47	83.9	102	2 S14592	Ig kappa chain V r
6	47	83.9	102	2 S14593	Ig kappa chain V r
7	47	83.9	102	2 E28195	Ig kappa chain V r
8	47	83.9	110	2 S26335	Ig kappa chain V r
9	47	83.9	112	2 D28195	Ig kappa chain V r
10	47	83.9	131	2 B39276	Ig kappa chain V r
11	46	82.1	103	2 PH1042	Ig light chain pre
12	46	82.1	113	2 PL0203	Ig light chain V r
13	45	80.4	114	2 A32987	anti-DNA autoantib
14	44	78.6	103	2 PH1040	Ig kappa chain V-I
15	44	78.6	112	2 A49715	Ig light chain V r
16	44	78.6	219	2 S16112	Ig kappa chain V r
17	43	76.8	101	2 S11126	Ig kappa chain V r
18	43	76.8	102	2 S14591	Ig kappa chain V r
19	43	76.8	112	2 S38719	Ig light chain V r
20	43	76.8	112	2 A36259	Ig kappa chain V r
21	42	75.0	93	2 PH1039	Ig light chain V r
22	42	75.0	112	2 PL0273	Ig kappa chain V r
23	42	75.0	112	2 A31807	Ig kappa chain V r
24	42	75.0	219	2 PC4203	Ig kappa chain (mo
25	42	75.0	389	2 H86676	hypothetical prote
26	41	73.2	103	2 PH1030	Ig light chain V r
27	41	73.2	112	2 H28840	Ig kappa chain V r
28	41	73.2	112	2 B31485	Ig kappa chain V r
29	41	73.2	112	2 A27887	Ig kappa chain V r

30 41 73.2 113 2 E30560 Ig kappa chain V r  
31 41 73.2 114 2 A34353 anti-peptide Fab,  
32 41 73.2 118 2 PT0359 Ig kappa chain V r  
33 41 73.2 131 2 B34904 Ig kappa chain pre  
34 41 73.2 131 2 S52449 Ig kappa chain V r  
35 41 73.2 131 2 C34904 Ig kappa chain pre  
36 41 73.2 219 2 S52028 Ig kappa chain - m  
37 41 73.2 225 2 JL0029 Ig kappa chain pre  
38 40 71.4 96 2 S55366 Ig kappa chain V r  
39 40 71.4 102 2 PH1035 Ig light chain V r  
40 40 71.4 119 2 A49032 Ig kappa chain V r  
41 39 69.6 111 2 S15673 Ig kappa chain V r  
42 39 69.6 112 2 C27887 Ig kappa chain V r  
43 38 67.9 103 2 PH1034 Ig light chain V r  
44 38 67.9 103 2 PH1038 Ig light chain V r  
45 38 67.9 103 2 PH1037 Ig light chain V r

#### ALIGNMENTS

##### RESULT 1

PH1043  
Ig light chain V region (clone 111.68) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: PH1043  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992

A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1043  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-103 <TIL>  
A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176AA5  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 56; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 0.0054;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9  
|||  
Db 94 FQSHVPWT 102

##### RESULT 2

S67944  
Ig kappa chain BrE-3 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 05-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C;Accession: S67944  
R;Couto, J.R.; Blank, E.W.; Peterson, J.A.; Ceriani, R.L.  
Hybridoma 12, 15-23, 1993

A;Title: Cloning of cDNAs encoding the variable domains of antibody BrE-3 and construct  
A;Reference number: S67944; MUID:93202671; PMID:8454302  
A;Accession: S67944  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-121 <COU>  
A;Cross-references: UNIPARC:UPI0001149C2; EMBL:Z22547; NID:g296068; PIDN:CAA80268.1;  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;25-104/Domain: immunoglobulin homology <IMM>

Query Match 94.6%; Score 53; DB 2; Length 121;  
Best Local Similarity 88.9%; Pred. No. 0.022;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9

Db 103 FQSHVPWT 111  
||||:||||

## RESULT 3

IG kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S14590; S14589  
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.  
submitted to the EMBL Data Library, March 1991  
A:Description: Natural polypeptide antibodies differ from Ag-induced antibodies in VH C  
A:Reference number: S14484  
A:Accession: S14590  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <CHE>  
A:Cross-references: UNIPARC:UPI0000115F40; EMBL:X58662; NID:G52927; PIDN:CAA41519.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 102;  
Best Local Similarity 88.9%; Pred. No. 0.21;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
||||:||||

Db 94 FQSHVPYT 102

## RESULT 4

IG kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S14594  
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.  
submitted to the EMBL Data Library, March 1991  
A:Description: Natural polypeptide antibodies differ from Ag-induced antibodies in VH C  
A:Reference number: S14484  
A:Accession: S14594  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <CHE>  
A:Cross-references: UNIPARC:UPI0000115F44; EMBL:X58666; NID:G52935; PIDN:CAA41523.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 102;  
Best Local Similarity 88.9%; Pred. No. 0.21;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
||||:||||

Db 94 FQSHVPYT 102

## RESULT 5

IG kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S14592  
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.  
submitted to the EMBL Data Library, March 1991  
A:Description: Natural polypeptide antibodies differ from Ag-induced antibodies in VH C  
A:Reference number: S14484  
A:Accession: S14592  
A>Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-102 <CHE>

A:Cross-references: UNIPARC:UPI0000115F42; EMBL:X58664; NID:G52931; PIDN:CAA41521.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 102;  
Best Local Similarity 88.9%; Pred. No. 0.21;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
||||:||||

Db 94 FQSHVPYT 102

## RESULT 6

IG kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S14593  
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.  
submitted to the EMBL Data Library, March 1991  
A:Description: Natural polypeptide antibodies differ from Ag-induced antibodies in VH C  
A:Reference number: S14484  
A:Accession: S14593  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <CHE>  
A:Cross-references: UNIPARC:UPI0000115F43; EMBL:X58665; NID:G52933; PIDN:CAA41522.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 102;  
Best Local Similarity 88.9%; Pred. No. 0.21;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
||||:||||

Db 94 FQSHVPYT 102

## RESULT 7

IG kappa chain V region (anti-haloperidol antibody E) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: E28195  
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
J. Biol. Chem. 263, 4059-4063, 1988  
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid  
A:Reference number: A28195; MUID:88153717; PMID:3267217  
A:Accession: E28195  
A:Molecule type: mRNA  
A:Residues: 1-102 <SHE>  
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B1B; EMBL:M29770  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;6-85/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 102;  
Best Local Similarity 88.9%; Pred. No. 0.21;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
||||:||||

Db 84 FQSHVPYT 92

## RESULT 8

S26335  
IG kappa chain V region - mouse



C;Species: Mus musculus (house mouse)  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 C;Accession: S26335  
 R;Stark, S.E.; Caton, A.J.  
 J. Exp. Med. 174, 613-624, 1991  
 A;Title: Antibodies that are specific for a single amino acid interchange in a protein e  
 A;Reference number: S26309; MUID:91341421; PMID:1908510  
 A;Accession: S26335  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-110 <STA>  
 A;Cross-references: UNIPARC:UPI0000115F78; EMBL:X59183; NID:G52314; PIDN:CAA41893.1; PID  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 110;  
 Best Local Similarity 88.9%; Pred. No. 0.23;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
 |||||:  
 Db 94 FQGSHPVPT 102

RESULT 9  
 D28195  
 Ig kappa chain V region (anti-haloperidol antibody D) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
 C;Accession: D28195  
 R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
 J. Biol. Chem. 263, 4059-4063, 1988  
 A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s  
 A;Reference number: A28195; MUID:88153717; PMID:3267217  
 A;Accession: D28195  
 A;Molecule type: mRNA  
 A;Residues: 1-112 <SHE>  
 A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B01; GB:M19769  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 112;  
 Best Local Similarity 88.9%; Pred. No. 0.23;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
 |||||:  
 Db 94 FQGSHPVPT 102

RESULT 10  
 B39276  
 Ig light chain precursor V-D-J region (6-19) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000  
 C;Accession: B39276  
 R;Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990  
 A;Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis an  
 A;Reference number: A39276; MUID:91088540; PMID:2263605  
 A;Accession: B39276  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-131 <REI>  
 A;Cross-references: UNIPARC:UPI0000115153; GB:M55313; NID:G198095; PIDN:AAA63385.1; PID  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: immunoglobulin  
 F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 131;  
 Best Local Similarity 88.9%; Pred. No. 0.28;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
 |||||:  
 Db 113 FQGSHPVPT 121

RESULT 11  
 PH1042  
 Ig light chain V region (clone 202.s38) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C;Accession: PH1042  
 R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B  
 A;Reference number: PH0971; MUID:92381444; PMID:1512540  
 A;Accession: PH1042  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-103 <TIL>  
 A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176AA4  
 A;Experimental source: B cell, strain [NZB x NZW]F1  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: immunoglobulin  
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 46; DB 2; Length 103;  
 Best Local Similarity 88.9%; Pred. No. 0.33;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
 |||||:  
 Db 94 FQGSHPVPT 102

RESULT 12  
 PL0203  
 anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
 C;Accession: PL0203  
 R;Smith, R.G.; Voss Jr., E.W.  
 Mol. Immunol. 27, 463-470, 1990  
 A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from  
 A;Reference number: PL0198; MUID:90309788; PMID:2114528  
 A;Accession: PL0203  
 A;Molecule type: mRNA  
 A;Residues: 1-113 <SMI>  
 A;Cross-references: UNIPARC:UPI0000113786; GB:X53643; NID:G50196; PIDN:CAA37694.1; PID:  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 F;16-95/Domain: immunoglobulin homology <IMM>  
 F;24-39/Region: complementarity-determining 1  
 F;55-61/Region: complementarity-determining 2  
 F;94-102/Region: complementarity-determining 3  
 F;101-113/Region: D region

Query Match 82.1%; Score 46; DB 2; Length 113;  
 Best Local Similarity 88.9%; Pred. No. 0.36;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
 |||||:  
 Db 94 FQGSHPVPT 102

RESULT 13  
 A32967  
 Ig kappa chain V-II region TE33 - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 21-Jan-2000  
 C;Accession: A32967  
 R;Levy, R.; Asulin, O.; Scherf, T.; Levitt, M.; Anglister, J.

Biochemistry 28, 7168-7175, 1989  
 A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predicted by 2D NMR and by sequence analysis  
 A;Reference number: A32967; MUID:90057406; PMID:2819059  
 A;Accession: A32967  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-114 <LEV>  
 A;Cross-references: UNIPARC:UPI0000114F5D; GB:M30481; NID:G197157; PIDN:AAA38935.1; PID:10000114F5D  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 114;

Best Local Similarity 77.8%; Pred. No. 0.54;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9

DB 94 FQGSHPWT 102

#### RESULT 14

PHI040

Ig light chain V region (clone 17s.83) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C;Accession: PHI040

R;Trillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PHI040

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-103 <TIL>

A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI00000176AA2

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 78.6%; Score 44; DB 2; Length 103;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9

DB 94 FQGSHPWT 102

#### RESULT 15

A49715

Ig kappa chain V region (anti-glucuronoxylomanan antibody 439) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 21-Jan-2000

C;Accession: A49715

R;Otterson, E.W.; Welch, W.H.; Kozel, T.R.

J. Biol. Chem. 269, 1858-1864, 1994

A;Title: Protein-polysaccharide interactions. A monoclonal antibody specific for the cap

A;Reference number: A49715; MUID:94124530; PMID:8294434

A;Accession: A49715

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-112 <OPT>

A;Cross-references: UNIPARC:UPI0000115509; GB:U01240; NID:G402265; PIDN:AAD10617.1; PID:10000115509

A;Note: authors translated the codon CTT for residue 99 as Val

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 78.6%; Score 44; DB 2; Length 112;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGSHPWT 9  
 DB 95 QGTHLPWT 102

Search completed: December 30, 2005, 13:34:54  
 Job time : 13.7742 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 81 Seconds  
(without alignments)  
78.392 Million cell updates/sec

Title: US-10-735-916A-6  
Perfect score: 56  
Sequence: 1 FQSHVPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	82.1	248	2	Q65ZQ7 9MURI
2	42	75.0	375	2	Q91YR3 MOUSE
3	42	75.0	389	2	Q9CIE7 LACTOCOC
4	42	75.0	504	2	Q4HV68 GIBZEL
5	41	73.2	112	2	Q53VP8 MOUSE
6	41	73.2	962	2	Q845Y7 9CHRO
7	41	73.2	962	2	Q845Y8 MICAE
8	41	73.2	993	2	Q48915 MICAE
9	41	73.2	2114	2	Q8RTG4 MICAE
10	41	73.2	2126	2	Q93LR1 MICAE
11	41	73.2	2126	2	Q93LR2 MICAE
12	41	73.2	2126	2	Q9S1A8 MICAE
13	40	71.4	201	2	Q5CFU2 CRYHO
14	40	71.4	982	2	Q51ZV2 MAGGR
15	40	71.4	2133	2	Q7WRQ4 9NOST
16	39.5	70.5	436	2	Q82DC5 STRAW
17	39	69.6	53	2	Q5C219 SCHUA
18	39	69.6	101	1	YB7J SCHPO
19	39	69.6	267	2	Q51HW6 MAGGR
20	39	69.6	348	2	Q854X6 9CAUD
21	39	69.6	463	2	Q6D073 ERWCT
22	39	69.6	508	2	Q6Z5V5 ORYSA
23	39	69.6	510	2	Q511B2 MAGGR
24	39	69.6	694	2	Q6NK77 CORDI
25	39	69.6	700	2	Q6Z5V6 ORYSA
26	39	69.6	1356	2	Q4IOD3 GIBZE
27	38.5	68.8	522	2	Q4J838 SULAC
28	38	67.9	173	2	Q53656 STIAU
29	38	67.9	217	2	Q51MF7 MAGGR
30	38	67.9	232	2	Q82WL3 NITRU
31	38	67.9	303	2	Q4Q3K2 LEIMA

32	38	67.9	342	2	Q850Y4 ORYSA
33	38	67.9	348	2	Q6LNP1 PHOPR
34	38	67.9	402	2	Q5MB05 MICROGADUS
35	38	67.9	460	2	Q8ZBA0 YERSINIA PE
36	38	67.9	461	2	Q66F83 YERPE
37	38	67.9	509	2	Q5QIB0 CAMAC
38	38	67.9	543	2	Q83X81 STRRO
39	38	67.9	564	2	Q53PM9 ORYSA
40	38	67.9	622	2	Q5MB06 MICROGADUS
41	38	67.9	655	2	Q8LN69 ORYSA
42	38	67.9	684	2	Q49319 ARATH
43	38	67.9	773	2	Q7YOC0 ORYSA
44	38	67.9	779	2	Q8H8E2 ORYSA
45	38	67.9	794	2	Q7XTH2 ORYSA

Q850Y4	oryza sativ
Q6LNP1	photobacter
Q5MB05	microgadus
Q8ZBA0	yersinia pe
Q66F83	yersinia ps
Q5QIB0	camptotheca
Q83X81	streptomyce
Q53PM9	oryza sativ
Q5MB06	microgadus
Q8LN69	oryza sativ
Q49319	arabidopsis
Q7YOC0	oryza sativ
Q8H8E2	oryza sativ
Q7XTH2	oryza sativ

#### ALIGNMENTS

##### RESULT 1

Q65ZQ7 9MURI  
ID Q65ZQ7\_9MURI PRELIMINARY; PRT; 248 AA.  
AC Q65ZQ7;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE B3(Fv)-PE40 (Fragment).  
GN Name=B3(Fv)-PE40;  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92020904; PubMed=1924323;  
RA Brinkmann U., Pai L.H., Fitzgerald D.J., Willingham M., Pastan I.;  
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete  
regression of a human carcinoma in mice";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).  
DR EMBL; S57990; AAB19971.2; -; mRNA.  
DR SNR; Q65ZQ7; 4-247.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IG; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON TER 248 248  
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 82.1%; Score 46; DB 2; Length 248;  
Best Local Similarity 88.9%; Pred. No. 7;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9

Db 229 FQSHVPFT 237

##### RESULT 2

Q91YR3 MOUSE  
ID Q91YR3\_MOUSE PRELIMINARY; PRT; 375 AA.  
AC Q91YR3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE Phf1 protein.  
GN Phf1 protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.

```

OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalios D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015077; AAH15077.1; -; mRNA.
DR Ensembl; ENSMUSG000000024193; Mus musculus.
DR MGI; MGI:98647; Phf1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002999; Tudor.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 2.
DR SMART; SM00249; PHD; 2.
DR SMART; SM00333; TUDOR; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
SQ SEQUENCE 375 AA; 41146 MW; 57D88E19A5BBB729 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 375;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGSHVPW 8
Db 359 EGSHVPW 365
:|||||

RESULT 3
Q9CIE7 LACIA PRELIMINARY; PRT; 389 AA.
AC Q9CIE7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cellulose-specific PTS system IIC component (EC 2.7.1.69).
GN Name=ptc; OrderedLocNames=LL0416;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IL1403;

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RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.CR-1697R;
RA Bolotin A., Wincker P., Mauer S., Jallion O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RL lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753 (2001).
DR EMBL; AB006278; AAK04514.1; -; Genomic_DNA.
DR PIR; H86676; H86676.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008982; F:protein-N(P1)-phosphohistidine-sugar phospho. .; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009401; F:phosphoenolpyruvate-dependent sugar phospho. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003352; Ptrans_EIIC.
DR InterPro; IPR004501; Pts_lac.
DR Pfam; PF02378; PTS_EIIC_1.
DR TIGRPFAMs; TIGR00410; lacE; 1.
KW Complete proteome.
SQ SEQUENCE 389 AA; 41700 MW; F49D2C3095FCF347 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 389;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGHVPWT 9
Db 325 FNGAIVPWT 333
|::|||

RESULT 4
Q4HV68 GIBZE PRELIMINARY; PRT; 504 AA.
AC Q4HV68;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG11140.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArelano K.,
RA Diaz J.S., Dodge K., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafer N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliou H., Venkataran V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

```

CC preliminary data.  
 DR EMBL; AACW01000459; EAA74791.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 504 AA; 55160 MW; 26098EA86A332C2F CRC64;

Query Match 75.0%; Score 42; DB 2; Length 504;  
 Best Local Similarity 66.7%; Pred. No. 72;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
 |||||:  
 Db 72 FVGSHPVWS 80

## RESULT 5

ID Q53VP8 MOUSE PRELIMINARY; PRT; 112 AA.  
 AC Q53VP8;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Kappa chain (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86136012; PubMed=3937730;  
 RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;  
 RT "The idiotypic network and the internal image; possible regulation of  
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
 RT antibodies in the GAT system.";  
 RL ENBO J. 4:3681-3688 (1985).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE OF 108-109.

RA Fougereau M.;  
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X03386; CAA27113.1; -; mRNA.  
 FT NON TER 1 1  
 FT NON TER 112 112

SQ SEQUENCE 112 AA; 12266 MW; C844B7881A89C18A CRC64;

Query Match 73.2%; Score 41; DB 2; Length 112;  
 Best Local Similarity 77.8%; Pred. No. 24;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
 |||||:  
 Db 94 FQGIHVPT 102

## RESULT 6

ID Q845Y7\_9CHRO PRELIMINARY; PRT; 962 AA.  
 AC Q845Y7;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Microcystin synthetase (Fragment).  
 GN Name=mcysB;  
 OS Microcystis viridis.  
 OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.  
 OX NCBI\_TaxID=44822;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NIES102;  
 RA Yoshida T., Shi R., Chinen H., Yuki Y., Yoshida M., Kondo R.,  
 RA Shingo H.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.

DR EMBL; AB092807; BAC57997.1; -; Genomic\_DNA.  
 DR HSSP; P14687; 1AMU.  
 DR GO; GO:0048037; F:cofactor binding; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR010071; AA\_adenyl\_dom.  
 DR InterPro; IPR009081; ACP\_like.  
 DR InterPro; IPR000873; AMP-bind.  
 DR InterPro; IPR001242; Condensatn.  
 DR InterPro; IPR006163; Phspanteth\_bind.  
 DR Pfam; PF00501; AMP-binding; 1.  
 DR Pfam; PF00668; Condensation; 1.  
 DR Pfam; PF00550; PP-binding; 1.  
 DR PRINTS; PR00154; AMPBINDING.  
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.  
 DR PROSITE; PS50075; ACP\_DOMAIN; 1.  
 DR PROSITE; PS00455; AMP\_BINDING; 1.  
 FT NON TER 1 1  
 FT NON TER 962 962

SQ SEQUENCE 962 AA; 108980 MW; 2510459A5CCD484F CRC64;

Query Match 73.2%; Score 41; DB 2; Length 962;  
 Best Local Similarity 66.7%; Pred. No. 21e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
 |||||:  
 Db 862 FVGSHPVPT 870

## RESULT 7

Q845Y8 MICAE  
 ID Q845Y8 MICAE PRELIMINARY; PRT; 962 AA.  
 AC Q845Y8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Microcystin synthetase (Fragment).  
 GN Name=mcysB;  
 OS Microcystis aeruginosa.  
 OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.  
 OX NCBI\_TaxID=1126;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NIES298;  
 RA Yoshida T., Shi R., Chinen H., Yuki Y., Yoshida M., Kondo R.,  
 RA Shingo H.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.

DR EMBL; AB092806; BAC57996.1; -; Genomic\_DNA.  
 DR HSSP; P14687; 1AMU.  
 DR GO; GO:0048037; F:cofactor binding; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR010071; AA\_adenyl\_dom.  
 DR InterPro; IPR009081; ACP\_like.  
 DR InterPro; IPR000873; AMP-bind.  
 DR InterPro; IPR001242; Condensatn.  
 DR InterPro; IPR001969; Pept\_Asp\_AS.  
 DR InterPro; IPR006163; Phspanteth\_bind.  
 DR Pfam; PF00501; AMP-binding; 1.  
 DR Pfam; PF00668; Condensation; 1.  
 DR Pfam; PF00550; PP-binding; 1.  
 DR PRINTS; PR00154; AMPBINDING.  
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.  
 DR PROSITE; PS50075; ACP\_DOMAIN; 1.  
 DR PROSITE; PS00455; AMP\_BINDING; 1.  
 DR PROSITE; PS00141; ASP\_PROTEASE; UNKNOWN\_1.  
 FT NON TER 1 1  
 FT NON TER 962 962

SQ SEQUENCE 962 AA; 108678 MW; 37F77CFD87F5FCB4 CRC64;

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Query Match          73.2%; Score 41; DB 2; Length 962;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FOGSHVPWT 9
DB      862 PKGSHLSWT 870

RESULT 8
Q48915 MICAE
ID Q48915 MICAE PRELIMINARY; PRT; 993 AA.
AC Q48915;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptide synthetase module (Fragment).
GN Name=peptide synthetase;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HUB 5-2-4;
RX MEDLINE=96162875; PubMed=8595871; DOI=10.1016/0378-1097(95)00469-6;
RA Meisner K., Dittmann E., Borner T.;
RT "Toxic and non-toxic strains of the cyanobacterium Microcystis
aeruginosa contain sequences homologous to peptide synthetase genes.";
RL FEMS Microbiol. Lett. 135:295-303(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HUB 5-2-4;
RA Juerchort K.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
family.
DR EMBL; Z28338; CA82192.1; -; Genomic_DNA.
DR PIR; S49111; S49111.
DR HSSP; Q30409; 1DNY.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA_adenyl_dom.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR006163; Phosphanteth_bind.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00668; Condensation; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
DR PROSITE; PS50075; ACP DOMAIN; 1.
DR PROSITE; PS00455; AMP BINDING; 1.
DR NON_TER 1
DR NON_TER 993
FT NON_TER 993
SQ SEQUENCE 993 AA; 112326 MW; 0EC0929E489CBB1E CRC64;

Query Match          73.2%; Score 41; DB 2; Length 993;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FOGSHVPWT 9
DB      874 PKGSHLSWT 882

RESULT 9
Q8RTG4 MICAE
ID Q8RTG4 MICAE PRELIMINARY; PRT; 2114 AA.
AC Q8RTG4;

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DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE McyB.
GN Name=mcvB;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UV027;
RA Raps S., Miller D., Ratner S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458094; AAL82383.1; -; Genomic_DNA.
DR HSSP; Q30409; 1DNY.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0031177; P:phosphopantetheine binding; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA_adenyl_dom.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR006163; Phosphanteth_bind.
DR Pfam; PF00501; AMP-binding; 2.
DR Pfam; PF00668; Condensation; 2.
DR Pfam; PF00550; PP-binding; 2.
DR PRINTS; PR00154; AMPBINDING.
DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
DR PROSITE; PS50075; ACP DOMAIN; 2.
DR PROSITE; PS00455; AMP BINDING; 2.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; 1.
SQ SEQUENCE 2114 AA; 240913 MW; 4549B6F61E600C66 CRC64;

Query Match          73.2%; Score 41; DB 2; Length 2114;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FOGSHVPWT 9
DB      1267 PKGSHLSWT 1275

RESULT 10
Q93LR1 MICAE
ID Q93LR1 MICAE PRELIMINARY; PRT; 2126 AA.
AC Q93LR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Microcystin synthetase.
GN Name=mcvB;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UV 027;
RA Botes E.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034602; AAK61391.1; -; Genomic_DNA.
DR HSSP; Q30409; 1DNY.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0031177; P:phosphopantetheine binding; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA_adenyl_dom.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; Condensatn.

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DR InterPro; IPR000977; DNA\_ligase.  
 DR InterPro; IPR006163; Phosphatase\_bind.  
 DR InterPro; IPR006162; Ppantne S.  
 DR Pfam; PF00501; AMP-binding; 2.  
 DR Pfam; PF00668; Condensation; 2.  
 DR Pfam; PF00550; PP-binding; 2.  
 DR PRINTS; PR00154; AMPBINDING.  
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.  
 DR PROSITE; PS00075; ACP DOMAIN; 2.  
 DR PROSITE; PS00455; AMP BINDING; 1.  
 DR PROSITE; PS00697; DNA\_LIGASE A1; UNKNOWN 1.  
 DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.  
 SQ SEQUENCE 2126 AA; 242439 MW; 6DB575F2A49B1933 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 2126;  
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9  
 |||||:  
 Db 1279 FKSHLSWT 1287

RESULT 11  
 Q93LR2 MICAE  
 ID Q93LR2 MICAE PRELIMINARY; PRT; 2126 AA.  
 AC Q93LR2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Microcystin synthetase.  
 GN Names=mcys;  
 OS Microcystis aeruginosa.  
 OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.  
 OX NCBI\_TaxID=1126;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PCC 7813;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY034601; AAK61390.1; -; Genomic\_DNA.  
 DR HSP; O30409; INDY.  
 DR GO; GO:0048037; F:cofactor binding; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0031177; F:phosphopantetheine binding; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR010071; AA-adenyl-dom.  
 DR InterPro; IPR009081; ACP-like.  
 DR InterPro; IPR000873; AMP-bind.  
 DR InterPro; IPR001242; Condensatn.  
 DR InterPro; IPR000977; DNA\_ligase.  
 DR InterPro; IPR001969; Pept\_Asp\_AS.  
 DR InterPro; IPR006163; Phosphatase\_bind.  
 DR InterPro; IPR006162; Ppantne S.  
 DR Pfam; PF00501; AMP-binding; 2.  
 DR Pfam; PF00668; Condensation; 2.  
 DR PRINTS; PR00154; AMPBINDING.  
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.  
 DR PROSITE; PS00075; ACP DOMAIN; 2.  
 DR PROSITE; PS00455; AMP BINDING; 2.  
 DR PROSITE; PS00141; ASP\_PROTEASE; UNKNOWN 1.  
 DR PROSITE; PS00697; DNA\_LIGASE A1; UNKNOWN 1.  
 DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.  
 SQ SEQUENCE 2126 AA; 242247 MW; 2A8438725198585C CRC64;

Query Match 73.2%; Score 41; DB 2; Length 2126;  
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9  
 |||||:  
 Db 1279 FKSHLSWT 1287

RESULT 12  
 Q9S1A8 MICAE  
 ID Q9S1A8 MICAE PRELIMINARY; PRT; 2126 AA.  
 AC Q9S1A8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE McyB protein.  
 GN Name=mcys;  
 OS Microcystis aeruginosa.  
 OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.  
 OX NCBI\_TaxID=1126;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-139;  
 RX MEDLINE=99398430; PubMed=10467167;  
 RA Nishizawa T., Asayama M., Fujii K., Harada K., Shirai M.;  
 RT "Genetic analysis of the peptide synthetase genes for a cyclic  
 heptapeptide microcystin in Microcystis spp.";  
 RL J. Biochem. 126:520-529 (1999).  
 DR EMBL; AB019578; BAA83993.1; -; Genomic\_DNA.  
 DR HSP; P14687; IAMU.  
 DR GO; GO:0048037; F:cofactor binding; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0031177; F:phosphopantetheine binding; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR010071; AA-adenyl-dom.  
 DR InterPro; IPR009081; ACP-like.  
 DR InterPro; IPR000873; AMP-bind.  
 DR InterPro; IPR001242; Condensatn.  
 DR InterPro; IPR000977; DNA\_ligase.  
 DR InterPro; IPR001969; Pept\_Asp\_AS.  
 DR InterPro; IPR006163; Phosphatase\_bind.  
 DR InterPro; IPR006162; Ppantne S.  
 DR Pfam; PF00501; AMP-binding; 2.  
 DR Pfam; PF00668; Condensation; 2.  
 DR PRINTS; PR00154; AMPBINDING.  
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.  
 DR PROSITE; PS00075; ACP DOMAIN; 2.  
 DR PROSITE; PS00455; AMP BINDING; 2.  
 DR PROSITE; PS00141; ASP\_PROTEASE; UNKNOWN 1.  
 DR PROSITE; PS00697; DNA\_LIGASE A1; UNKNOWN 1.  
 DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.  
 SQ SEQUENCE 2126 AA; 242242 MW; D7EFC6C9F6F43AB3 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 2126;  
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9  
 |||||:  
 Db 1279 FKSHLSWT 1287

RESULT 13  
 Q5CFU2 CRYHO  
 ID Q5CFU2 CRYHO PRELIMINARY; PRT; 201 AA.  
 AC Q5CFU2;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=Chro.70128;  
 OS Cryptosporidium hominis.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
 OC Cryptosporidiidae; Cryptosporidium.  
 OX NCBI\_TaxID=237895;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=TU502;

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RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
RA Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
RA Bankier A.T., Peterson D.L., Abrahamson M.S., Kapur V., Tzipori S.,
RA Buck G.A.;
RT "The genome of Cryptosporidium hominis.";
RL Nature 431:1107-1112(2004).
DR EMBL; AAE01000406; EAL35474.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004518; F:nuclease activity; IEA.
DR InterPro; IPR012337; RNAseH fold.
KW Hydrolase; Hypothetical protein; Nuclease.
SQ SEQUENCE 201 AA; 23518 MW; FA6A8F84A00E9AA CRC64;

Query Match 71.4%; Score 40; DB 2; Length 201;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSHVPW 8
DB 121 QGSHCPW 127

RESULT 14
Q51ZY2 MAGGR
ID Q51ZY2_MAGGR PRELIMINARY; PRT; 982 AA.
AC Q51ZY2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MGO5904.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachi H., Ambruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitskayn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseilis M., Karlsson E.,
RA Kells C., Kieu A., Kiener P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokytang T., Lokytang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marbella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., McGhee T., Meldrim J., Menes L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pigani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Teamia T., Tsomo N., Vallee B., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,

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RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU01000839; EAA52776.1; -; Genomic DNA.
DR InterPro; IPR012351; Cycokine_4_hlx.
DR InterPro; IPR012340; NA-bind_OB_sub.
DR InterPro; IPR009007; Pept_Aspartc_cat.
KW Hypothetical protein.
SQ SEQUENCE 982 AA; 106107 MW; EC7E86B1E6911520 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 982;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QGSHVPWT 9
DB 554 GSHWPWT 560

RESULT 15
Q7WRQ4_9NCST
ID Q7WRQ4_9NCST PRELIMINARY; PRT; 2133 AA.
AC Q7WRQ4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Peptide synthetase.
GN Name=mcysB;
OS Anabaena circinalis 90.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=46234;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14766543; DOI=10.1128/ASM.70.2.686-692.2004;
RA Rouhiainen L., Vakkilainen T., Siemer B.L., Buikema W., Haselkorn R.,
RA Sivonen K.;
RT "Genes coding for hepatotoxic heptapeptides (microcystins) in the
RT cyanobacterium Anabaena strain 90.";
RL Appl. Environ. Microbiol. 70:686-692 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Rouhiainen L., Vakkilainen T., Lumby-Siemer B., Buikema W.,
RA Haselkorn R., Sivonen K.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY212249; AAO62587.1; -; Genomic DNA.
DR EMBL; AJ536156; CAD60102.1; -; Genomic DNA.
DR HSSP; P14687; IAMU.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0031177; F:phosphopantetheine binding; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA_adenyl_dom.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR006163; Phosphateth_bind.
DR InterPro; IPR006162; Ppantne_S.

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DR Pfam; PF00501; AMP-binding; 2.  
 DR Pfam; PF00668; Condensation; 2.  
 DR Pfam; PF00550; PP-binding; 2.  
 DR PRINTS; PR00154; AMPBINDING.  
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.  
 DR PROSITE; PS00075; ACP\_DOMAIN; 2.  
 DR PROSITE; PS00455; AMP\_BINDING; 2.  
 DR PROSITE; PS00697; DNA\_LIGASE\_A1; UNKNOWN 1.  
 DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 2.  
 SQ SEQUENCE 2133 AA; 243072 MW; AF806DB0F9372FE7 CRC64;  
 Query Match 71.4%; Score 40; DB 2; Length 2133;  
 Best Local Similarity 66.7%; Pred. No. 7e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 FQSHVPWT 9  
 Db 1286 FNGSHLSWT 1294

Search completed: December 30, 2005, 13:33:26  
 Job time : 84 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 66.9194 Seconds  
(without alignments)  
56.194 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQSHVPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
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2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	56	100.0	9	3	US-09-995-529-36
3	56	100.0	9	4	US-10-470-045-48
4	56	100.0	9	5	US-10-735-916A-6
5	56	100.0	49	4	US-10-470-045-94
6	56	100.0	112	3	US-09-995-529-10
7	56	100.0	112	3	US-09-995-529-10
8	56	100.0	112	4	US-10-153-401-15
9	56	100.0	112	4	US-10-308-817-172
10	56	100.0	112	4	US-10-308-817-172
11	56	100.0	112	4	US-10-308-817-180
12	56	100.0	112	4	US-10-308-817-181
13	56	100.0	112	4	US-10-308-817-182
14	56	100.0	112	4	US-10-453-698-172
15	56	100.0	112	4	US-10-453-698-179
16	56	100.0	112	4	US-10-453-698-180
17	56	100.0	112	4	US-10-453-698-181
18	56	100.0	112	4	US-10-453-698-182
19	56	100.0	112	4	US-10-258-728-4
20	56	100.0	112	4	US-10-258-728-25
21	56	100.0	112	4	US-10-258-728-26
22	56	100.0	112	4	US-10-258-728-27
23	56	100.0	112	4	US-10-258-728-28
24	56	100.0	112	5	US-10-735-916A-54
25	56	100.0	112	5	US-10-735-916A-56
26	56	100.0	112	5	US-10-735-916A-61
27	56	100.0	112	5	US-10-735-916A-65

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28 56 100.0 122 5 US-10-735-916A-49 Sequence 49, Appl
29 56 100.0 131 5 US-10-735-916A-63 Sequence 63, Appl
30 56 100.0 131 5 US-10-735-916A-67 Sequence 67, Appl
31 56 100.0 149 3 US-09-990-205-2 Sequence 2, Appl
32 56 100.0 149 4 US-10-153-401-2 Sequence 84, Appl
33 56 100.0 249 6 US-11-093-103-84 Sequence 66, Appl
34 56 100.0 263 4 US-10-153-401-66 Sequence 72, Appl
35 53 94.6 9 3 US-09-947-839-72 Sequence 66, Appl
36 53 94.6 131 3 US-09-947-839-11 Sequence 11, Appl
37 52 92.9 9 3 US-09-995-529-128 Sequence 128, App
38 52 92.9 9 3 US-09-995-529-132 Sequence 132, App
39 52 92.9 9 3 US-09-995-529-138 Sequence 138, App
40 52 92.9 9 3 US-09-995-529-138 Sequence 128, App
41 52 92.9 9 3 US-09-995-529-132 Sequence 132, App
42 52 92.9 9 3 US-09-995-529-138 Sequence 138, App
43 51 91.1 9 3 US-09-995-529-139 Sequence 139, App
44 51 91.1 9 3 US-09-995-529-140 Sequence 140, App
45 51 91.1 9 3 US-09-995-529-141 Sequence 141, App

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#### ALIGNMENTS

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RESULT 1
US-09-995-529-36
; Sequence 36, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-36

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Query Match 100.0%; Score 56; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FQSHVPWT 9
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Db 1 FQSHVPWT 9

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RESULT 2
US-09-995-529-36
; Sequence 36, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-36

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Query Match 100.0%; Score 56; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
 |||||  
 Db 1 FQGSHPVPT 9

## RESULT 3

US-10-470-045-48  
 ; Sequence 48, Application US/10470045  
 ; Publication No. US20040146505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Scancell Limited  
 ; APPLICANT: Durrant, Linda Gillian  
 ; APPLICANT: Parsons, Tina  
 ; TITLE OF INVENTION: Substances  
 ; FILE REFERENCE: P32181WO/NJL  
 ; CURRENT APPLICATION NUMBER: US/10/470,045  
 ; CURRENT FILING DATE: 2003-07-24  
 ; PRIOR APPLICATION NUMBER: GB 0102145.0  
 ; PRIOR FILING DATE: 2001-01-26  
 ; NUMBER OF SEQ ID NOS: 101  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 48  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-470-045-48

Query Match 100.0%; Score 56; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
 |||||  
 Db 1 FQGSHPVPT 9

## RESULT 4

US-10-735-916A-6  
 ; Sequence 6, Application US/10735916A  
 ; Publication No. US2005084906A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GOETSCH, Liliane  
 ; APPLICANT: CORVAIA, Nathalie  
 ; APPLICANT: LEGER, Olivier  
 ; APPLICANT: DUFLOS, Alain  
 ; APPLICANT: BECK, Alain  
 ; APPLICANT: HAEUW, Jean-Francois  
 ; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
 ; FILE REFERENCE: 017753-183  
 ; CURRENT APPLICATION NUMBER: US/10/735,916A  
 ; CURRENT FILING DATE: 2003-12-15  
 ; PRIOR APPLICATION NUMBER: FR 03/08 538  
 ; PRIOR FILING DATE: 2003-07-11  
 ; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
 ; PRIOR FILING DATE: 2003-01-20  
 ; PRIOR APPLICATION NUMBER: FR 02/00 653  
 ; PRIOR FILING DATE: 2002-01-18  
 ; PRIOR APPLICATION NUMBER: FR 02/00 654  
 ; PRIOR FILING DATE: 2002-01-18  
 ; PRIOR APPLICATION NUMBER: FR 02/05 753  
 ; PRIOR FILING DATE: 2002-05-07  
 ; NUMBER OF SEQ ID NOS: 156  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-735-916A-6

Query Match 100.0%; Score 56; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
 |||||  
 Db 1 FQGSHPVPT 9

## RESULT 5

US-10-470-045-94  
 ; Sequence 94, Application US/10470045  
 ; Publication No. US20040146505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Scancell Limited  
 ; APPLICANT: Durrant, Linda Gillian  
 ; APPLICANT: Parsons, Tina  
 ; TITLE OF INVENTION: Substances  
 ; FILE REFERENCE: P32181WO/NJL  
 ; CURRENT APPLICATION NUMBER: US/10/470,045  
 ; CURRENT FILING DATE: 2003-07-24  
 ; PRIOR APPLICATION NUMBER: GB 0102145.0  
 ; PRIOR FILING DATE: 2001-01-26  
 ; NUMBER OF SEQ ID NOS: 101  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 94  
 ; LENGTH: 49  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-470-045-94

Query Match 100.0%; Score 56; DB 4; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 0.077;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
 |||||  
 Db 34 FQGSHPVPT 42

## RESULT 6

US-09-995-529-10  
 ; Sequence 10, Application US/09995529  
 ; Publication No. US20030099655A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Watkins, Jeffrey D.  
 ; APPLICANT: Huse, William D.  
 ; APPLICANT: Tang, Ying  
 ; TITLE OF INVENTION: Humanized Collagen Antibodies and  
 ; TITLE OF INVENTION: Related Methods  
 ; FILE REFERENCE: P-IX 4976  
 ; CURRENT APPLICATION NUMBER: US/09/995,529  
 ; CURRENT FILING DATE: 2001-11-26  
 ; NUMBER OF SEQ ID NOS: 358  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 112  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-995-529-10

Query Match 100.0%; Score 56; DB 3; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
 |||||  
 Db 94 FQGSHPVPT 102

## RESULT 7

US-09-995-529-10

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; Sequence 10, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-10

Query Match      100.0%; Score 56; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
DB      94 FQGSHPVPT 102

RESULT 8
US-10-153-401-15
; Sequence 15, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-153-401-15

Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
DB      94 FQGSHPVPT 102

RESULT 9
US-10-308-817-172
; Sequence 172, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 172
; LENGTH: 112
; TYPE: PRT
; ORGANISM: mouse
US-10-308-817-172

Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
DB      94 FQGSHPVPT 102

RESULT 10
US-10-308-817-179
; Sequence 179, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 179
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-308-817-179

Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
DB      94 FQGSHPVPT 102
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RESULT 11
US-10-308-817-180
; Sequence 180, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 180
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-308-817-180
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

RESULT 12
US-10-308-817-181
; Sequence 181, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 181
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-308-817-181
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

RESULT 13
US-10-308-817-182
; Sequence 182, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-308-817-182
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

RESULT 14
US-10-453-698-172
; Sequence 172, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 172
; LENGTH: 112
; TYPE: PRT
; ORGANISM: mouse
; OTHER INFORMATION:
US-10-453-698-172
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

RESULT 15
US-10-453-698-179
; Sequence 179, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-453-698-179
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

Search completed: December 30, 2005, 14:14:52
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OM protein' - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 3.33871 Seconds  
(without alignments)  
20.187 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	56	100.0	9	7	US-11-125-837-15
3	56	100.0	9	7	US-11-105-708-19
4	56	100.0	112	7	US-11-012-353-54
5	56	100.0	112	7	US-11-012-353-56
6	56	100.0	112	7	US-11-012-353-61
7	56	100.0	112	7	US-11-012-353-65
8	56	100.0	122	7	US-11-012-353-49
9	56	100.0	131	7	US-11-012-353-63
10	56	100.0	131	7	US-11-012-353-67
11	56	100.0	131	7	US-11-125-837-23
12	47	83.9	113	6	US-10-932-334-59
13	47	83.9	113	6	US-10-932-334-61
14	47	83.9	251	6	US-10-512-184-30
15	47	83.9	320	6	US-10-512-184-67
16	47	83.9	569	6	US-10-512-184-66
17	47	83.9	618	6	US-10-512-184-48
18	46	82.1	112	7	US-11-012-353-55
19	46	82.1	113	6	US-10-932-334-66
20	46	82.1	113	6	US-10-932-334-68
21	46	82.1	116	7	US-11-065-943-49
22	45	80.4	113	6	US-10-932-334-65
23	44	78.6	112	7	US-11-012-353-57
24	43	76.8	113	6	US-10-932-334-69
25	43	76.8	131	6	US-10-789-273-14

26 75.0 113 6 US-10-932-334-62  
27 41 73.2 9 6 US-10-932-334-6  
28 41 73.2 113 6 US-10-932-334-8  
29 41 73.2 113 6 US-10-932-334-9  
30 41 73.2 113 6 US-10-932-334-10  
31 41 73.2 113 6 US-10-932-334-11  
32 41 73.2 113 6 US-10-932-334-12  
33 41 73.2 113 6 US-10-932-334-58  
34 41 73.2 113 6 US-10-932-334-63  
35 41 73.2 113 6 US-10-932-334-64  
36 41 73.2 113 6 US-10-932-334-82  
37 41 73.2 113 6 US-10-932-334-83  
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40 41 73.2 113 6 US-10-932-334-86  
41 41 73.2 113 6 US-10-932-334-90  
42 41 73.2 113 6 US-10-932-334-94  
43 41 73.2 132 6 US-10-932-334-50  
44 40 71.4 100 6 US-10-932-334-56  
45 40 71.4 113 6 US-10-932-334-60

#### ALIGNMENTS

RESULT 1  
US-11-012-353-6  
; Sequence 6, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOTSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFIOS, ALAIN  
; APPLICANT: HAEUM, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; PRIOR FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-6

Query Match 100.0%; Score 56; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPWT 9  
| | | | |  
Db 1 FQGSHPWT 9

RESULT 2  
US-11-125-837-15  
; Sequence 15, Application US/11125837

```
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-15

Query Match          100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9

RESULT 3
US-11-105-708-19
; Sequence 19, Application US/11/105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
; APPLICANT: Pernasetti, Flavia
; APPLICANT: Freimark, Bruce
; APPLICANT: Van Epps, Dennis
; APPLICANT: Brooks, Peter C
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
; FILE REFERENCE: 30797-704.501
; CURRENT APPLICATION NUMBER: US/11/105,708
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 09/478,977
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: 60/152,496
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/143,534
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/114,878
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/114,877
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-105-708-19

Query Match          100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9

RESULT 4
US-11-012-353-54
; Sequence 54, Application US/11/012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-54

Query Match          100.0%; Score 56; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

RESULT 5
US-11-012-353-56
; Sequence 56, Application US/11/012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
```

; SEQ ID NO 56  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-56

Query Match 100.0%; Score 56; DB 7; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.00059;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
Db 94 FQGSHPVPT 102

## RESULT 6

US-11-012-353-61  
; Sequence 61, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 61  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-61

Query Match 100.0%; Score 56; DB 7; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.00059;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
Db 94 FQGSHPVPT 102

## RESULT 7

US-11-012-353-65  
; Sequence 65, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 61  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-61

Query Match 100.0%; Score 56; DB 7; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.00059;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
Db 94 FQGSHPVPT 102

## RESULT 8

US-11-012-353-49  
; Sequence 49, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 49  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-49

Query Match 100.0%; Score 56; DB 7; Length 122;  
Best Local Similarity 100.0%; Pred. No. 0.00064;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9

; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 65  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-65

Query Match 100.0%; Score 56; DB 7; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.00059;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
Db 94 FQGSHPVPT 102

## RESULT 8

US-11-012-353-49  
; Sequence 49, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 49  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-49

Query Match 100.0%; Score 56; DB 7; Length 122;  
Best Local Similarity 100.0%; Pred. No. 0.00064;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9

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Db          104 FQSHVPWT 112
|||||
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 67
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-67

Query Match          100.0%; Score 56; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FQSHVPWT 9
Db          113 FQSHVPWT 121
|||||
RESULT 11
US-11-125-837-23
; Sequence 23, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-23

Query Match          100.0%; Score 56; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FQSHVPWT 9
Db          113 FQSHVPWT 121
|||||
RESULT 12
US-10-932-334-59
; Sequence 59, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
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```
Db          104 FQSHVPWT 112
|||||
; Sequence 63, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 63
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-63

Query Match          100.0%; Score 56; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FQSHVPWT 9
Db          113 FQSHVPWT 121
|||||
RESULT 10
US-11-012-353-67
; Sequence 67, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
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;
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-59

Query Match      83.9%; Score 47; DB 6; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
Db 94 FQSHVPYT 102

RESULT 13
US-10-932-334-61
; Sequence 61, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-61

Query Match      83.9%; Score 47; DB 6; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
Db 94 FQSHVPYT 102

RESULT 14
US-10-512-184-30
; Sequence 30, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VD2 with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: Originates from Mus musculus.
US-10-512-184-30

Query Match      83.9%; Score 47; DB 6; Length 251;
Best Local Similarity 88.9%; Pred. No. 0.056;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

---

```
;
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-59

Query Match      83.9%; Score 47; DB 6; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
Db 94 FQSHVPYT 102

RESULT 13
US-10-932-334-61
; Sequence 61, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-61

Query Match      83.9%; Score 47; DB 6; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
Db 94 FQSHVPYT 102

RESULT 14
US-10-512-184-30
; Sequence 30, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VD2 with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: Originates from Mus musculus.
US-10-512-184-30

Query Match      83.9%; Score 47; DB 6; Length 251;
Best Local Similarity 88.9%; Pred. No. 0.056;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 FQSHVPWT 9
Db 231 FQSHVPYT 239

RESULT 15
US-10-512-184-67
; Sequence 67, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising AG - linker - scFv VD2.
US-10-512-184-67

Query Match      83.9%; Score 47; DB 6; Length 320;
Best Local Similarity 88.9%; Pred. No. 0.07;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
Db 300 FQSHVPYT 308

Search completed: December 30, 2005, 14:15:21
Job time : 4.33871 secs
```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:52:54 ; Search time 182 Seconds  
(without alignments)  
21.728 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQSHVPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 203235

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_21:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*  
9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	5	ABP52345 Fv region
2	56	100.0	9	7	ADD94151 Mouse HUI
3	56	100.0	9	7	ADJ76840 CDR seque
4	56	100.0	9	9	ADZ67010 Murine in
5	55	98.2	9	8	ADS88735 CDR deriv
6	52	92.9	9	7	ADD94253 Mouse HUI
7	52	92.9	9	7	ADD94243 Mouse HUI
8	52	92.9	9	7	ADD94247 Mouse HUI
9	51	91.1	9	7	ADD94260 Mouse HUI
10	51	91.1	9	7	ADD94256 Mouse HUI
11	51	91.1	9	7	ADD94254 Mouse HUI
12	51	91.1	9	7	ADD94258 Mouse HUI
13	51	91.1	9	7	ADD94257 Mouse HUI
14	51	91.1	9	7	ADD94255 Mouse HUI
15	50	89.3	9	7	ADD94242 Mouse HUI
16	50	89.3	9	7	ADD94241 Mouse HUI
17	50	89.3	9	7	ADD94245 Mouse HUI
18	49	87.5	9	7	ADD94246 Mouse HUI
19	49	87.5	9	7	ADD94244 Mouse HUI
20	48	85.7	9	7	ADD94252 Mouse HUI
21	47	83.9	9	2	AAR40218 Humanised
22	47	83.9	9	2	AAR70455 VL sequen
23	47	83.9	9	6	ABP72122 Mouse FGF
24	7	83.9	9	7	ADD28190 Mouse lec

25	47	83.9	9	7	ADD94250	Add94250 Mouse HUI
26	47	83.9	9	7	ADZ67010	Adz67010 Murine in
27	47	83.9	9	7	ADL35324	Adl35324 Murine an
28	47	83.9	9	8	ADP84870	Adp84870 Complemen
29	47	83.9	9	9	ABB03714	Aeb03714 Murine 5B
30	46	82.1	9	7	ADD94251	Add94251 Mouse HUI
31	46	82.1	9	7	ADD94249	Add94249 Mouse HUI
32	46	82.1	9	8	ADM78083	Adm78083 Human SJB
33	46	82.1	9	8	ADM78107	Adm78107 Human SJB
34	46	82.1	9	8	ADM78125	Adm78125 Human SJB
35	46	82.1	9	8	ADM78131	Adm78131 Human SJB
36	45	80.4	9	4	AAB86296	Aab86296 Murine de
37	45	80.4	9	7	ADD94473	Add94473 Mouse ant
38	45	80.4	9	7	ADD94248	Add94248 Mouse HUI
39	45	80.4	9	9	AEA34943	Aea34943 Human ant
40	45	80.4	9	9	AEI17184	Aebi17184 EphA2-spe
41	45	80.4	9	9	AEA42984	Aea42984 EphA2 ant
42	43	76.8	9	6	ABP58278	Abp58278 Murine mo
43	43	76.8	9	7	ADH61994	Adh61994 Mouse ant
44	43	76.8	9	8	ADR19274	Adr19274 Glycosyla
45	42	75.0	9	2	AAW70922	Aaw70922 CDR3 of t

#### ALIGNMENTS

RESULT 1  
ABP52345  
ID ABP52345 standard; peptide; 9 AA.  
XX  
AC ABP52345;  
XX  
DT 17-OCT-2002 (first entry)  
XX  
DE Fv region SC100 antibody CDR-L3 amino acid sequence.  
XX  
KW Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;  
KW tumour; immune response; cancer; vaccine; antibody.  
XX  
OS Mus musculus.  
OS Synthetic.  
XX  
PN WO200258728-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 28-JAN-2002; 2002WO-GB000354.  
XX  
PR 26-JAN-2001; 2001GB-00002145.  
XX  
XX (SCAN-) SCANCEL LTD.  
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
Durrant LG, Parsons T, Robins A;  
WPI; 2002-608418/65.  
Use of polypeptides and nucleic acids encoding the polypeptides, in  
manufacturing medicament for stimulating a cytotoxic T cell response and  
for preventing or treating cancer, e.g. colorectal, lung, breast or  
ovarian cancer.  
Example 11; Page 46; 87pp; English.  
The present invention describes the use of a polypeptide (I) in the  
manufacture of a medicament for stimulating a cytotoxic T cell response,  
where (I) comprises a first portion comprising the part of human Fc that  
binds to CD64 and a second portion comprising one or more heterologous T  
cell epitopes. Also described is a method of stimulating a cytotoxic T  
cell response in a patient such as a mammal, preferably human, by  
administering (I) to the patient. (I) has cytostatic activity and can be  
used in vaccine production. (I) and the nucleic acid encoding (I) are  
useful in the manufacture of a medicament for stimulating cytotoxic T

CC	cryptic collagen site antibody HUI77 variable region light chain CDR
CC	which is related to the invention.
XX	
SQ	Sequence 9 AA;
	Query Match            100.0%;   Score 56;   DB 7;   Length 9;
	Best Local Similarity   100.0%;   Pred. No. 2e+06;
	Matches     9;   Conservative   0;   Mismatches     0;   Indels     0;   Gaps     0;
QY	1 FQGSHVPWT 9                 1 FQGSHVPWT 9
DB	
RESULT 3	
ADJ76840	
ID	AUJ76840 standard; peptide; 9 AA.
XX	AC ADJ76840;
XX	
DT	06-MAY-2004 (first entry)
DE	CDR sequence for anti-IGF-1R antibody.
XX	
KW	cystostatic; antipsoriatic; antibody;
KW	insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW	or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW	ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW	CDR.
XX	
OS	Mus musculus.
XX	
PN	WO2003059951-A2.
XX	
FD	24-JUL-2003.
XX	
PF	20-JAN-2003; 2003WO-FR000178.
XX	
PR	18-JAN-2002; 2002FR-00000653.
PR	18-JAN-2002; 2002FR-00000654.
PR	07-MAY-2002; 2002FR-00005753.
XX	
PA	(FABR ) FABRE MEDICAMENT SA PIERRE.
XX	
PI	Goetsch L, Corvaia N, Leger O;
XX	
DR	WPI; 2003-569653/53.
DR	N-ESDB; ADJ76839.
PT	New antibodies that bind to human insulin-like growth factor receptor,
PT	useful for treatment, prevention and diagnosis of cancers.
XX	
FS	Claim 1; SEQ ID NO 6; 164pp; French.
XX	
CC	The invention relates to an isolated antibody (Ab), and its functional
CC	fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC	1R) and optionally: (i) inhibit natural binding of insulin-like growth
CC	factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC	kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC	treat diseases associated with overexpression and/or abnormal activity of
CC	IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
CC	hyperactivity of signal transduction pathways mediated by interaction of
CC	these receptors with their ligands. Especially they inhibit
CC	transformation of normal cells to tumor cells, inhibit growth and/or
CC	proliferation of tumor cells, so are useful against cancers of the
CC	prostate, lung, breast, endometrium and colon, also osteosarcoma, and
CC	also for treating psoriasis. Ab are also used to diagnose diseases caused
CC	by abnormal expression of IGF-1R and/or EGFR. This sequence represents an
CC	CDR sequence used to generate the Ab of the invention.
XX	
SQ	Sequence 9 AA;
	Query Match            100.0%;   Score 56;   DB 7;   Length 9;



Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
 DB 1 FQSHVPWT 9

RESULT 4  
 ADZ67010  
 ID ADZ67010 standard; peptide; 9 AA.  
 AC ADZ67010;  
 XX  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:6.  
 XX  
 KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2005084906-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 PF 16-DEC-2003; 2003US-00735916.  
 XX  
 PR 18-JAN-2002; 2002FR-0000653.  
 PR 18-JAN-2002; 2002FR-0000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 PR 20-JAN-2003; 2003WO-FR000178.  
 PR 11-JUL-2003; 2003FR-00008538.  
 XX  
 XX (GOET/) GOETSCH L.  
 PA (CORV/) CORVAIA N.  
 PA (LEGE/) LEGER O.  
 PA (DUFL/) DUFLOS A.  
 PA (HAU/) HAEUW J.  
 PA (BECK/) BECK A.  
 XX  
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 PI WPI; 2005-321968/33.  
 XX  
 DR N-PSDB; ADZ67009.  
 XX  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX  
 PS Claim 1; SEQ ID NO 6; 125pp; English.  
 XX  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended

CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC scarring from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 100.0%; Score 56; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
 DB 1 FQSHVPWT 9

RESULT 5  
 ADS88735  
 ID ADS88735 standard; peptide; 9 AA.  
 XX  
 AC ADS88735;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 XX CDR derived from the VL region of an anti RSV G glycoprotein antibody.  
 XX  
 KW G glycoprotein; respiratory syncytial virus;  
 KW respiratory syncytial virus infection; RSV; RSV infection;  
 KW complementarity determining region; CDR.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2004083373-A2.  
 XX  
 PD 30-SEP-2004.  
 XX  
 XX 22-MAR-2004; 2004WO-GB001239.  
 XX  
 XX 22-MAR-2003; 2003GB-00006618.  
 XX  
 PA (TYNE-) UNIV NEWCASTLE-UPON-TYNE.  
 XX  
 XX Toms G, Routledge E, Mekseepalard C;  
 PI WPI; 2004-691033/67.  
 XX  
 DR N-PSDB; ADS88741.  
 XX  
 XX New antibody against the G glycoprotein of RSV with a variable region  
 PT having a first and second domain from a VL and VH region, respectively,  
 PT useful for treating respiratory syncytial virus (RSV) infections.  
 XX  
 PS Claim 1; SEQ ID NO 3; 93pp; English.  
 XX  
 XX The specification describes an against the G glycoprotein of respiratory  
 CC syncytial virus, with a variable region comprising a first domain from a  
 CC variable light chain region and a second domain a variable heavy chain  
 CC region. The antibodies of the invention are useful for treating and

CC preventing the development of infections caused by the respiratory  
CC syncytial virus (RSV). The present sequence represents a complementarity  
CC determining region (CDR) derived from the variable light chain (VL)  
CC region of an antibody directed against the G glycoprotein of RSV. This  
CC peptide is used to construct antibodies of the invention.

XX Sequence 9 AA;

Query Match 98.2%; Score 55; DB 8; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
DB 1 FQGSHPVPT 9  
|||||

RESULT 6  
ADD94253  
ID ADD94253 standard; peptide; 9 AA.

XX ADD94253;

XX 29-JAN-2004 (first entry)

DE Mouse HUI77 mutant light chain CDR amino acid sequence SeqID138.

XX grafted antibody; complementarity determining region; CDR; light CDR;  
KW heavy CDR; cryptic collagen epitope; solid tumour;  
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
KW collagen agonist; collagen antagonist; cancer metastasis;  
KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;  
KW mutant; mutein.

XX Synthetic.  
OS Mus musculus.

XX WO2003046204-A2.

XX 05-JUN-2003.

XX 26-NOV-2002; 2002WO-US038147.

XX 26-NOV-2001; 2001US-00995529.

PR 06-DEC-2001; 2001US-00011250.

XX (CELL-) CELL MATRIX INC.

XX Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;

XX WPI; 2003-513649/48.

XX New cryptic collagen antibody with one or more complementarity  
PT determining regions, useful for diagnosing and treating disorders  
PT associated with angiogenesis, tumor growth and/or cancer metastasis.

XX Claim 24; SEQ ID NO 138; 232pp; English.

XX This invention relates to a novel grafted antibody or its functional  
CC fragment comprising one or more complementarity determining regions  
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
CC acid (aa) substitution where the antibody has specific binding activity  
CC for a cryptic collagen epitope. The growth of all solid tumours requires  
CC new blood vessel growth; angiogenesis, inhibition of which is an approach  
CC to limiting tumour growth. The invention may allow development of  
CC therapeutics with a cytostatic activity as a collagen agonist or  
CC antagonist. The invention is useful for diagnosing and treating disorders  
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
CC present sequence is the amino acid sequence of a mutant mouse anti-  
CC cryptic collagen site antibody HUI77 variable region light chain CDR  
CC which may be used during the creation of an antibody of the invention.

XX Sequence 9 AA;

Query Match 92.9%; Score 52; DB 7; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
DB 1 FQGSHPVPT 9  
|||||

RESULT 7  
ADD94243  
ID ADD94243 standard; peptide; 9 AA.

XX ADD94243;

XX 29-JAN-2004 (first entry)

DE Mouse HUI77 mutant light chain CDR amino acid sequence SeqID128.

XX grafted antibody; complementarity determining region; CDR; light CDR;  
KW heavy CDR; cryptic collagen epitope; solid tumour;  
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
KW collagen agonist; collagen antagonist; cancer metastasis;  
KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;  
KW mutant; mutein.

XX Synthetic.  
OS Mus musculus.

XX WO2003046204-A2.

XX 05-JUN-2003.

XX 26-NOV-2002; 2002WO-US038147.

XX 26-NOV-2001; 2001US-00995529.

PR 06-DEC-2001; 2001US-00011250.

XX (CELL-) CELL MATRIX INC.

XX Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;

XX WPI; 2003-513649/48.

XX New cryptic collagen antibody with one or more complementarity  
PT determining regions, useful for diagnosing and treating disorders  
PT associated with angiogenesis, tumor growth and/or cancer metastasis.

XX Claim 24; SEQ ID NO 128; 232pp; English.

XX This invention relates to a novel grafted antibody or its functional  
CC fragment comprising one or more complementarity determining regions  
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
CC acid (aa) substitution where the antibody has specific binding activity  
CC for a cryptic collagen epitope. The growth of all solid tumours requires  
CC new blood vessel growth; angiogenesis, inhibition of which is an approach  
CC to limiting tumour growth. The invention may allow development of  
CC therapeutics with a cytostatic activity as a collagen agonist or  
CC antagonist. The invention is useful for diagnosing and treating disorders  
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
CC present sequence is the amino acid sequence of a mutant mouse anti-  
CC cryptic collagen site antibody HUI77 variable region light chain CDR  
CC which may be used during the creation of an antibody of the invention.

XX Sequence 9 AA;

Query Match 92.9%; Score 52; DB 7; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9  
DB 1 FQGSHPVPT 9  
|||||



KW heavy CDR; cryptic collagen epitope; solid tumour;  
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
 KW collagen agonist; collagen antagonist; cancer metastasis;  
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;  
 KW mutant; mutein.  
 XX  
 XX Synthetic.  
 OS Mus musculus.  
 XX WO2003046204-A2.  
 PN 05-JUN-2003.  
 XX  
 XX 26-NOV-2002; 2002WO-US038147.  
 XX  
 XX 26-NOV-2001; 2001US-00995529.  
 PR 06-DEC-2001; 2001US-00011250.  
 XX  
 XX (CELL-) CELL MATRIX INC.  
 PA  
 PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;  
 XX WPI; 2003-513649/48.  
 XX  
 XX New cryptic collagen antibody with one or more complementarity  
 PT determining regions, useful for diagnosing and treating disorders  
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
 XX  
 XX Claim 24; SEQ ID NO 141; 232pp; English.  
 XX  
 CC This invention relates to a novel grafted antibody or its functional  
 CC fragment comprising one or more complementarity determining regions  
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
 CC acid (aa) substitution where the antibody has specific binding activity  
 CC for a cryptic collagen epitope. The growth of all solid tumours requires  
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
 CC to limiting tumour growth. The invention may allow development of  
 CC therapeutics with a cytostatic activity as a collagen agonist or  
 CC antagonist. The invention is useful for diagnosing and treating disorders  
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
 CC present sequence is the amino acid sequence of a mutant mouse anti-  
 CC cryptic collagen site antibody HUI77 variable region light chain CDR  
 CC which may be used during the creation of an antibody of the invention.  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 91.1%; Score 51; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FQGSHPVW 8  
 Db 1 FQGSHPVW 8  
 |||||  
 |||||  
 RESULT 11  
 ADD94254  
 ID ADD94254 standard; peptide; 9 AA.  
 AC ADD94254;  
 XX  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX Mouse HUI77 mutant light chain CDR amino acid sequence SeqID139.  
 DE  
 XX grafted antibody; complementarity determining region; CDR; light CDR;  
 KW heavy CDR; cryptic collagen epitope; solid tumour;  
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
 KW collagen agonist; collagen antagonist; cancer metastasis;  
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;  
 KW mutant; mutein.  
 XX  
 XX Synthetic.  
 OS

OS Mus musculus.  
 XX WO2003046204-A2.  
 PN 05-JUN-2003.  
 XX  
 XX 26-NOV-2002; 2002WO-US038147.  
 XX  
 XX 26-NOV-2001; 2001US-00995529.  
 PR 06-DEC-2001; 2001US-00011250.  
 XX  
 XX (CELL-) CELL MATRIX INC.  
 PA  
 PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;  
 XX WPI; 2003-513649/48.  
 XX  
 XX New cryptic collagen antibody with one or more complementarity  
 PT determining regions, useful for diagnosing and treating disorders  
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
 XX  
 XX Claim 24; SEQ ID NO 139; 232pp; English.  
 XX  
 CC This invention relates to a novel grafted antibody or its functional  
 CC fragment comprising one or more complementarity determining regions  
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
 CC acid (aa) substitution where the antibody has specific binding activity  
 CC for a cryptic collagen epitope. The growth of all solid tumours requires  
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
 CC to limiting tumour growth. The invention may allow development of  
 CC therapeutics with a cytostatic activity as a collagen agonist or  
 CC antagonist. The invention is useful for diagnosing and treating disorders  
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
 CC present sequence is the amino acid sequence of a mutant mouse anti-  
 CC cryptic collagen site antibody HUI77 variable region light chain CDR  
 CC which may be used during the creation of an antibody of the invention.  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 91.1%; Score 51; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FQGSHPVW 8  
 Db 1 FQGSHPVW 8  
 |||||  
 |||||  
 RESULT 12  
 ADD94258  
 ID ADD94258 standard; peptide; 9 AA.  
 AC ADD94258;  
 XX  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX Mouse HUI77 mutant light chain CDR amino acid sequence SeqID143.  
 DE  
 XX grafted antibody; complementarity determining region; CDR; light CDR;  
 KW heavy CDR; cryptic collagen epitope; solid tumour;  
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
 KW collagen agonist; collagen antagonist; cancer metastasis;  
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;  
 KW mutant; mutein.  
 XX  
 XX Synthetic.  
 OS Mus musculus.  
 XX WO2003046204-A2.  
 PN 05-JUN-2003.  
 XX  
 XX 26-NOV-2002; 2002WO-US038147.  
 PF

XX PR 26-NOV-2001; 2001US-00995529.  
 PR 06-DEC-2001; 2001US-00011250.  
 XX PA (CELL-) CELL MATRIX INC.  
 XX PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;  
 XX DR WPI; 2003-513649/48.  
 XX XX  
 XX PR New cryptic collagen antibody with one or more complementarity  
 PT determining regions, useful for diagnosing and treating disorders  
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
 XX PS Claim 24; SEQ ID NO 143; 232pp; English.  
 XX XX  
 XX CC This invention relates to a novel grafted antibody or its functional  
 CC fragment comprising one or more complementarity determining regions  
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
 CC acid (aa) substitution where the antibody has specific binding activity  
 CC for a cryptic collagen epitope. The growth of all solid tumours requires  
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
 CC to limiting tumour growth. The invention may allow development of  
 CC therapeutics with a cytostatic activity as a collagen agonist or  
 CC antagonist. The invention is useful for diagnosing and treating disorders  
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
 CC present sequence is the amino acid sequence of a mutant mouse anti-  
 CC cryptic collagen site antibody HUI77 variable region light chain CDR  
 CC which may be used during the creation of an antibody of the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 91.1%; Score 51; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FQSGHVPW 8  
 Db 1 FQSGHVPW 8  
 |||||  
 |||||  
 RESULT 13  
 ID ADD94257 standard; peptide; 9 AA.  
 AC ADD94257;  
 XX 29-JAN-2004 (first entry)  
 DT Mouse HUI77 mutant light chain CDR amino acid sequence SeqID142.  
 XX DE  
 XX KW grafted antibody; complementarity determining region; CDR; light CDR;  
 KW heavy CDR; cryptic collagen epitope; solid tumour;  
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
 KW collagen agonist; collagen antagonist; cancer metastasis;  
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;  
 KW mutant; mutein.  
 XX OS Synthetic.  
 OS Mus musculus.  
 XX WO2003046204-A2.  
 XX 05-JUN-2003.  
 XX 26-NOV-2002; 2002WO-US038147.  
 XX 26-NOV-2001; 2001US-00995529.  
 XX 06-DEC-2001; 2001US-00011250.  
 XX (CELL-) CELL MATRIX INC.  
 XX PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;

XX WPI; 2003-513649/48.  
 XX PR New cryptic collagen antibody with one or more complementarity  
 PT determining regions, useful for diagnosing and treating disorders  
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
 XX PS Claim 24; SEQ ID NO 142; 232pp; English.  
 XX XX  
 XX CC This invention relates to a novel grafted antibody or its functional  
 CC fragment comprising one or more complementarity determining regions  
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
 CC acid (aa) substitution where the antibody has specific binding activity  
 CC for a cryptic collagen epitope. The growth of all solid tumours requires  
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
 CC to limiting tumour growth. The invention may allow development of  
 CC therapeutics with a cytostatic activity as a collagen agonist or  
 CC antagonist. The invention is useful for diagnosing and treating disorders  
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
 CC present sequence is the amino acid sequence of a mutant mouse anti-  
 CC cryptic collagen site antibody HUI77 variable region light chain CDR  
 CC which may be used during the creation of an antibody of the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 91.1%; Score 51; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FQSGHVPW 8  
 Db 1 FQSGHVPW 8  
 |||||  
 |||||  
 RESULT 14  
 ID ADD94255 standard; peptide; 9 AA.  
 AC ADD94255;  
 XX 29-JAN-2004 (first entry)  
 DT Mouse HUI77 mutant light chain CDR amino acid sequence SeqID140.  
 XX DE  
 XX KW grafted antibody; complementarity determining region; CDR; light CDR;  
 KW heavy CDR; cryptic collagen epitope; solid tumour;  
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
 KW collagen agonist; collagen antagonist; cancer metastasis;  
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;  
 KW mutant; mutein.  
 XX OS Synthetic.  
 OS Mus musculus.  
 XX WO2003046204-A2.  
 XX 05-JUN-2003.  
 XX 26-NOV-2002; 2002WO-US038147.  
 XX 26-NOV-2001; 2001US-00995529.  
 XX 06-DEC-2001; 2001US-00011250.  
 XX (CELL-) CELL MATRIX INC.  
 XX PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;  
 XX WPI; 2003-513649/48.  
 XX PR New cryptic collagen antibody with one or more complementarity  
 PT determining regions, useful for diagnosing and treating disorders  
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
 XX

PS Claim 24; SEQ ID NO 140; 232pp; English.

XX This invention relates to a novel grafted antibody or its functional

CC fragment comprising one or more complementarity determining regions

CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino

CC acid (aa) substitution where the antibody has specific binding activity

CC for a cryptic collagen epitope. The growth of all solid tumours requires

CC new blood vessel growth, angiogenesis, inhibition of which is an approach

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CC therapeutics with a cytostatic activity as a collagen agonist or

CC antagonist. The invention is useful for diagnosing and treating disorders

CC associated with angiogenesis, tumour growth and/or cancer metastasis. The

CC present sequence is the amino acid sequence of a mutant mouse anti-

CC cryptic collagen site antibody HUI77 variable region light chain CDR

CC which may be used during the creation of an antibody of the invention.

XX

SQ Sequence 9 AA;

Query Match 91.1%; Score 51; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPW 8

DB 1 FQGSHPW 8

RESULT 15

ADD94242

ID ADD94242 standard; peptide; 9 AA.

XX

AC ADD94242;

XX

DT 29-JAN-2004 (first entry)

XX

DE Mouse HUI77 mutant light chain CDR amino acid sequence SeqID127.

XX

KW grafted antibody; complementarity determining region; CDR; light CDR;

KW heavy CDR; cryptic collagen epitope; solid tumour;

KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;

KW collagen agonist; collagen antagonist; cancer metastasis;

KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;

KW mutant; mutein.

XX

OS Synthetic.

OS Mus musculus.

XX

PN WO2003046204-A2.

XX

PD 05-JUN-2003.

XX

PF 26-NOV-2002; 2002WO-US038147.

XX

PR 26-NOV-2001; 2001US-00995529.

PR 06-DEC-2001; 2001US-00011250.

XX

PA (CELL-) CELL MATRIX INC.

XX

PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;

XX

DR WPI; 2003-513649/48.

XX

PT New cryptic collagen antibody with one or more complementarity

PT determining regions, useful for diagnosing and treating disorders

PT associated with angiogenesis, tumor growth and/or cancer metastasis.

XX

PS Claim 24; SEQ ID NO 127; 232pp; English.

XX

CC This invention relates to a novel grafted antibody or its functional

CC fragment comprising one or more complementarity determining regions

CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino

CC acid (aa) substitution where the antibody has specific binding activity

CC for a cryptic collagen epitope. The growth of all solid tumours requires

CC new blood vessel growth, angiogenesis, inhibition of which is an approach

CC to limiting tumour growth. The invention may allow development of

CC therapeutics with a cytostatic activity as a collagen agonist or

CC antagonist. The invention is useful for diagnosing and treating disorders

CC associated with angiogenesis, tumour growth and/or cancer metastasis. The

CC present sequence is the amino acid sequence of a mutant mouse anti-

CC cryptic collagen site antibody HUI77 variable region light chain CDR

CC which may be used during the creation of an antibody of the invention.

XX

CC new blood vessel growth, angiogenesis, inhibition of which is an approach

CC to limiting tumour growth. The invention may allow development of

CC therapeutics with a cytostatic activity as a collagen agonist or

CC antagonist. The invention is useful for diagnosing and treating disorders

CC associated with angiogenesis, tumour growth and/or cancer metastasis. The

CC present sequence is the amino acid sequence of a mutant mouse anti-

CC cryptic collagen site antibody HUI77 variable region light chain CDR

CC which may be used during the creation of an antibody of the invention.

XX

SQ Sequence 9 AA;

Query Match 89.3%; Score 50; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGSHPWT 9

DB 2 QGSHPWT 9

Search completed: December 30, 2005, 15:08:40

Job time : 183 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:05:21 ; Search time 37 Seconds  
(without alignments)  
23.404 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPVWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 185

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Pir1.\*
- 2: Pir2.\*
- 3: Pir3.\*
- 4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	32.1	9	2 JS0302	xenopsin-related p
2	18	32.1	9	2 A60320	xenopsin-related p
3	18	32.1	9	2 T31612	hypothetical prote
4	18	32.1	9	2 I46023	growth hormone rec
5	18	32.1	9	2 A60522	sperm-activating p
6	16	28.6	9	2 A43848	cell surface adhes
7	16	28.6	9	2 D57444	neuropeptide Grb-A
8	15	26.8	9	2 S77984	cytochrome-c oxida
9	13	23.2	9	1 AKLQIM	locustamyoinhibiti
10	13	23.2	9	2 A61230	calsequestrin, car
11	13	23.2	9	2 D28834	fibrinogen beta ch
12	12	21.4	9	2 C24180	fibrinogen beta ch
13	12	21.4	9	2 E28854	neuropeptide B -
14	12	21.4	9	2 C60070	gastrin - domestic
15	12	21.4	9	2 S65913	pyrimidine synthe
16	12	21.4	9	2 S36850	ig heavy chain V r
17	12	21.4	9	2 G41946	T-cell receptor ga
18	12	21.4	9	2 A42266	peptidylglycine mo
19	12	21.4	9	2 A12872	transaldolase [EC
20	12	21.4	9	2 A11497	transaldolase [EC
21	12	21.4	9	2 A61620	locustamyotropin I
22	12	21.4	9	2 PC7078	unidentified 48.7K
23	12	21.4	9	2 S39437	D-amino-acid oxida
24	11	19.6	9	1 YPPG	thymic factor - pi
25	11	19.6	9	2 A61364	isotocin - common
26	11	19.6	9	2 A60957	thymocyte growth p
27	11	19.6	9	2 A24244	adipokinetic hormo
28	11	19.6	9	2 S07205	litorin 2-Glu - Au
29	11	19.6	9	2 S07204	litorin I - Austra

ALIGNMENTS

RESULT 1

JS0302  
xenopsin-related peptide 2 - turkey  
N:Contains: xenopsin-related peptide 1  
C:Species: Meleagris gallopavo (common turkey)  
C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C:Accession: JS0302  
R:Carraway, R.E.; Cochran, D.E.; Mitra, S.P.  
Regul. Pept. 22, 303-314, 1988  
A>Title: Xenopsin-related peptide generated in avian gastric extracts.  
A:Reference number: JS0302; MUID:89042995; PMID:2460902  
A:Accession: JS0302  
A:Molecule type: protein  
A:Residues: 1-9 <CAR>  
A:Cross-references: UNIPROT:Q7LZ66; UNIPARC:UPI0000178409  
C:Comment: The peptides are present within several tissues primarily in large molecular weight fractions of the stomach and liver of the turkey.  
C:Superfamily: Yeast coatomer complex alpha chain; WD repeat homology  
C:Keywords: neuropeptide  
F:1-9/Product: xenopsin-related peptide 2 #status experimental <XP2>  
F:2-9/Product: xenopsin-related peptide 1 #status experimental <XP1>

Query Match 32.1%; Score 18; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PW 8  
Db 6 PW 7

RESULT 2

A60320  
xenopsin-related peptide 2 - rat  
N:Contains: xenopsin-related peptide 1  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 09-Jul-2004  
C:Accession: A60320  
R:Carraway, R.E.; Mitra, S.P.; Muraki, K.  
Regul. Pept. 29, 229-239, 1990  
A>Title: Isolation and structures of xenopsin-related peptides from rat stomach, liver and brain.  
A:Reference number: A60320; MUID:91018491; PMID:2217904  
A:Accession: A60320  
A:Molecule type: protein  
A:Residues: 1-9 <CAR>  
A:Cross-references: UNIPROT:Q7M078; UNIPARC:UPI0000178409  
A>Note: The authors purified these peptides from pepsin-treated extracts of stomach, liver and brain of the rat.  
C:Comment: Xenopsin and xenopsin-related peptides are similar to neurotensin in sequence and function.  
C:Superfamily: Yeast coatomer complex alpha chain; WD repeat homology  
C:Keywords: neuropeptide  
F:1-9/Product: xenopsin-related peptide 2 #status experimental <MAT1>  
F:2-9/Product: xenopsin-related peptide 1 #status experimental <MAT2>

Query Match 32.1%; Score 18; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8  
||  
DB 6 PW 7

## RESULT 3

T31612  
hypothetical protein Y50E8A.h - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C;Accession: T31612  
R;Steward, C.  
submitted to the EMBL Data Library, September 1999  
A;Reference number: Z21047  
A;Accession: T31612  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-9 <WIL>  
A;Cross-references: UNIPARC:UPI000017BCA0; EMBL:AL117200; NID:e1549770; PIDN:CAR55051.1;  
A;Experimental source: clone Y50E8A  
C;Genetics:  
A;Gene: CESP:Y50E8A.h

Query Match 32.1%; Score 18; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSH 5  
||  
DB 3 GSH 5

## RESULT 4

I46023  
growth hormone receptor - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I46023  
R;Hauser, S.D.; McGrath, M.P.; Collier, R.J.; Krivi, G.G.  
Mol. Cell. Endocrinol. 72, 187-200, 1990  
A;Title: Cloning and in vivo expression of bovine growth hormone receptor mRNA.  
A;Reference number: I46023; MUID:91146804; PMID:2289631  
A;Accession: I46023  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-9 <HAU>  
A;Cross-references: UNIPROT:Q28121; UNIPARC:UPI0000086CAB; EMBL:U24113; NID:g775221; PID  
C;Genetics:  
A;Gene: GHR

Query Match 32.1%; Score 18; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8  
||  
DB 4 PW 5

## RESULT 5

A60522  
sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)  
C;Species: Diadema setosum  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 05-Oct-2004  
C;Accession: A60522  
R;Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzuki  
Comp. Biochem. Physiol. B 95, 423-429, 1990  
A;Title: A species-specific sperm-activating peptide from the egg jelly of the sea urchin  
A;Reference number: A60522; MUID:90227916; PMID:2158412

A;Accession: A60522  
A;Molecule type: protein  
A;Residues: 1-9 <YOS>  
A;Cross-references: UNIPROT:Q7M4D5; UNIPARC:UPI000017A4D9  
F;2-9/Disulfide bonds: #status experimental

Query Match 32.1%; Score 18; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8  
||  
DB 3 PW 4

## RESULT 6

A43848  
cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)  
C;Species: Staphylococcus aureus  
C;Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A43848  
R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.  
Infect. Immun. 60, 899-906, 1992  
A;Title: Binding of heparan sulfate to Staphylococcus aureus.  
A;Reference number: A43848; MUID:92176005; PMID:1541563  
A;Accession: A43848  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <LIA>  
A;Cross-references: UNIPROT:Q9R5M1; UNIPARC:UPI0000089726  
A;Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 28.6%; Score 16; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WT 9  
||  
DB 2 WT 3

## RESULT 7

D57444  
neuropeptide Grb-AST B4 - two-spotted cricket  
C;Species: Gryllus bimaculatus (two-spotted cricket)  
C;Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 09-Jul-2004  
C;Accession: D57444  
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.  
J. Biol. Chem. 270, 21103-21108, 1995  
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cr  
A;Reference number: A57444; MUID:95403341; PMID:7673141  
A;Accession: D57444  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <LOR>  
A;Cross-references: UNIPROT:Q7M3N6; UNIPARC:UPI000017BE1A

Query Match 28.6%; Score 16; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGS 4  
||  
DB 5 FHGS 8

## RESULT 8

S77984  
cytochrome-c oxidase (BC 1.9.3.1) chain Via - bigeye tuna (fragment)  
C;Species: Thunnus obesus (bigeye tuna)  
C;Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: S77984  
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.



submitted to the Protein Sequence Database, June 1997

A;Reference number: S77980  
A;Accession: S77984  
A;Molecule type: protein  
A;Residues: 1-9 <ARN>  
A;Cross-references: UNIPROT:P80975; UNIPARC:UPI0000128149  
A;Experimental source: heart  
C;Genetics:  
A;Genome: nuclear  
C;Function:  
A;Pathway: oxidative phosphorylation; respiratory chain  
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 26.8%; Score 15; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QGSHVPW 8  
| : | : |  
Db 3 QPBFVPY 9

## RESULT 9

AKUQIM

Locustamyoinhibiting peptide - migratory locust  
C;Species: Locusta migratoria (migratory locust)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A60065

R;Schooofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.  
Regul. Pept. 36, 111-119, 1991  
A;Title: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MIP)  
A;Reference number: A60065; MUID:92179466; PMID:1796179

A;Accession: A60065  
A;Molecule type: protein  
A;Residues: 1-9 <SCH>  
A;Cross-references: UNIPROT:P31799; UNIPARC:UPI000012877A  
C;Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and d  
C;Superfamily: locustamyoinhibiting peptide  
C;Keywords: amidated carboxyl end; hormone  
F;9/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 23.2%; Score 13; DB 1; Length 9;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 FQSHVPW 8  
| : | : |  
Db 2 WQDLNAGW 9

## RESULT 10

A61230

Calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)  
N;Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin-  
C;Species: Rana pipiens (northern leopard frog)

C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: A61230  
R;McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.  
Circ. Res. 69, 344-359, 1991

A;Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular d  
rdium.

A;Reference number: A61230; MUID:91316784; PMID:1860177

A;Accession: A61230  
A;Molecule type: protein  
A;Residues: 1-9 <MCL>  
A;Cross-references: UNIPROT:Q71Z81; UNIPARC:UPI00001776B8  
C;Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protei  
C;Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to c  
C;Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi  
C;Superfamily: calsequestrin  
C;Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skelet

Query Match 23.2%; Score 13; DB 2; Length 9;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QGSHVP 7  
| : | : |  
Db 2 EGLNFP 7

## RESULT 11

D28854

Fibrinopeptide B - olive baboon  
C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)  
C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 09-Jul-2004  
C;Accession: D28854

R;Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. 94, 1973-1978, 1983  
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropi

A;Reference number: A91973; MUID:84161822; PMID:6423621  
A;Accession: D28854  
A;Molecule type: protein  
A;Residues: 1-9 <NAK>

A;Cross-references: UNIPROT:P19344; UNIPARC:UPI000012A77F  
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

Query Match 23.2%; Score 13; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQG 3  
| : | : |  
Db 6 FRG 8

## RESULT 12

C24180

Fibrinogen beta chain - Japanese macaque (fragment)  
N;Contents: fibrinopeptide B  
C;Species: Macaca fuscata (Japanese macaque)

C;Date: 05-Jun-1988 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
C;Accession: C24180  
R;Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. 97, 1487-1492, 1985

A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (

A;Reference number: A91990; MUID:85289140; PMID:3928610  
A;Accession: C24180  
A;Molecule type: protein  
A;Residues: 1-9 <NAK>

A;Cross-references: UNIPROT:P19345; UNIPARC:UPI000012A77B  
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

Query Match 21.4%; Score 12; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQG 3  
| : | : |  
Db 6 FSG 8

## RESULT 13

E28854

Fibrinopeptide B - hamadryas baboon  
C;Species: Papio hamadryas (hamadryas baboon)  
C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 09-Jul-2004  
C;Accession: E28854

R;Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. 94, 1973-1978, 1983  
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropi

A;Reference number: A91973; MUID:84161822; PMID:6423621  
A;Accession: E28854  
A;Molecule type: protein  
A;Residues: 1-9 <NAK>

A;Cross-references: UNIPROT:P19343; UNIPARC:UPI000012A780  
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 21.4%; Score 12; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQG 3  
 Db 6 FHG 8

## RESULT 14

C60070  
 gastrin - domestic ferret (fragment)  
 C;Species: Mustela putorius furo (domestic ferret)  
 C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 18-Jun-1993  
 C;Accession: C60070  
 R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.  
 Regul. Pept. 25, 223-233, 1989  
 A;Title: The constitution and properties of phosphorylated and unphosphorylated C-terminal  
 A;Reference number: A60070; PMID:89331947; PMID:2756156  
 A;Accession: C60070  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <DES>  
 A;Cross-references: UNIPARC:UPI000017C439

Query Match 21.4%; Score 12; DB 2; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QGSHVP 7  
 Db 4 EGDERP 9

## RESULT 15

S65913  
 pyrimidine synthesis multifunctional protein CAD - golden hamster (fragment)  
 C;Species: Mesocricetus auratus (golden hamster)  
 C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
 C;Accession: S65913  
 R;Hemmings, B.; Carrey, E.A.  
 Eur. J. Biochem. 231, 220-225, 1995  
 A;Title: Mammalian dihydroorotase; secondary structure, and interactions with other proteins  
 A;Reference number: S65913; PMID:95354692; PMID:7628474  
 A;Accession: S65913  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <HEM>  
 A;Cross-references: UNIPARC:UPI000017C614

Query Match 21.4%; Score 12; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HV 6  
 Db 1 HV 2

Search completed: December 30, 2005, 15:14:17  
 Job time : 38 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 15:02:14 ; Search time 230 Seconds  
(without alignments)  
27.608 Million cell updates/sec

Title: US-10-735-916A-6  
Perfect score: 56  
Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 873

Minimum DB seq length: 9  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	39.3	9	2	Q9UCQ9_HUMAN
2	19	33.9	9	2	Q6QF45_HUMAN
3	19	33.9	9	2	Q924N8_MOUSE
4	18	32.1	9	1	COW_CONVE
5	18	32.1	9	2	Q9UMF3_HUMAN
6	18	32.1	9	2	Q9UQW0_HUMAN
7	18	32.1	9	2	Q7M4D5_DIASE
8	18	32.1	9	2	Q28121_BOVIN
9	18	32.1	9	2	Q38366_BPPHX
10	18	32.1	9	2	Q7M078_RAT
11	18	32.1	9	2	Q7LZ66_MELGA
12	17	30.4	9	2	Q51LX3_MAGGR
13	17	30.4	9	2	Q67AR4_HUMAN
14	17	30.4	9	2	Q67AR6_HUMAN
15	17	30.4	9	2	Q67AR7_HUMAN
16	17	30.4	9	2	Q67AT1_HUMAN
17	17	30.4	9	2	Q67AT2_HUMAN
18	16	28.6	9	2	Q7M3N6_GRYBI
19	16	28.6	9	2	Q6LAP5_MACEU
20	16	28.6	9	2	Q47410_ECOLI
21	16	28.6	9	2	Q9RSM1_STAAU
22	16	28.6	9	2	Q673W5_TYTRA
23	16	28.6	9	2	Q673W6_9CORV
24	16	28.6	9	2	Q673W7_9CORV
25	16	28.6	9	2	Q673W8_9CORV
26	16	28.6	9	2	Q673W9_9CORV
27	16	28.6	9	2	Q673X0_9CORV
28	16	28.6	9	2	Q673X1_9CORV
29	16	28.6	9	2	Q673X2_9CORV
30	16	28.6	9	2	Q673X3_9CORV
31	16	28.6	9	2	Q673X4_9CORV

32	16	28.6	9	2	Q673X5_9CORV	Q673x5 platysteira
33	16	28.6	9	2	Q673X6_ORIXA	Q673x6 oriolus xan
34	16	28.6	9	2	Q673X7_9CORV	Q673x7 nilaus afer
35	16	28.6	9	2	Q673X8_9CORV	Q673x8 bias flammu
36	16	28.6	9	2	Q673X9_9CORV	Q673x9 malaconotus
37	16	28.6	9	2	Q673Y0_LANCL	Q673y0 lanus coll
38	16	28.6	9	2	Q673Y1_9CORV	Q673y1 lanioturdus
39	16	28.6	9	2	Q673Y2_9CORV	Q673y2 laniarius f
40	16	28.6	9	2	Q673Y3_9CORV	Q673y3 laniarius f
41	16	28.6	9	2	Q673Y4_9CORV	Q673y4 laniarius b
42	16	28.6	9	2	Q673Y5_9CORV	Q673y5 laniarius a
43	16	28.6	9	2	Q673Y6_9CORV	Q673y6 platysteira
44	16	28.6	9	2	Q673Y7_9CORV	Q673y7 dryoscopus
45	16	28.6	9	2	Q673Y8_9CORV	Q673y8 dryoscopus

## ALIGNMENTS

## RESULT 1

Q9UCQ9\_HUMAN PRELIMINARY; PRT; 9 AA.  
AC Q9UCQ9;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE AUTOTAXIN (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=92129337; PubMed=1733949;  
RA Stracke M.L., Kruttsch H.C., Unsworth E.J., Arestad A., Cioce V.,  
RA Schiffrmann E., Liotta L.A.;  
RT "Identification, purification, and partial sequence analysis of  
RT autotaxin, a novel motility-stimulating protein.";  
RL J. Biol. Chem. 267:2524-2529(1992).  
DR GO; GO:0006928; P:cell motility; NAS.  
FT NON TER 1 1  
FT TER 9 9  
SQ SEQUENCE 9 AA; 1136 MW; 9A3CAB14536772CA CRC64;  
Query Match 39.3%; Score 22; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. NO. 2.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VPW 8

Db 3 VPW 5

## RESULT 2

Q6QF45\_HUMAN PRELIMINARY; PRT; 9 AA.  
AC Q6QF45;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)  
DE Cytochrome P450 4F12 (Fragment).  
GN Name=CYP4F12;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Cauffiez C., Klinzig F., Rat E., Tournel G., Allorge D., Chevalier D.,  
RA Lovecchio T., Pottier N., Colombel J.-F., Lhermitte M.,  
RA D'halluin J.-C., Broly F., Lo-Guidice J.-M.;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY544783; AAS49384.1; -; Genomic DNA.  
 DR EMBL; AY544784; AAS49385.1; -; Genomic DNA.  
 DR EMBL; AY544785; AAS49386.1; -; Genomic DNA.  
 DR EMBL; AY544782; AAS49383.1; -; Genomic DNA.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1059 MW; 970A676735B72735 CRC64;

Query Match 33.9%; Score 19; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VFW 8

DB 6 LPW 8

# RESULT 3

Q924N8 MOUSE  
 ID Q924N8 PRELIMINARY; PRT; 9 AA.  
 AC Q924N8  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Niemann Pick type C1 protein (Fragment).  
 GN Name=Npcl;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BLKS;  
 RA Gevry N.Y., Lacroix D.A., Murphy B.D.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF184964; AAK83683.1; -; Genomic DNA.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 890 MW; 2C4E2DC761E1EDD8 CRC64;

Query Match 33.9%; Score 19; DB 2; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GSHVP 7

DB 2 GAHP 6

# RESULT 4

Q924N8 CONVE STANDARD; PRT; 9 AA.  
 ID CONVE  
 AC P83047;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Contryphan-Vn.  
 OS Conus ventricosus (Mediterranean cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=117992;  
 RN [1]  
 RP PROTEIN SEQUENCE, SYNTHESIS, DISULFIDE BONDS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RA MEDLINE=21547785; PubMed=11688995; DOI=10.1006/bbrc.2001.5833;  
 RA Maesilia G.R., Schinina M.E., Ascenzi P., Polticelli F.;  
 RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean  
 snail Conus ventricosus.";  
 RL Biochem. Biophys. Res. Commun. 288:908-913(2001).  
 FT NON\_TER 9  
 SQ STRUCTURE BY NMR, SYNTHESIS, DISULFIDE BONDS, AND FUNCTION.  
 RP PubMed=12646193; DOI=10.1016/S0006-291X(03)00331-0;

RA Masilia G.R., Eliseo T., Grolleau F., Lapiere B., Barbier J.,  
 RA Bournaud R., Molgo J., Cicero D.O., Paci M., Schinina M.E.,  
 RA Ascenzi P., Polticelli F.;  
 RT "Contryphan-Vn: a modulator of Ca2+-dependent K+ channels.";  
 RL Biochem. Biophys. Res. Commun. 303:238-246(2003).  
 CC -!- FUNCTION: Affects both voltage-gated and calcium-dependent  
 potassium channel activities, with composite and diversified  
 effects in invertebrate and vertebrate systems.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- PTM: The cis isomer is the most abundant and is thus thought to be  
 the functionally relevant conformer.  
 CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI; RANGE=1-9; NOTE=Ref.1.  
 CC -!- SIMILARITY: Belongs to the contryphan family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.

PDB: 1NKN; NMR: A=1-9.  
 3D-structure; Amidation; D-amino acid; Direct protein sequencing;  
 KW Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;  
 KW Toxin.  
 FT MOD\_RES 5 5 D-tryptophan.  
 FT MOD\_RES 9 9 Cysteine amide.  
 FT DISULFID 3 9  
 SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 32.1%; Score 18; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8

DB 4 PW 5

# RESULT 5

Q9UMF3 HUMAN  
 ID Q9UMF3 HUMAN PRELIMINARY; PRT; 9 AA.  
 AC Q9UMF3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PD-1 protein (Fragment).  
 GN Name=PD-1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RX MEDLINE=97473511; PubMed=9332365; DOI=10.1016/S0378-1119(97)00260-6;  
 RA Finger L.R., Pu J., Wasseerman R., Vibhakar R., Louie E., Hardy R.R.,  
 RA Burrows P.D., Billips L.D.;  
 RT "The human PD-1 gene: complete cDNA, genomic organization, and  
 developmentally regulated expression in B cell progenitors.";  
 RL Gene 197:177-187(1997).  
 DR EMBL; U64864; AAC51774.1; -; Genomic DNA.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1067 MW; DD4A676DC6C76046 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8

DB 7 PW 8

```
RESULT 6
O9UQW0_HUMAN
ID Q9UQW0_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q9UQW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Prolactin precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84182507; PubMed=6325171;
RA Truong A.T., Duez C., Belayew A., Renard A., Pictet R.L., Bell G.I.,
RA Martial J.A.;
RT "Isolation and characterization of the human prolactin gene.";
RL EMBO J. 3:429-437(1984).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93076813; PubMed=1332868;
RA Peers B., Nalida A.M., Monget P., Voz M.L., Belayew A., Martial J.A.;
RT "Binding of a 100-kDa ubiquitous factor to the human prolactin
RT promoter is required for its basal and hormone-regulated activity.";
RL Eur. J. Biochem. 210:53-58(1992).
DR EMBL; X00368; CAA25108.1; -; Genomic_DNA.
KW Signal.
FT NON TER 1 1 Potential.
FT SIGNAL <1 8
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1060 MW; 0A1A6775B8733054 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB ||
  ||
  7 PW 8

RESULT 7
Q7M4D5_DIASE
ID Q7M4D5_DIASE PRELIMINARY; PRT; 9 AA.
AC Q7M4D5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sperm-activating peptide SAP-IV.
OS Diadema setosum (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;
OC Diadema.
OX NCBI_TaxID=31175;
RN [1]
RP PROTEIN SEQUENCE.
RA Yoshino K.I., Kurita M., Yamaguchi M., Nomura K., Takao T.,
RA Shimonishi Y., Suzuki N.;
RT "A species-specific sperm-activating peptide from the egg jelly of the
RT sea urchin Diadema setosum.";
RL Comp. Biochem. Physiol. 95:423-429(1990).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=2158412;
RA Yoshino K., Kurita M., Yamaguchi M., Nomura K., Takao T.,
RA Shimonishi Y., Suzuki N.;
RT "A species-specific sperm-activating peptide from the egg jelly of the
RT sea urchin Diadema setosum.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 95:423-429(1990).
DR PIR; A60522; A60522.
```

```
SQ SEQUENCE 9 AA; 849 MW; 9639CDD87863676E CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB ||
  ||
  3 PW 4

RESULT 8
Q28121_BOVIN
ID Q28121_BOVIN PRELIMINARY; PRT; 9 AA.
AC Q28121;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Names=GHR;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96043217; PubMed=7486254;
RA Moody D.E., Pomp D., Barendse W., Momack J.E.;
RT "Assignment of the growth hormone receptor gene to bovine chromosome
RT 20 using linkage analysis and somatic cell mapping.";
RL Anim. Genet. 26:341-343(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91146804; PubMed=2289631; DOI=10.1016/0303-7207(90)90143-V;
RA Hauser S.D., McGrath M.F., Collier R.J., Krivi G.G.;
RT "Cloning and in vivo expression of bovine growth hormone receptor
RT mRNA.";
RL Mol. Cell. Endocrinol. 72:187-200(1990).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Moody D.M., Pomp D.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U24113; AAA91014.1; -; Genomic_DNA.
DR PIR; I46023; I46023.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1 1
FT NON TER 9 9
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1182 MW; D11E42C9D36769D6 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB ||
  ||
  4 PW 5

RESULT 9
Q38366_BPPHX
ID Q38366_BPPHX PRELIMINARY; PRT; 9 AA.
AC Q38366;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DSC-2001 (TrEMBLrel. 19, Last annotation update)
DE E gene product (Fragment).
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

```
RX MEDLINE=88118956; PubMed=2963134;
RA Buckley K.J., Hayashi M.;
RT "Role of premature translational termination in the regulation of
RT expression of the phi X174 lysis gene.";
RL J. Mol. Biol. 198;599-607(1987).
DR EMBL; X07809; CAA30668.1; -; Genomic_DNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1207 MW; C093B37731B36412 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 VPWT 9
DB 2 VWT 5

RESULT 10
Q7M078 RAT PRELIMINARY; PRT; 9 AA.
AC Q7M078
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Xenopsin-related peptide 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91018491; PubMed=2217904; DOI=10.1016/0167-0115(90)90085-B;
RA Carraway R.E., Mitra S.P., Muraki K.;
RT "Isolation and structures of xenopsin-related peptides from rat
RT stomach, liver and brain.";
RL Regul. Pept. 29:229-239(1990).
DR PIR; A60320; A60320.
SQ SEQUENCE 9 AA; 1193 MW; E9FE436774032761 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 6 PW 7

RESULT 11
Q7LZ66 MELGA PRELIMINARY; PRT; 9 AA.
AC Q7LZ66
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Xenopsin-related peptide 2.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89042995; PubMed=2460902; DOI=10.1016/0167-0115(88)90107-3;
RA Carraway R.E., Cochran D.E., Mitra S.P.;
RT "Xenopsin-related peptide generated in avian gastric extracts.";
RL Regul. Pept. 22:303-314(1988).
DR PIR; JS0302; JS0302.
SQ SEQUENCE 9 AA; 1193 MW; E9FE436774032761 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 6 PW 7

RESULT 12
Q51LX3 MAGGR PRELIMINARY; PRT; 9 AA.
AC Q51LX3
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG02768.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhaltier B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Fische H.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Galtsova E., Gnerre S.,
RA Gnikre A., Goette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseis M., Karlsson E.,
RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalov A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okaawa O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tensing P., Tefaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Venkataran V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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CC -I- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACU01001555; EAA47525.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 9 AA; 1003 MW; DF9FC5A6D1F5BDC6 CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.2e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSH 5  
|  
|  
|  
Db 2 QASH 5

## RESULT 13

Q67AR4 HUMAN  
ID Q67AR4\_HUMAN PRELIMINARY; PRT; 9 AA.  
AC Q67AR4;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN Name=HLA-DPB1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Wood J.M., Simons M.J., Ashdown M.L.;  
RT "HLA-DPB1 3' intron 1";  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY375795; AAQ88089.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1154 MW; 1AF0C40866D9C73B CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQG 3  
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|  
|  
Db 4 FQG 6

## RESULT 14

Q67AR6 HUMAN  
ID Q67AR6\_HUMAN PRELIMINARY; PRT; 9 AA.  
AC Q67AR6;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN Name=HLA-DPB1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Wood J.M., Simons M.J., Ashdown M.L.;  
RT "HLA-DPB1 3' intron 1";  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY375793; AAQ88087.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1154 MW; 1AF0C40866D9C73B CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQG 3  
|  
|  
|  
Db 4 FQG 6

## RESULT 15

Q67AR7 HUMAN  
ID Q67AR7\_HUMAN PRELIMINARY; PRT; 9 AA.  
AC Q67AR7;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN Name=HLA-DPB1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Wood J.M., Simons M.J., Ashdown M.L.;  
RT "HLA-DPB1 3' intron 1";  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY375792; AAQ88086.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1154 MW; 1AF0C40866D9C73B CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQG 3  
|  
|  
|  
Db 4 FQG 6

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Job time : 232 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 15:02:40 ; Search time 50 Seconds  
(without alignments)  
14.882 Million cell updates/sec

Title: US-10-735-916A-6  
Perfect score: 56  
Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 25369

Minimum DB seq length: 9  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	94.6	9	1	US-07-977-696C-72
2	53	94.6	9	1	US-08-129-330B-72
3	53	94.6	9	2	US-08-976-288A-72
4	53	94.6	9	2	US-09-947-839B-72
5	47	83.9	9	1	US-07-977-696C-34
6	47	83.9	9	1	US-08-129-330B-34
7	47	83.9	9	1	US-08-560-558B-31
8	47	83.9	9	2	US-08-134-346A-21
9	47	83.9	9	2	US-08-976-288A-34
10	47	83.9	9	2	US-09-217-268B-31
11	47	83.9	9	2	US-09-947-839B-34
12	46	82.1	9	1	US-08-053-171-29
13	39	69.6	9	2	US-09-724-409-5
14	39	69.6	9	2	US-09-724-530-5
15	39	69.6	9	2	US-09-328-296-5
16	37	66.1	9	2	US-08-649-100-15
17	37	66.1	9	2	US-08-649-100-31
18	36	64.3	9	2	US-10-226-795-30
19	35	62.5	9	2	US-09-771-415-15
20	34	60.7	9	1	US-08-488-161-6
21	34	60.7	9	2	US-09-273-685-6
22	34	60.7	9	2	US-09-440-781-24
23	34	60.7	9	4	PCT-US95-11934-6
24	32	57.1	9	2	US-09-440-781-26
25	32	57.1	9	2	US-09-771-415-14
26	32	57.1	9	2	US-09-518-737-10
27	32	57.1	9	2	US-09-996-288-61

28	32	57.1	9	2	US-09-996-265-61	Sequence 61, Appl
29	31	55.4	9	2	US-08-836-561-39	Sequence 39, Appl
30	31	55.4	9	2	US-09-434-122-39	Sequence 39, Appl
31	31	55.4	9	2	US-09-440-781-25	Sequence 25, Appl
32	31	55.4	9	2	US-09-771-415-5	Sequence 5, Appl
33	31	55.4	9	2	US-09-771-415-16	Sequence 16, Appl
34	31	55.4	9	2	US-09-996-288-6	Sequence 6, Appl
35	31	55.4	9	2	US-09-996-265-6	Sequence 6, Appl
36	31	55.4	9	2	US-08-908-469-6	Sequence 10, Appl
37	31	55.4	9	2	US-10-135-636-10	Sequence 10, Appl
38	30	53.6	9	1	US-08-350-260A-364	Sequence 364, App
39	30	53.6	9	1	US-08-350-260A-425	Sequence 425, App
40	30	53.6	9	2	US-09-104-337A-364	Sequence 364, App
41	30	53.6	9	2	US-09-104-337A-425	Sequence 425, App
42	30	53.6	9	2	US-09-889-480A-6	Sequence 6, Appl
43	27	48.2	9	1	US-08-244-626-8	Sequence 8, Appl
44	27	48.2	9	1	US-09-440-781-23	Sequence 23, Appl
45	27	48.2	9	2	US-08-908-469-125	Sequence 125, Appl

## ALIGNMENTS

RESULT 1  
US-07-977-696C-72  
; Sequence 72, Application US/07977696C  
; Patent No. 5792852  
; GENERAL INFORMATION:  
; APPLICANT: do Couto, Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides with Specificity  
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination  
; TITLE OF INVENTION: and Therapeutic Methods.  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/977,696C  
; FILING DATE: 11-16-92  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel Ph.D., Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: P66 38227  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 748-6868  
; TELEFAX: (510) 748-6868  
; TELEX: n.a.  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-977-696C-72

Query Match 94.6%; Score 53; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9

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Db      1 FOGTHVPWT 9
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-72

Query Match      94.6%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FOGSHVPWT 9
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Db      1 FOGTHVPWT 9
||||:|||||

RESULT 4
US-09-947-839B-72
; Sequence 72, Application US/09947839B
; Patent No. 6936706
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; Ceriani Dr., Roberto L.
; Peterson Dr., Jerry A.
; Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; for Carcinomas and Kit and Diagnostic Vaccination
; and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. Amzel & Assoc.
; STREET: P.O.Box 159
; CITY: Gladwyne
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19035
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/129,930
; FILING DATE: September 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. 6315997ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-976-288A-72

Query Match      94.6%; Score 53; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FOGSHVPWT 9
||||:|||||
Db      1 FOGTHVPWT 9
||||:|||||

RESULT 3
US-08-976-288A-72
; Sequence 72, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; Ceriani Dr., Roberto L.
; Peterson Dr., Jerry A.
; Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; Carcinoma Specificity, and Kit and
; Diagnostic Vaccination and
; TITLE OF INVENTION: Diagnostic Vaccination and
; Therapeutic Methods
; NUMBER OF SEQUENCES: 96
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APPLICATION NUMBER: US/09/947,839B  
FILING DATE: 06-Sep-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: CRFC-083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-649-0609  
TELEFAX: 240-359-0299  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-09-947-839B-72

Query Match 94.6%; Score 53; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPEWT 9  
Db 1 FQSHVPEWT 9

RESULT 5  
US-07-977-696C-34  
Sequence 34, Application US/07977696C  
Patent No. 5792852  
GENERAL INFORMATION:  
APPLICANT: do Couto, Fernando J.R.  
APPLICANT: Ceriani Dr., Roberto L.  
APPLICANT: Peterson Dr., Jerry A.  
APPLICANT: Padlan Dr., Eduardo A.  
TITLE OF INVENTION: Analogue Peptides with Specificity  
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination  
TITLE OF INVENTION: and Therapeutic Methods.  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,696C  
FILING DATE: 11-16-92  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Ph.D., Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P66 38227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 748-6868  
TELEFAX: (510) 748-6688  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-977-696C-34

Query Match 83.9%; Score 47; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPEWT 9  
Db 1 FQSHVPEWT 9

RESULT 6  
US-08-129-930B-34  
Sequence 34, Application US/08129930B  
Patent No. 5804187  
GENERAL INFORMATION:  
APPLICANT: do Couto Dr., Fernando J.R.  
APPLICANT: Ceriani Dr., Roberto L.  
APPLICANT: Peterson Dr., Jerry A.  
APPLICANT: Padlan Dr., Eduardo A.  
TITLE OF INVENTION: Analogue Peptides with Broad  
TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
TITLE OF INVENTION: Diagnostic Vaccination and  
TITLE OF INVENTION: Therapeutic Methods  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: V. AMZEL & ASSOC.  
STREET: 2055 No. 5804187th Broadway, Suite 201  
CITY: Walnut Creek  
STATE: California  
COUNTRY: USA  
ZIP: 94596  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/129,930B  
FILING DATE: September 30, 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Ph.D., Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: CRFCC-008A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 521-1333  
TELEFAX: (510) 521-3541  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-129-930B-34

Query Match 83.9%; Score 47; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPEWT 9  
Db 1 FQSHVPEWT 9

RESULT 7  
US-08-560-558E-31  
Sequence 31, Application US/08560558E  
Patent No. 5891996  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Humanized and chimeric monoclonal  
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor  
US-08-560-558E-31

;; TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.  
;; NUMBER OF SEQUENCES: 34  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA  
;; STREET: P.O. Box 2250  
;; CITY: Salt Lake City  
;; STATE: Utah  
;; COUNTRY: United States of America  
;; ZIP: 84110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: WINDOWS95  
;; SOFTWARE: WordPerfect 5.1/5.2  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/560,558E  
;; FILING DATE: No. 5891996ember 17, 1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Turner, Allen C.  
;; REGISTRATION NUMBER: 33,041  
;; REFERENCE/DOCKET NUMBER: 2720US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (801) 532-1922  
;; TELEFAX: (801) 531-9168  
;; INFORMATION FOR SEQ ID NO: 31:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; US-08-560-558E-31

Query Match 83.9%; Score 47; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
Db 1 FQSHVPWT 9

RESULT 8  
US-08-134-346A-21  
; Sequence 21, Application US/08134346A  
; Patent No. 6281335  
; GENERAL INFORMATION:  
; APPLICANT: do Couto, F.J.R.  
; APPLICANT: Ceriani, R.L.C.  
; APPLICANT: Petersen, J.A.  
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrager, Chong & Flaherty  
; STREET: 300 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10022-7499  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/134,346A  
; FILING DATE: 08-OCT-1993  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Onofrio, Dara L.

;; REGISTRATION NUMBER: 34,889  
;; REFERENCE/DOCKET NUMBER: CLT 149,608  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-826-6565  
;; TELEFAX: 212-826-5909  
;; INFORMATION FOR SEQ ID NO: 21:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-134-346A-21

Query Match 83.9%; Score 47; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9  
Db 1 FQSHVPWT 9

RESULT 9  
US-08-976-288A-34  
; Sequence 34, Application US/08976288A  
; Patent No. 6315997  
; GENERAL INFORMATION:  
; APPLICANT: do Couto Dr., Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides With Broad  
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
; TITLE OF INVENTION: Diagnostic Vaccination and  
; TITLE OF INVENTION: Therapeutic Methods  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder & Poplawski  
; STREET: 444 South Flower St., 19th Floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/976,288A  
; FILING DATE: No. 6315997ember 21, 1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/129,930  
; FILING DATE: September 30, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/977,696  
; FILING DATE: No. 6315997ember 16, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Viviana Amzel Ph.D.  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: P6639938  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 622-7700  
; TELEFAX: (213) 489-4210  
; TELEX: n.a.  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-976-288A-34

Query Match 83.9%; Score 47; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.6e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9  
Db 1 FQSHVPYT 9

## RESULT 10

US-09-217-268B-31

; Sequence 31, Application US/09217268B

; Patent No. 6506883

; GENERAL INFORMATION:

; APPLICANT: Mateo de Acosta del Rio, Christina M

; APPLICANT: Rodriguez, Rolando P

; APPLICANT: Frias, Ernesto M

; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epitopes of the Human Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use

; FILE REFERENCE: 2720.1US

; CURRENT APPLICATION NUMBER: US/09/217,268B

; CURRENT FILING DATE: 1998-12-21

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Murine

; FEATURE:

; NAME/KEY: MISC FEATURE

; OTHER INFORMATION: CDR of murine R3 antibody

US-09-217-268B-31

Query Match

Best Local Similarity 83.9%; Score 47; DB 2; Length 9;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9  
Db 1 FQSHVPYT 9

## RESULT 11

US-09-947-839B-34

; Sequence 34, Application US/09947839B

; Patent No. 6936706

; GENERAL INFORMATION:

; APPLICANT: do Couto, Fernando J.R.

; APPLICANT: Peterson Dr., Roberto L.

; APPLICANT: Padlan Dr., Eduardo A.

; TITLE OF INVENTION: Analogue Peptides with Specificity for Carcinomas and Kit and Diagnostic Vaccination and Therapeutic Methods.

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: V. Amzel &amp; Assoc.

; STREET: P.O.Box 159

; CITY: Gladwyne

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19035

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/947,839B

; FILING DATE: 06-Sep-2001

; CLASSIFICATION: &lt;Unknown&gt;

; ATTORNEY/AGENT INFORMATION:

; NAME: Amzel Viviana

; REGISTRATION NUMBER: 30,930

; REFERENCE/DOCKET NUMBER: CRFC-083

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-649-0609

; TELEFAX: 240-359-0299

; TELEX: n.a.

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-09-947-839B-34

Query Match

Best Local Similarity 83.9%; Score 47; DB 2; Length 9;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9  
Db 1 FQSHVPYT 9

## RESULT 12

US-08-053-171-29

; Sequence 29, Application US/08053171

; Patent No. 5562903

; GENERAL INFORMATION:

; APPLICANT: Co. Loibner

; TITLE OF INVENTION: Antibody Derivatives

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/053,171

; FILING DATE: 22-APR-1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-54-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1-9

; OTHER INFORMATION: /note= "Third

; OTHER INFORMATION: complementarity-determining region (CDR3) of  
; OTHER INFORMATION: BR55-2 antibody light chain"

US-08-053-171-29

Query Match

83.1%; Score 46; DB 1; Length 9;

Best Local Similarity 88.9%; Pred. No. 4.6e+05; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 0;

QY 1 FQSHVPWT 9  
|:|||||:  
Db 1 FQSHVPWT 9

## RESULT 13

US-09-724-409-5  
; Sequence 5, Application US/09724409  
; Patent No. 6838261  
; GENERAL INFORMATION:  
; APPLICANT: Siegall, Clay  
; APPLICANT: Wahl, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005  
; CURRENT APPLICATION NUMBER: US/09/724,409  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/328,296  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-724-409-5

Query Match 69.6%; Score 39; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9  
|:|||||:  
Db 2 QTTHVPWT 9

## RESULT 14

US-09-724-530-5  
; Sequence 5, Application US/09724530  
; Patent No. 6843989  
; GENERAL INFORMATION:  
; APPLICANT: Siegall, Clay  
; APPLICANT: Wahl, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005  
; CURRENT APPLICATION NUMBER: US/09/724,530  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/328,296  
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-724-530-5

Query Match 69.6%; Score 39; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9  
|:|||||:  
Db 2 QTTHVPWT 9

## RESULT 15

US-09-328-296-5  
; Sequence 5, Application US/09328296  
; Patent No. 6946129  
; GENERAL INFORMATION:  
; APPLICANT: Siegall, Clay  
; APPLICANT: Wahl, Alan  
; APPLICANT: Francisco, Joseph  
; APPLICANT: Fell, H. Perry  
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF  
; FILE REFERENCE: 9632-005  
; CURRENT APPLICATION NUMBER: US/09/328,296  
; CURRENT FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-328-296-5

Query Match 69.6%; Score 39; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9  
|:|||||:  
Db 2 QTTHVPWT 9

Search completed: December 30, 2005, 15:13:33  
JOB time : 50 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 15:12:47 ; Search time 160 Seconds  
(without alignments)  
23.503 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPVPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 68385

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	3	US-09-995-529-36
2	56	100.0	9	3	US-09-995-529-36
3	56	100.0	9	4	US-10-470-045-48
4	56	100.0	9	5	US-10-735-916A-6
5	53	94.6	9	3	US-09-947-839-72
6	52	92.9	9	3	US-09-995-529-128
7	52	92.9	9	3	US-09-995-529-132
8	52	92.9	9	3	US-09-995-529-138
9	52	92.9	9	3	US-09-995-529-128
10	52	92.9	9	3	US-09-995-529-132
11	52	92.9	9	3	US-09-995-529-138
12	51	91.1	9	3	US-09-995-529-139
13	51	91.1	9	3	US-09-995-529-140
14	51	91.1	9	3	US-09-995-529-141
15	51	91.1	9	3	US-09-995-529-142
16	51	91.1	9	3	US-09-995-529-143
17	51	91.1	9	3	US-09-995-529-145
18	51	91.1	9	3	US-09-995-529-139
19	51	91.1	9	3	US-09-995-529-140
20	51	91.1	9	3	US-09-995-529-141
21	51	91.1	9	3	US-09-995-529-142
22	51	91.1	9	3	US-09-995-529-143
23	51	91.1	9	3	US-09-995-529-145
24	50	89.3	9	3	US-09-995-529-126
25	50	89.3	9	3	US-09-995-529-127
26	50	89.3	9	3	US-09-995-529-130
27	50	89.3	9	3	US-09-995-529-126

28	50	89.3	9	3	US-09-995-529-127	Sequence 127, App
29	50	89.3	9	3	US-09-995-529-130	Sequence 130, App
30	49	87.5	9	3	US-09-995-529-129	Sequence 129, App
31	49	87.5	9	3	US-09-995-529-131	Sequence 131, App
32	49	87.5	9	3	US-09-995-529-129	Sequence 129, App
33	49	87.5	9	3	US-09-995-529-131	Sequence 131, App
34	48	85.7	9	3	US-09-995-529-137	Sequence 137, App
35	48	85.7	9	3	US-09-995-529-137	Sequence 137, App
36	47	83.9	9	3	US-09-217-268B-31	Sequence 31, Appl
37	47	83.9	9	3	US-09-995-529-135	Sequence 135, App
38	47	83.9	9	3	US-09-947-839-34	Sequence 34, Appl
39	47	83.9	9	3	US-09-995-529-135	Sequence 135, App
40	47	83.9	9	4	US-10-434-469-12	Sequence 12, Appl
41	47	83.9	9	5	US-10-482-105-10	Sequence 10, Appl
42	47	83.9	9	5	US-10-409-611-81	Sequence 81, Appl
43	47	83.9	9	5	US-10-409-608A-23	Sequence 23, Appl
44	47	83.9	9	5	US-10-500-207A-12	Sequence 12, Appl
45	47	83.9	9	6	US-11-009-443-6	Sequence 6, Appl

#### ALIGNMENTS

RESULT 1  
US-09-995-529-36  
; Sequence 36, Application US/09995529  
; Publication No. US2003009655A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; TITLE OF INVENTION: Related Methods  
; FILE REFERENCE: P-IX 4976  
; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-995-529-36

Query Match 100.0%; Score 56; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
| | | | | | | |  
Db 1 FQGSHPVPT 9

RESULT 2  
US-09-995-529-36  
; Sequence 36, Application US/09995529  
; Publication No. US20040091482A9  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; TITLE OF INVENTION: Related Methods  
; FILE REFERENCE: P-IX 4976  
; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-995-529-36

Query Match 100.0%; Score 56; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9  
DB 1 FQGSHPWT 9

RESULT 3  
US-10-470-045-48  
; Sequence 48, Application US/10470045  
; Publication No. US20040146505A1  
; GENERAL INFORMATION:  
; APPLICANT: Scancell Limited  
; APPLICANT: Durrant, Linda Gillian  
; APPLICANT: Parsons, Tina  
; TITLE OF INVENTION: Substances  
; FILE REFERENCE: P32181WQ/NJL  
; CURRENT APPLICATION NUMBER: US/10/470,045  
; CURRENT FILING DATE: 2003-07-24  
; PRIOR APPLICATION NUMBER: GB 0102145.0  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-470-045-48

Query Match 100.0%; Score 56; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9  
DB 1 FQGSHPWT 9

RESULT 4  
US-10-735-916A-6  
; Sequence 6, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GORTSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFILOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-6

Query Match 100.0%; Score 56; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9  
DB 1 FQGSHPWT 9

RESULT 5  
US-09-947-839-72  
; Sequence 72, Application US/09947839  
; Publication No. US20030138428A1  
; GENERAL INFORMATION:  
; APPLICANT: do Couto Dr., Fernando J.R.  
; Ceriani Dr., Roberto L.  
; Peterson Dr., Jerry A.  
; Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides With Broad  
; Carcinoma Specificity, and Kit and  
; Diagnostic Vaccination and  
; Therapeutic Methods  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder & Poplawski  
; STREET: 444 South Flower St., 19th Floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/09/947,839  
; FILING DATE: 06-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/976,288  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 07/977,696  
; FILING DATE: No. US20030138428A1ember 16, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Viviana Amzel Ph.D.  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: P6639938  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 622-7700  
; TELEFAX: (213) 489-4210  
; TELEX: n.a.  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-09-947-839-72

Query Match 94.6%; Score 53; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9  
DB 1 FQGSHPWT 9

RESULT 6  
US-09-995-529-128



; Sequence 128, Application US/09995529  
; Publication No. US2003009655A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; FILE REFERENCE: P-IX 4976  
; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 128  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic antibody mutation  
US-09-995-529-128

Query Match 92.9%; Score 52; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
Db 1 FQGSHPVPT 9

## RESULT 7

US-09-995-529-132  
; Sequence 132, Application US/09995529  
; Publication No. US2003009655A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; FILE REFERENCE: P-IX 4976  
; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 132  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic antibody mutation  
US-09-995-529-132

Query Match 92.9%; Score 52; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
Db 1 FQGSHPVPT 9

## RESULT 8

US-09-995-529-138  
; Sequence 138, Application US/09995529  
; Publication No. US2003009655A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; FILE REFERENCE: P-IX 4976

; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 138  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic antibody mutation  
US-09-995-529-138

Query Match 92.9%; Score 52; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
Db 1 FQGSHPVPT 9

## RESULT 9

US-09-995-529-128  
; Sequence 128, Application US/09995529  
; Publication No. US20040091482A9  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; FILE REFERENCE: P-IX 4976  
; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 128  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic antibody mutation  
US-09-995-529-128

Query Match 92.9%; Score 52; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9  
Db 1 FQGSHPVPT 9

## RESULT 10

US-09-995-529-132  
; Sequence 132, Application US/09995529  
; Publication No. US20040091482A9  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; FILE REFERENCE: P-IX 4976  
; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 132  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

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; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-132

Query Match          92.9%; Score 52; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
DB 1 FQGSHPWT 9

RESULT 11
US-09-995-529-138
; Sequence 138, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-138

Query Match          92.9%; Score 52; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
DB 1 FQGSHPWT 9

RESULT 12
US-09-995-529-139
; Sequence 139, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-139

Query Match          91.1%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPW 8
DB 1 FQGSHPW 8

RESULT 13
US-09-995-529-140
; Sequence 140, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-140

Query Match          91.1%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPW 8
DB 1 FQGSHPW 8

RESULT 14
US-09-995-529-141
; Sequence 141, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-141

Query Match          91.1%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPW 8
DB 1 FQGSHPW 8

RESULT 15
US-09-995-529-142
; Sequence 142, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
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```
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-142
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Query Match          91.1%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 FQGSHPVW 8
         |||||
Db      1 FQGSHPVW 8
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Search completed: December 30, 2005, 15:26:42
Job time : 161 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:13:42 ; Search time 13 seconds  
(without alignments)

5.185 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 6541

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.\*

1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	7 US-11-012-353-6	Sequence 6, Appl
2	56	100.0	9	7 US-11-125-837-15	Sequence 15, Appl
3	56	100.0	9	7 US-11-105-708-19	Sequence 19, Appl
4	41	73.2	9	6 US-10-932-334-6	Sequence 6, Appl
5	39	69.6	9	7 US-11-102-743-5	Sequence 5, Appl
6	37	66.1	9	7 US-11-125-837-3	Sequence 3, Appl
7	32	57.1	9	7 US-11-009-939-40	Sequence 40, Appl
8	32	57.1	9	7 US-11-097-812-196	Sequence 196, Appl
9	31	55.4	9	7 US-11-193-512-39	Sequence 39, Appl
10	29	51.8	9	6 US-10-473-037-8	Sequence 8, Appl
11	27	48.2	9	6 US-10-507-662-60	Sequence 60, Appl
12	26	46.4	9	6 US-10-507-662-59	Sequence 59, Appl
13	24	42.9	9	7 US-11-045-024-46	Sequence 46, Appl
14	24	42.9	9	7 US-11-045-024-3770	Sequence 3770, Ap
15	24	42.9	9	7 US-11-045-024-7048	Sequence 7048, Ap
16	24	42.9	9	7 US-11-045-024-13595	Sequence 13595, A
17	23	41.1	9	7 US-11-009-939-20	Sequence 20, Appl
18	22	39.3	9	7 US-11-010-748A-303	Sequence 303, App
19	22	39.3	9	7 US-11-010-748A-304	Sequence 304, App
20	22	39.3	9	7 US-11-045-024-45	Sequence 45, Appl
21	22	39.3	9	7 US-11-045-024-47	Sequence 47, Appl
22	22	39.3	9	7 US-11-045-024-3769	Sequence 3769, Ap
23	22	39.3	9	7 US-11-045-024-3771	Sequence 3771, Ap
24	22	39.3	9	7 US-11-045-024-6971	Sequence 6971, Ap
25	22	39.3	9	7 US-11-045-024-7067	Sequence 7067, Ap

#### ALIGNMENTS

##### RESULT 1

US-11-012-353-6  
; Sequence 6, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GORTSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFILOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-6

Query Match 100.0%; Score 56; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9

Db 1 FQGSHPWT 9

##### RESULT 2

US-11-125-837-15  
; Sequence 15, Application US/11125837

Sequence 13572, A  
Sequence 13594, A  
Sequence 13597, A  
Sequence 13604, A  
Sequence 13630, A  
Sequence 13638, A  
Sequence 45, Appl  
Sequence 301, App  
Sequence 302, App  
Sequence 305, App  
Sequence 306, App  
Sequence 10563, A  
Sequence 12365, A  
Sequence 13976, A  
Sequence 1135, Ap  
Sequence 4056, Ap  
Sequence 4058, Ap  
Sequence 12607, A  
Sequence 13736, A  
Sequence 72, Appl

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; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-15

Query Match      100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9
|||||

RESULT 3
US-11-105-708-19
; Sequence 19, Application US/11105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
; APPLICANT: Pernasetti, Flavia
; APPLICANT: Freimark, Bruce
; APPLICANT: Van Epps, Dennis
; APPLICANT: Brooks, Peter C
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
; FILE REFERENCE: 30797-704.501
; CURRENT APPLICATION NUMBER: US/11/105,708
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 09/478,977
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: 60/152,496
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/143,534
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/114,878
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/114,877
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-105-708-19

Query Match      100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9
|||||

RESULT 4
US-10-932-334-6
; Sequence 6, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain complementarity determining region
US-10-932-334-6

Query Match      73.2%; Score 41; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.3e+04;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9
|||||

RESULT 5
US-11-102-743-5
; Sequence 5, Application US/11102743
; Publication No. US20050266002A1
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/11/102,743
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-102-743-5

Query Match      69.6%; Score 39; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QGSHPVPT 9
Db      2 QTHVPT 9
|:|||||

RESULT 6
US-11-125-837-3
; Sequence 3, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
```

; FILE REFERENCE: 13062-011001  
; CURRENT APPLICATION NUMBER: US/11/125,837  
; CURRENT FILING DATE: 2005-05-10  
; PRIOR APPLICATION NUMBER: US 60/569,892  
; PRIOR FILING DATE: 2004-05-10  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-125-837-3

Query Match 66.1%; Score 37; DB 7; Length 9;  
Best Local Similarity 77.8%; Pred. No. 4.3e+04;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9  
Db 1 FQGSYVELT 9

RESULT 7  
US-11-009-939-40  
; Sequence 40, Application US/11009939  
; Publication No. US20050265998A1  
; GENERAL INFORMATION:  
; APPLICANT: Elson, Greg Christopher Andrew  
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof  
; FILE REFERENCE: 23135-402  
; CURRENT APPLICATION NUMBER: US/11/009,939  
; CURRENT FILING DATE: 2005-12-10  
; PRIOR APPLICATION NUMBER: 60/528,811  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,812  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,962  
; PRIOR FILING DATE: 2003-12-10  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-009-939-40

Query Match 57.1%; Score 32; DB 7; Length 9;  
Best Local Similarity 62.5%; Pred. No. 4.3e+04;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QGSHVPWT 9  
Db 2 QGNTFPWT 9

RESULT 8  
US-11-097-812-196  
; Sequence 196, Application US/11097812  
; Publication No. US20050281828A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Kretz-Rommel, Anke  
; APPLICANT: Dakapagari, Naveen  
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN  
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)  
; CURRENT APPLICATION NUMBER: US/11/097,812  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 11/016,647  
; PRIOR FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: PCT/US04/06570  
; PRIOR FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: US 60/548,385

; PRIOR FILING DATE: 2004-02-28  
; PRIOR APPLICATION NUMBER: US 60/529,500  
; PRIOR FILING DATE: 2003-12-15  
; PRIOR APPLICATION NUMBER: US 60/451,816  
; PRIOR FILING DATE: 2003-03-04  
; NUMBER OF SEQ ID NOS: 207  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 196  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: mouse  
US-11-097-812-196

Query Match 57.1%; Score 32; DB 7; Length 9;  
Best Local Similarity 62.5%; Pred. No. 4.3e+04;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QGSHVPWT 9  
Db 2 QSKEVPWT 9

RESULT 9  
US-11-193-512-39  
; Sequence 39, Application US/11193512  
; Publication No. US20050272918A1  
; GENERAL INFORMATION:  
; APPLICANT: KOIKE, Masamichi  
; FURUYA, Akiko  
; NAKAMURA, Kazuyasu  
; IIDA, Akihiro  
; ANAZAWA, Hideharu  
; HANAI, Nobuo  
; TAKATSU, Kiyoshi  
; TITLE OF INVENTION: Antibody Against Human Interleukin-5  
; RECEPTOR Alpha Chain  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/193,512  
; FILING DATE: 01-Aug-2005  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/10/283,349  
; FILING DATE: 29-Oct-2002  
; APPLICATION NUMBER: US/08/836,561  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: JP 232384/95  
; FILING DATE: 11-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lawrence, III, Stanton T  
; REGISTRATION NUMBER: 25,736  
; REFERENCE/DOCKET NUMBER: 7005-115-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

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;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-11-193-512-39

Query Match      55.4%; Score 31; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9
DB 2 QSKDVPWT 9

RESULT 10
US-10-473-037-8
; Sequence 8, Application US/10473037
; Publication No. US20050260206A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374WO1
; CURRENT APPLICATION NUMBER: US/10/473,037
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-8

Query Match      51.8%; Score 29; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.3e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9
DB 2 QYSKLPWT 9

RESULT 11
US-10-507-662-60
; Sequence 60, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-60

Query Match      48.2%; Score 27; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VPWT 9
   ||||

```

```

DB 6 VPWT 9

RESULT 12
US-10-507-662-59
; Sequence 59, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-59

Query Match      46.4%; Score 26; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VPWT 9
DB 6 IPWT 9

RESULT 13
US-11-045-024-46
; Sequence 46, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060, 0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-46

Query Match      42.9%; Score 24; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 SHVPW 8
       :||||
Db      5 TNVPW 9
```

## RESULT 14

```
US-11-045-024-3770
; Sequence 3770, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 3770
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3770
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Query Match      42.9%; Score 24; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      4 SHVPW 8
       :||||
Db      5 TNVPW 9
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## RESULT 15

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US-11-045-024-7048
; Sequence 7048, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7048
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7048
```

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Query Match      42.9%; Score 24; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY      4 SHVPW 8
       :||||
Db      5 TNVPW 9
```

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Search completed: December 30, 2005, 15:27:03
Job time : 16 secs
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# OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 13.4516 Seconds  
(without alignments)  
36.877 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

- Issued Patents AA:\*\*
- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	480	2	US-09-252-991A-19202
2	35	87.5	275	2	US-09-489-039A-12128
3	35	87.5	277	2	US-09-583-110-2944
4	35	87.5	278	2	US-09-769-787-19
5	35	87.5	290	2	US-09-107-433-4262
6	35	87.5	550	2	US-09-252-991A-17547
7	35	87.5	739	2	US-09-540-236-3594
8	34	85.0	144	1	US-09-108-051-2
9	34	85.0	144	2	US-09-440-833-2
10	34	85.0	180	2	US-08-913-159-13
11	34	85.0	301	2	US-09-328-352-7439
12	34	85.0	326	2	US-09-489-039A-9700
13	34	85.0	349	2	US-09-270-767-45401
14	34	85.0	516	2	US-09-489-039A-12893
15	34	85.0	609	2	US-09-949-016-6846
16	34	85.0	984	2	US-09-171-461-14
17	34	85.0	984	2	US-09-970-711-14
18	34	85.0	1091	2	US-09-328-352-5758
19	33	82.5	324	2	US-09-549-8488-34
20	33	82.5	324	2	US-09-688-069-34
21	33	82.5	347	2	US-09-902-540-13914
22	33	82.5	601	2	US-09-902-540-12462
23	32	80.0	114	1	US-08-741-437-3
24	32	80.0	114	1	US-09-134-593-3
25	32	80.0	143	2	US-09-270-767-33503
26	32	80.0	143	2	US-09-270-767-48720
27	32	80.0	289	1	US-08-741-437-1

28	32	80.0	289	1	US-08-741-437-4	Sequence 4, Appli
29	32	80.0	289	1	US-09-134-593-1	Sequence 1, Appli
30	32	80.0	289	1	US-09-134-593-4	Sequence 4, Appli
31	32	80.0	289	2	US-09-538-092-1335	Sequence 1335, Ap
32	32	80.0	339	2	US-09-583-110-3067	Sequence 3067, Ap
33	32	80.0	348	2	US-09-107-433-2966	Sequence 2966, Ap
34	32	80.0	411	2	US-09-540-236-3549	Sequence 3549, Ap
35	32	80.0	533	2	US-09-252-991A-25841	Sequence 25841, A
36	32	80.0	545	2	US-08-976-0638-10	Sequence 10, Appl
37	32	80.0	613	1	US-08-484-101B-46	Sequence 46, Appl
38	32	80.0	613	1	US-08-484-101B-48	Sequence 48, Appl
39	32	80.0	613	2	US-08-714-524D-46	Sequence 46, Appl
40	32	80.0	613	2	US-08-714-524D-48	Sequence 48, Appl
41	32	80.0	738	2	US-09-328-352-4315	Sequence 4315, Ap
42	32	80.0	886	2	US-09-769-787-126	Sequence 126, App
43	32	80.0	2504	2	US-09-328-352-5821	Sequence 5821, Ap
44	31	77.5	94	2	US-09-543-681A-7919	Sequence 7919, Ap
45	31	77.5	120	2	US-09-591-181-199	Sequence 199, App

## ALIGNMENTS

RESULT 1  
US-09-252-991A-19202  
; Sequence 19202, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19202  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19202

Query Match 90.0%; Score 36; DB 2; Length 480;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
Db 194 GGFLWN 199

## RESULT 2

US-09-489-039A-12128  
; Sequence 12128, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 12128  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12128

Query Match 87.5%; Score 35; DB 2; Length 275;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 103 GGYTWN 108

RESULT 3  
US-09-583-110-2944  
; Sequence 2944, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 2944  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-2944

Query Match 87.5%; Score 35; DB 2; Length 277;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 66 GGYTWN 71

RESULT 4  
US-09-769-787-19  
; Sequence 19, Application US/09769787  
; Patent No. 6936252  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/F21129WO  
; CURRENT APPLICATION NUMBER: US/09/769,787  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-769-787-19

Query Match 87.5%; Score 35; DB 2; Length 278;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 66 GGYTWN 71

Db 67 GGYTWN 72  
RESULT 5  
US-09-107-433-4262  
; Sequence 4262, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
; THERAPEUTICS

NUMBER OF SEQUENCES: 5206  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: <Unknown>  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: <Unknown>  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,433  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/ 085131  
FILING DATE: May 12, 1998  
APPLICATION NUMBER: 60/051553  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 4262:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 290 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...290  
SEQUENCE DESCRIPTION: SEQ ID NO: 4262:  
US-09-107-433-4262

Query Match 87.5%; Score 35; DB 2; Length 290;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 79 GGYTWN 84

RESULT 6  
US-09-252-991A-17547  
; Sequence 17547, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17547  
; LENGTH: 550  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17547

Query Match 87.5%; Score 35; DB 2; Length 550;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
|||  
Db 257 GGYWN 262

## RESULT 7

US-09-540-236-3594  
; Sequence 3594, Application US/09540236  
; Patent No. 6673910

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 3594

; LENGTH: 739

; TYPE: PRT

; ORGANISM: M.catarrhalis

US-09-540-236-3594

Query Match 87.5%; Score 35; DB 2; Length 739;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
|||  
Db 339 GGYLWN 344

## RESULT 8

US-09-108-051-2  
; Sequence 2, Application US/09108051  
; Patent No. 5985576

; GENERAL INFORMATION:

; APPLICANT: Ellingson, Jay L.E.

; APPLICANT: Stabel, Judith R.

; TITLE OF INVENTION: Species-Specific Genetic Identification

; TITLE OF INVENTION: of Mycobacterium Paratuberculosis

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Curtis P. Ribando

; STREET: 1815 N. University Street

; CITY: Peoria

; STATE: IL

; COUNTRY: US

; ZIP: 61604

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/108,051

; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ribando, Curtis P.  
; REGISTRATION NUMBER: 27,976  
; REFERENCE/DOCKET NUMBER: 0229.97  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 309/681-6513  
; TELEFAX: 309/681-6688  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 144 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-108-051-2

Query Match 85.0%; Score 34; DB 1; Length 144;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYLWN 6  
|||  
Db 30 GYLWN 34

## RESULT 9

US-09-440-833-2

; Sequence 2, Application US/09440833

; Patent No. 6277580

; GENERAL INFORMATION:

; APPLICANT: Ellingson, Jay L.E.

; APPLICANT: Stabel, Judith R.

; TITLE OF INVENTION: Species-Specific Genetic Identification

; TITLE OF INVENTION: of Mycobacterium Paratuberculosis

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Curtis P. Ribando

; STREET: 1815 N. University Street

; CITY: Peoria

; STATE: IL

; COUNTRY: US

; ZIP: 61604

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/440,833

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/108,051

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Ribando, Curtis P.

; REGISTRATION NUMBER: 27,976

; REFERENCE/DOCKET NUMBER: 0229.97

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 309/681-6513

; TELEFAX: 309/681-6688

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 144 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-440-833-2

Query Match 85.0%; Score 34; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 GYLWN 6
      |||||
Db     30 GYLWN 34

RESULT 10
US-08-913-159-13
; Sequence 13, Application US/08913159
; Patent No. 6300109
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Plasmid-derived type II
; TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,159
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0179/95
; FILING DATE: 17-FEB-1995
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-913-159-13

Query Match      85.0%; Score 34; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      |||||
Db     57 GYLWN 61

RESULT 11
US-09-328-352-7439
; Sequence 7439, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7439
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7439

Query Match      85.0%; Score 34; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      |||||
Db     215 GYLWN 219

RESULT 12
US-09-489-039A-9700
; Sequence 9700, Application US/09489039A
```

```
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9700
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9700

Query Match      85.0%; Score 34; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      |||||
Db     240 GYLWN 244

RESULT 13
US-09-270-767-45401
; Sequence 45401, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45401
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45401

Query Match      85.0%; Score 34; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLW 5
      |||||
Db     57 GGYLW 61

RESULT 14
US-09-489-039A-12893
; Sequence 12893, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12893
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12893
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Query Match 85.0%; Score 34; DB 2; Length 516;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLW 5  
|  
|  
|  
|  
Db 491 GGYLW 495

RESULT 15  
US-09-949-016-6846  
; Sequence 6846, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6846  
; LENGTH: 609  
; TYPE: PRT  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(609)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-949-016-6846

Query Match 85.0%; Score 34; DB 2; Length 609;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLMN 6  
|  
|  
|  
|  
Db 294 GYLMN 298

Search completed: December 30, 2005, 13:37:18  
Job time : 14.4516 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 53.3226 Seconds  
(without alignments)  
49.440 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	40	100.0	6	7	ADJ76842
2	40	100.0	6	9	ADZ67012 Murine in
3	40	100.0	117	7	ADJ76903
4	40	100.0	117	7	ADJ76909
5	40	100.0	117	7	ADJ76917
6	40	100.0	117	7	ADJ76913
7	40	100.0	117	9	ADZ67083 Human ant
8	40	100.0	117	9	ADZ67087 Human ant
9	40	100.0	117	9	ADZ67073 Murine im
10	40	100.0	117	9	ADZ67079 Human ant
11	40	100.0	127	7	ADJ76886 Anti-IGF-
12	40	100.0	127	9	ADZ67056 Murine im
13	40	100.0	135	7	ADJ76911
14	40	100.0	135	7	ADJ76919
15	40	100.0	135	7	ADJ76915
16	40	100.0	135	9	ADZ67089 Human ant
17	40	100.0	135	9	ADZ67081 Human ant
18	40	100.0	135	9	ADZ67085 Human ant
19	40	100.0	544	7	ADZ670198 C. neofo
20	37	92.5	1471	4	ABBS8739 Drosophil
21	36	90.0	480	7	ABO70456 Pseudomon
22	35	87.5	83	5	ABU05763 M. tuberc
23	35	87.5	121	7	ADJ80377 Antibody
24	35	87.5	125	7	ADP03868 Murine-ex

25	35	87.5	125	7	ADP03876	Adp03876 Murine-ex
26	35	87.5	257	7	ADB75644	Adb75644 TM1 scFv
27	35	87.5	275	7	ABO65611	Abo65611 Klebsiell
28	35	87.5	277	8	ADK46429	Adk46429 Streptoco
29	35	87.5	279	3	AAy81519	Aay81519 Streptoco
30	35	87.5	285	6	ABU02392	Abu02392 S. pneumo
31	35	87.5	290	8	ADR95627	Adr95627 Novel S.
32	35	87.5	290	9	AEA59497	Aea59497 Streptoco
33	35	87.5	400	7	ADC87483	Adc87483 Human GPC
34	35	87.5	550	7	ABO68801	Abo68801 Pseudomon
35	35	87.5	739	8	ADL05908	Adl05908 M. catarr
36	34	85.0	57	5	ABG80748	Abg80748 C-type le
37	34	85.0	71	4	ABBI7537	Abbi7537 Human ner
38	34	85.0	72	4	AAG73998	Aag73998 Human col
39	34	85.0	96	4	AAM92258	Aam92258 Human dig
40	34	85.0	103	3	AAG29147	Aag29147 Arabidops
41	34	85.0	107	3	AAG29146	Aag29146 Arabidops
42	34	85.0	109	4	AAU20236	Aau20236 Human nov
43	34	85.0	137	4	ABB59022	Abb59022 Drosophil
44	34	85.0	139	3	AAB41367	Aab41367 Human ORF
45	34	85.0	139	5	ABP34716	Abp34716 Human ORF

## ALIGNMENTS

RESULT 1  
ADJ76842

ID ADJ76842 standard; peptide; 6 AA.

AC ADJ76842;

DT 06-MAY-2004 (first entry)

DE CDR sequence for anti-IGF-1R antibody.

KW cytostatic; antipsoriatic; antibody;

KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
or epidermal growth factor receptor; EGFR; signal transduction pathway;

KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
CDR.

OS Mus musculus.

PN WO2003059951-A2.

PD 24-JUL-2003.

PF 20-JAN-2003; 2003WO-FR000178.

PR 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-000005753.

PA (FABR ) FABRE MEDICAMENT SA PIERRE.

PI Goetech L, Corvaia N, Leger O;

DR WPI; 2003-569653/53.

DR N-PSDB; ADJ76841.

PT New antibodies that bind to human insulin-like growth factor receptor,  
useful for treatment, prevention and diagnosis of cancers.

XX Claim 1; SEQ ID NO 8; 164pp; French.

CC The invention relates to an isolated antibody (Ab), and its functional  
fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
1R) and optionally: (i) inhibit natural binding of insulin-like growth  
factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
treat diseases associated with overexpression and/or abnormal activity of  
IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 40; DB 7; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 |||||  
 Db 1 GGYLWN 6

RESULT 2

ID ADZ67012 standard; peptide; 6 AA.

XX ADZ67012;

AC (first entry)

DT 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:8.  
 XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasia; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUFLO/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

XX Goetech L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX N-PSDB; ADZ67011.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.

XX Claim 1; SEQ ID NO 8; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 40; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 |||||  
 Db 1 GGYLWN 6

RESULT 3

ADJ76903

ID ADJ76903 standard; protein; 117 AA.

XX ADJ76903;

XX 06-MAY-2004 (first entry)

XX Anti-IGF-1R related protein #16.

XX cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX Homo sapiens.

XX WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;  
 XX WPI; 2003-569653/53.  
 XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.  
 XX  
 XX Disclosure; SEQ ID NO 69; 164pp; French.  
 XX  
 CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 XX Sequence 117 AA;  
 SQ

Query Match 100.0%; Score 40; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLMN 6  
 DB 31 GGYLMN 36  
 |||||

RESULT 4  
 ADJ76909  
 ID ADJ76909 standard; protein; 117 AA.

XX AC ADJ76909;  
 XX 06-MAY-2004 (first entry)  
 XX DE Anti-IGF-1R related protein #22.  
 XX cytotstatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 75; 164pp; French.  
 XX  
 CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 XX Sequence 117 AA;  
 SQ

Query Match 100.0%; Score 40; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLMN 6  
 DB 31 GGYLMN 36  
 |||||

RESULT 5  
 ADJ76917  
 ID ADJ76917 standard; protein; 117 AA.

XX AC ADJ76917;

XX 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #26.

XX cytotstatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 83; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 |||||  
 Db 31 GGYLWN 36

# RESULT 6

ADJ76913  
 ID ADJ76913 standard; protein; 117 AA.

XX AC ADJ76913;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #24.

XX KW cytostatic; antipsoriatic; antibody;

KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX DR WPI; 2003-569653/53.

XX PT New antibodies that bind to human insulin-like growth factor receptor,

XX PT useful for treatment, prevention and diagnosis of cancers.

XX PS Disclosure; SEQ ID NO 79; 164pp; French.

XX CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the

CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 |||||  
 Db 31 GGYLWN 36

# RESULT 7

ADZ67083  
 ID ADZ67083 standard; protein; 117 AA.

XX AC ADZ67083;

XX DT 30-JUN-2005 (first entry)

XX DE Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.

XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW heavy chain variable region.

XX OS Homo sapiens.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOET/) GOETSCH L.

XX PA (CORV/) CORVAIA N.

XX PA (LEGE/) LEGER O.

XX PA (DUFLO/) DUFLOS A.

XX PA (HAEU/) HAEUW J.

XX PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX DR WPI; 2005-321968/33.

XX PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 XX PT antibody or its functional fragment, being capable of binding human IGF-  
 XX PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 XX PT useful for treating cancer.

XX PS Example 13; SEQ ID NO 79; 125pp; English.

XX CC The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in

CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 9; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 DB 31 GGYLWN 36  
 |||||

# RESULT 8

ID ADZ67087 standard; protein; 117 AA.

XX AC ADZ67087;

XX DT 30-JUN-2005 (first entry)

XX DE Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.

XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW heavy chain variable region.

XX OS Homo sapiens.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-0000653.

XX PR 18-JAN-2002; 2002FR-0000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.  
 PA (LEGE/) LEGER O.  
 PA (DUFLO/) DUFLOS A.  
 PA (HAEU/) HAEUW J.  
 XX (BECK/) BECK A.

PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 DR WPI; 2005-321968/33.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.

XX Example 13; SEQ ID NO 83; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 DB 31 GGYLWN 36  
 |||||

# RESULT 9

ID ADZ67073

XX ADZ67073 standard; protein; 117 AA.

XX AC ADZ67073;

XX DT 30-JUN-2005 (first entry)

XX DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW immunoglobulin; heavy chain variable region.  
 XX Mus musculus.  
 XX US2005084906-A1.  
 XX 21-APR-2005.  
 XX 16-DEC-2003; 2003US-00735916.  
 XX 18-JAN-2002; 2002FR-00000653.  
 XX 18-JAN-2002; 2002FR-00000654.  
 XX 07-MAY-2002; 2002FR-00005753.  
 XX 20-JAN-2003; 2003WO-FR000178.  
 XX 11-JUL-2003; 2003FR-00008538.  
 XX (GOET/) GOETSCH L.  
 XX (CORV/) CORVAIA N.  
 XX (LEGE/) LEGER O.  
 XX (DUF/) DUFLOS A.  
 XX (HAU/) HAEUW J.  
 XX (BECK/) BECK A.  
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 PI WPI; 2005-321968/33.  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX Example 13; SEQ ID NO 69; 125pp; English.  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1- and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-

CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX Sequence 117 AA;  
 SQ Query Match 100.0%; Score 40; DB 9; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGYLWN 6  
 Db |||||  
 31 GGYLWN 36  
 RESULT 10  
 ADZ67079  
 ID ADZ67079 standard; protein; 117 AA.  
 XX AC ADZ67079;  
 XX 30-JUN-2005 (first entry)  
 XX Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.  
 DE Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW heavy chain variable region.  
 XX Homo sapiens.  
 XX US2005084906-A1.  
 XX 21-APR-2005.  
 XX 16-DEC-2003; 2003US-00735916.  
 XX 18-JAN-2002; 2002FR-00000653.  
 XX 18-JAN-2002; 2002FR-00000654.  
 XX 07-MAY-2002; 2002FR-00005753.  
 XX 20-JAN-2003; 2003WO-FR000178.  
 XX 11-JUL-2003; 2003FR-00008538.  
 XX (GOET/) GOETSCH L.  
 XX (CORV/) CORVAIA N.  
 XX (LEGE/) LEGER O.  
 XX (DUF/) DUFLOS A.  
 XX (HAU/) HAEUW J.  
 XX (BECK/) BECK A.  
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 PI WPI; 2005-321968/33.  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX Example 13; SEQ ID NO 75; 125pp; English.  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment

CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6

Db 31 GGYLWN 36

# RESULT 11

ADJ76886  
 ID ADJ76886 standard; protein; 127 AA.

XX AC ADJ76886;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #4.

XX KW cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX OS Mus musculus.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX XX WPI; 2003-569653/53.

XX

PT New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.  
 XX PS Disclosure; SEQ ID NO 52; 164pp; French.

XX CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells; inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 127 AA;

Query Match 100.0%; Score 40; DB 7; Length 127;

Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6

Db 41 GGYLWN 46

# RESULT 12

ADZ67056  
 ID ADZ67056 standard; protein; 127 AA.

XX AC ADZ67056;

XX DT 30-JUN-2005 (first entry)

XX DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.

XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW immunoglobulin; heavy chain variable region.

XX OS Mus musculus.

XX FH Key Location/Qualifiers  
 FT Peptide 1..10  
 FT /note= "leader peptide"

FT Region 41..46

FT /note= "CDR1"

FT Region 61..76

FT /note= "CDR2"

FT Region 109..116

FT /note= "CDR3"

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX (GORT/) GOETSCH L.  
 PA (CORV/) CORVAIA N.  
 PA (LEGE/) LEGER O.  
 PA (DUF/) DUFLOS A.  
 PA (HAEU/) HAEUW J.  
 PA (BECK/) BECK A.  
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 XX WPI: 2005-321968/33.  
 DR N-PSDB; AD267055.  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX Example 8; SEQ ID NO 52; 125pp; English.  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (AD267006 and AD267014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX Sequence 127 AA;  
 SQ  
 Query Match 100.0%; Score 40; DB 9; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGYLWN 6  
 |||||  
 Db 41 GGYLWN 46  
 RESULT 13  
 ID ADJ76911 standard; protein; 135 AA.  
 XX  
 AC ADJ76911;  
 XX

DT 06-MAY-2004 (first entry)  
 XX Anti-IGF-IR related protein #23.  
 DE cytotatic; antipsoriatic; antibody;  
 XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX Homo sapiens.  
 OS WO2003059951-A2.  
 XX 24-JUL-2003.  
 PD 20-JAN-2003; 2003WO-FR000178.  
 PF 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA Goetsch L, Corvaia N, Leger O;  
 XX WPI: 2003-569653/53.  
 PI New antibodies that bind to human insulin-like growth factor receptor,  
 DR useful for treatment, prevention and diagnosis of cancers.  
 PT Disclosure; SEQ ID NO 77; 164pp; French.  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-IR. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX Sequence 135 AA;  
 SQ  
 Query Match 100.0%; Score 40; DB 7; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGYLWN 6  
 |||||  
 Db 49 GGYLWN 54  
 RESULT 14  
 ID ADJ76919 standard; protein; 135 AA.  
 XX  
 AC ADJ76919;  
 XX 06-MAY-2004 (first entry)  
 DT Anti-IGF-1R related protein #27.  
 DE cytotatic; antipsoriatic; antibody;  
 XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW



KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO2003059951-A2.  
 PN  
 XX  
 XX 24-JUL-2003.  
 PD  
 XX  
 XX 20-JAN-2003; 2003WO-FR000178.  
 PF  
 XX  
 XX 18-JAN-2002; 2002FR-00000653.  
 PR  
 XX 18-JAN-2002; 2002FR-00000654.  
 PR  
 XX 07-MAY-2002; 2002FR-00005753.  
 XX  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA  
 XX  
 XX Goetsch L, Corvaia N, Leger O;  
 PI  
 XX  
 XX WPI; 2003-569653/53.  
 DR  
 XX  
 XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 85; 164pp; French.  
 PS  
 XX  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 135 AA;  
 Query Match 100.0%; Score 40; DB 7; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGYLWN 6  
 |||||  
 Db 49 GGYLWN 54  
 RESULT 15  
 ADJ76915  
 ID ADJ76915 standard; protein; 135 AA.  
 XX  
 AC ADJ76915;  
 XX  
 XX 06-MAY-2004 (first entry)  
 DT  
 XX  
 XX Anti-IGF-1R related protein #25.  
 DE  
 XX  
 KW cytostatic; antiproliferative; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO2003059951-A2.  
 PN  
 XX

PD 24-JUL-2003.  
 XX  
 XX 20-JAN-2003; 2003WO-FR000178.  
 PF  
 XX  
 XX 18-JAN-2002; 2002FR-00000653.  
 PR  
 XX 18-JAN-2002; 2002FR-00000654.  
 PR  
 XX 07-MAY-2002; 2002FR-00005753.  
 XX  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA  
 XX  
 XX Goetsch L, Corvaia N, Leger O;  
 PI  
 XX  
 XX WPI; 2003-569653/53.  
 DR  
 XX  
 XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 81; 164pp; French.  
 PS  
 XX  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 135 AA;  
 Query Match 100.0%; Score 40; DB 7; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGYLWN 6  
 |||||  
 Db 49 GGYLWN 54  
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 Job time : 55.3226 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 8.51613 Seconds  
(without alignments)  
67.789 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	277	2 D42400	membrane protein M
2	36	90.0	479	2 T44446	D-rhamnose synthase
3	36	90.0	479	2 F82964	phosphomannose iso
4	36	90.0	530	2 S01430	chlorophyll a/b-bi
5	35	87.5	70	2 AF2508	transposase asl724
6	35	87.5	258	2 AD0615	probable membrane
7	35	87.5	259	2 C90754	hypothetical prote
8	35	87.5	259	2 G64831	probable membrane
9	35	87.5	259	2 A85618	hypothetical prote
10	35	87.5	277	2 D98085	hypothetical prote
11	35	87.5	278	2 E95221	sugar ABC transpor
12	35	87.5	440	2 F69322	hypothetical prote
13	35	87.5	481	2 A38598	mannose-6-phosphat
14	35	87.5	481	2 B83201	phosphomannose iso
15	35	87.5	1001	2 AG1979	hypothetical prote
16	34	85.0	107	2 H84839	late embryogenesis
17	34	85.0	155	2 S78774	perlucin - Haloti
18	34	85.0	159	2 AB2051	hypothetical prote
19	34	85.0	167	2 G71548	hypothetical prote
20	34	85.0	274	2 E95912	hypothetical prote
21	34	85.0	286	2 T22354	hypothetical prote
22	34	85.0	304	2 T05587	hypothetical prote
23	34	85.0	318	2 AI1945	hypothetical prote
24	34	85.0	323	2 F69454	signal-transducing
25	34	85.0	323	2 T26536	hypothetical prote
26	34	85.0	325	2 AD3140	hypothetical prote
27	34	85.0	325	2 H98147	hypothetical prote
28	34	85.0	330	2 B95900	probable ABC trans
29	34	85.0	356	2 C97265	mannose-1-phosphat

30 34 85.0 390 2 D81289 probable aminotran  
31 34 85.0 394 2 AB1870 hypothetical prote  
32 34 85.0 395 2 S50986 MAF1 protein - yea  
33 34 85.0 406 2 T50894 hydroxynurosporen  
34 34 85.0 436 2 H87697 mannose-1-phosphat  
35 34 85.0 448 1 H69386 mannose-6-phosphat  
36 34 85.0 476 2 AH2968 mannose-1-phosphat  
37 34 85.0 476 2 C98314 mannose-6-phosphat  
38 34 85.0 494 2 S30187 ba-type ubiquinol  
39 34 85.0 667 2 A97176 cytochrome O ubiq  
40 34 85.0 667 2 AG2593 hypoxia inducible  
41 34 85.0 705 2 JC7771 N-acetylmuramoyl-L  
42 34 85.0 705 2 A41322 cationic amino aci  
43 34 85.0 736 2 C69451 100K protein - fow  
44 34 85.0 798 2 JN0878 hypothetical prote  
45 34 85.0 1482 2 T34010

#### ALIGNMENTS

##### RESULT 1

D42400

membrane protein MamG - Streptococcus mutans

C;Species: Streptococcus mutans

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: D42400

R;Russell, R.R.; Aduese-Opoku, J.; Sutcliffe, I.C.; Tao, L.; Ferretti, J.J.

J. Biol. Chem. 267, 4631-4637, 1992

A;Title: A binding protein-dependent transport system in Streptococcus mutans responsi

A;Reference number: A42400; MUID:92165821; PMID:1537846

A;Accession: D42400

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-277 <RUS>

A;Cross-references: UNIPROT:Q00751; UNIPARC:UPI000012F61F; GB:M77351; GB:M19349; GB:M30

A;Note: sequence extracted from NCBI backbone (NCBIN:83895, NCBI:P:83891)

C;Superfamily: maltose transport protein malG

C;Keywords: transmembrane protein

Query Match 90.0%; Score 36; DB 2; Length 277;  
Best Local Similarity 83.3%; Pred. No. 18;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
||| ||  
Db 66 GGYFWN 71

##### RESULT 2

T44446

D-rhamnose synthase protein wbpW [imported] - Pseudomonas aeruginosa

C;Species: Pseudomonas aeruginosa

C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C;Accession: T44446

R;Rocchetta, H.L.; Pacan, J.C.; Lam, J.S.

Mol. Microbiol. 29, 1419-1434, 1998

A;Title: Synthesis of the A-band polysaccharide sugar D-rhamnose requires Rmd and WbpW;

A;Reference number: Z22772; MUID:98453140; PMID:9781879

A;Accession: T44446

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-479 <ROC>

A;Cross-references: UNIPROT:O87266; UNIPARC:UPI000000BBB2C; EMBL:AF0009956; NID:G3249548;

A;Experimental source: strain PAOI

C;Genetics:

A;Gene: wbpW

C;Superfamily: Helicobacter mannose-6-phosphate isomerase

Query Match 90.0%; Score 36; DB 2; Length 479;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 GGYLWN 6
      ||:||||
Db      193 GGFLWN 198

RESULT 3
F82964
phosphomannose isomerase/GDP-mannose WbpW PA5452 [imported] - Pseudomonas aeruginosa (str
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F82964
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F82964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <STO>
A:Cross-references: UNIPROT:Q9HTB7; UNIPARC:UPI00000C6012; GB:AE004958; GB:AE004091; NID
A:Gene: wbpW; PA5452
C:Genetics:
C:Superfamily: Helicobacter mannose-6-phosphate isomerase

Query Match      90.0%; Score 36; DB 2; Length 479;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      ||:||||
Db      193 GGFLWN 198

RESULT 4
S01430
chlorophyll a/b-binding protein LH38 precursor - Euglena gracilis (fragment)
N:Alternate names: light-harvesting complex I apoprotein
C:Species: Euglena gracilis
C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: S01430
R:Houlne, G.; Schantz, R.
Mol. Gen. Genet. 213, 479-486, 1988
A:Title: Characterization of cDNA sequences for LHCI apoproteins in Euglena gracilis: Th
A:Reference number: S01429; MUID:89039737; PMID:3141775
A:Accession: S01430
A:Molecule type: mRNA
A:Residues: 1-530 <HOU>
A:Cross-references: UNIPROT:P08976; UNIPARC:UPI000012E61A; EMBL:X12861; NID:g18421; PIDN
F;1-178/Product: chlorophyll a/b-binding protein LH38a (fragment) #status predicted <WAT
F;179-360/Product: chlorophyll a/b-binding protein LH38b #status predicted <WAT>
F;361-530/Product: chlorophyll a/b-binding protein LH38c (fragment) #status predicted <M

Query Match      90.0%; Score 36; DB 2; Length 530;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      ||:||||
Db      468 GGFLWN 473

RESULT 5
AF2508
transposase asl7246 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2508
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

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Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2508
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-70 <KUR>
A:Cross-references: UNIPROT:Q8YKP7; UNIPARC:UPI00000CEFA4C; GB:BA000020; PIDN:BA078330.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl7246
A:Genome: plasmid

Query Match      87.5%; Score 35; DB 2; Length 70;
Best Local Similarity 83.3%; Pred. No. 6; 7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      ||:||||
Db      37 GGHLWN 42

RESULT 6
AD0615
probable membrane protein STY092 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 12-Jul-2004
C:Accession: AD0615
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conner, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
.; S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Barry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <PAR>
A:Cross-references: UNIPARC:UPI000005A069; GB:AL513382; PIDN:CAD05390.1; PID:g16502152;
C:Genetics:
A:Gene: STY0992
C:Superfamily: conserved hypothetical protein H11262

Query Match      87.5%; Score 35; DB 2; Length 258;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      ||:||||
Db      87 GGYTWN 92

RESULT 7
C90754
hypothetical protein ECs1003 [imported] - Escherichia coli (strain O157:H7, substrain R
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 12-Jul-2004
C:Accession: C90754
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C90754
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <HAY>
A:Cross-references: UNIPROT:P36565; UNIPARC:UPI000013A5A1; GB:BA000007; PIDN:BA034426.1
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:

```

A;Gene: ECa1003  
C;Superfamily: conserved hypothetical protein HI1262

Query Match 87.5%; Score 35; DB 2; Length 259;  
Best Local Similarity 83.3%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
||| ||  
Db 87 GGYTWN 92

## RESULT 8

G64831  
A;Title: probable membrane protein ycbC - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 12-Jul-2004  
C;Accession: G64831

A;Authors: R.; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen

A.; Rode, D.J.; Mau, B.; Shao, Y.

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: G64831

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-259 <BLAT>

A;Cross-references: UNIPROT:P36565; UNIPARC:UPI000013A5A1; GB:AE000194; GB:U000096; MID:9

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: ycbC

C;Superfamily: conserved hypothetical protein HI1262

C;Keywords: transmembrane protein

F;13-29/Domain: transmembrane #status predicted <TM1>

F;39-55/Domain: transmembrane #status predicted <TM2>

Query Match 87.5%; Score 35; DB 2; Length 259;  
Best Local Similarity 83.3%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
||| ||  
Db 87 GGYTWN 92

## RESULT 9

A85618

hypothetical protein ycbC [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 12-Jul-2004

C;Accession: A85618

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A85618

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-259 <STO>

A;Cross-references: UNIPROT:P36565; UNIPARC:UPI000013A5A1; GB:AE005174; NID:g12514089; H

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: ycbC

C;Superfamily: conserved hypothetical protein HI1262

Query Match 87.5%; Score 35; DB 2; Length 259;  
Best Local Similarity 83.3%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
||| ||  
Db 87 GGYTWN 92

## RESULT 10

D98085

hypothetical protein msmG [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004

C;Accession: D98085

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Bursgett, S.; DeHoff, B.S.;

e, P.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: D98085

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-277 <KUR>

A;Cross-references: UNIPROT:Q8DNI0; UNIPARC:UPI00000E36DD; GB:AE007317; PIDN:AAL00513.1

C;Genetics:

A;Gene: msmG

C;Superfamily: maltose transport protein malG

Query Match 87.5%; Score 35; DB 2; Length 277;  
Best Local Similarity 83.3%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
||| ||  
Db 66 GGYTWN 71

## RESULT 11

E95221

sugar ABC transporter, permease protein SP1895 [imported] - Streptococcus pneumoniae (s

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004

C;Accession: E95221

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison

A;Title: Complete Genome Sequence of a Virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95221

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-278 <KUR>

A;Cross-references: UNIPROT:Q97NW4; UNIPARC:UPI00000C9CFA; GB:AE005672; PIDN:AAK75966.1

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP1895

C;Superfamily: maltose transport protein malG

Query Match 87.5%; Score 35; DB 2; Length 278;  
Best Local Similarity 83.3%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
||| ||  
Db 67 GGYTWN 72

## RESULT 12

F69322

hypothetical protein AF0582 - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C;Accession: F69322

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: F69322  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-440 <KLE>  
A;Cross-references: UNIPROT:O29673; UNIPARC:UPI0000057054; GB:AE0001064; GB:AE000782; NID

Query Match 87.5%; Score 35; DB 2; Length 440;  
Best Local Similarity 83.3%; Pred. No. 45;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
||| ||  
DB 218 GGYWN 223

RESULT 13  
A38598  
mannose-6-phosphate isomerase (EC 5.3.1.8) / mannose-1-phosphate guanylyltransferase (GP  
N;Alternate names: phosphomannose isomerase  
C;Species: Pseudomonas aeruginosa  
C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 09-Jul-2004  
C;Accession: A38598; A25638  
R;Shinabarger, D.; Berry, A.; May, T.B.; Rothmel, R.; Fialho, A.; Chakrabarty, A.M.  
J. Biol. Chem. 266, 2080-2088, 1991  
A;Title: Purification and characterization of phosphomannose isomerase-guanosine diphosph  
inosa.  
A;Reference number: A38598; MUID:91115815; PMID:1846611  
A;Accession: A38598  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-481 <SHI>  
A;Cross-references: UNIPROT:P07874; UNIPARC:UPI000016PCF0; GB:M14037; NID:g151503; PIDN:  
R;Darling, A.; Prantz, B.; Vanags, R.I.; Chakrabarty, A.M.  
Gene 42, 293-302, 1986  
A;Title: Nucleotide sequence analysis of the phosphomannose isomerase gene (pmi) of Pseu  
A;Reference number: A25638; MUID:86276004; PMID:3089876  
A;Accession: A25638  
A;Molecule type: DNA  
A;Residues: 1-25, 'FL', 28-39, 'L', 41-57, 'A', 59-106, 108-114, 'I', 116-358, 'EV', 361-478, 'A', 48  
A;Cross-references: UNIPARC:UPI0000176197  
A;Note: the nucleotide sequence given predicts 26-Leu, 27-Val, 115-Leu, 359-Asp, and 360  
C;Superfamily: Helicobacter mannose-6-phosphate isomerase  
C;Keywords: intramolecular oxidoreductase; isomerase; nucleotidyltransferase

Query Match 87.5%; Score 35; DB 2; Length 481;  
Best Local Similarity 83.3%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
||| ||  
DB 188 GGYWN 193

RESULT 14  
B83201  
phosphomannose isomerase / guanosine 5'-diphospho-D-mannose pyrophosphorylase PA3551 [im  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: B83201  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Harbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: B83201  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-481 <STO>  
A;Cross-references: UNIPROT:P07874; UNIPARC:UPI0000125847; GB:AE004776; GB:AE004091; NID  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: algA; PA3551  
C;Superfamily: Helicobacter mannose-6-phosphate isomerase

Query Match 87.5%; Score 35; DB 2; Length 481;  
Best Local Similarity 83.3%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
||| ||  
DB 188 GGYWN 193

RESULT 15  
AG1979  
hypothetical protein alr1386 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AG1979  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An.  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AG1979  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1001 <KUR>  
A;Cross-references: UNIPROT:Q8YX32; UNIPARC:UPI000000CE0A1; GB:BA0000019; PIDN:BAE73343.1.  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr1386

Query Match 87.5%; Score 35; DB 2; Length 1001;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
||| ||  
DB 667 GGYLWD 672

Search completed: December 30, 2005, 13:34:55  
Job time : 9.51613 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 54 Seconds  
(without alignments)  
78.392 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	467	Q9EXY5	Escherichia coli
2	40	100.0	492	Q31278	Acetobacter
3	40	100.0	492	Q8RR87	Acetobacter
4	40	100.0	560	Q55VE7	Cryne
5	40	100.0	560	Q5KKT9	Cryne
6	37	92.5	368	Q4PIK9	Ustila
7	37	92.5	425	Q6EVV9	Yersinia
8	37	92.5	1097	Q9VA99	Drome
9	37	92.5	1109	Q8IM19	Drome
10	37	92.5	1199	Q6NP40	Drome
11	37	92.5	1279	Q522J8	MAGGR
12	36	90.0	277	Q5MGM	STRMU
13	36	90.0	281	Q4K774	PSEF5
14	36	90.0	370	Q4IPC3	GIBZE
15	36	90.0	430	Q6WN42	PSED
16	36	90.0	479	Q8T266	PSEAE
17	36	90.0	479	Q9HTB7	PSEAE
18	36	90.0	483	Q4K774	PSEF5
19	36	90.0	483	Q4K774	PSEF5
20	36	90.0	485	Q4K774	PSEF5
21	36	90.0	530	Q4K774	PSEF5
22	36	90.0	798	Q4UP17	XANCP
23	36	90.0	798	Q8P3J4	XANCP
24	36	90.0	801	Q5H632	XANOR
25	36	90.0	814	Q52DW1	MAGGR
26	35	87.5	70	Q8YKP7	ANASP
27	35	87.5	83	Q7U1K5	MYCBO
28	35	87.5	83	Q8VRH3	MYCTU
29	35	87.5	86	Q5BD31	EMENI
30	35	87.5	87	Q5WGF8	BACSK
31	35	87.5	111	Q70IV0	CLODI

32	35	87.5	111	2	Q70IV1	CLODI
33	35	87.5	121	2	Q5FN84	GLUOX
34	35	87.5	147	2	Q4IVK8	AZOVI
35	35	87.5	148	2	Q4KAB9	PSEF5
36	35	87.5	148	2	Q880D2	PSEF5
37	35	87.5	209	2	Q8A573	BACTN
38	35	87.5	221	2	Q5YMI3	NOCPA
39	35	87.5	223	2	Q7NWT8	CHRCO
40	35	87.5	258	2	Q57R07	SALCH
41	35	87.5	258	2	Q5PGF7	SALPA
42	35	87.5	258	2	Q827Z8	SALTI
43	35	87.5	258	2	Q82Q88	SALTY
44	35	87.5	259	1	YCBC	ECOLI
45	35	87.5	259	2	Q8FJA7	ECOL6

#### ALIGNMENTS

RESULT 1  
Q9EXY5\_ECOLI  
ID Q9EXY5\_ECOLI PRELIMINARY; PRT; 467 AA.  
AC Q9EXY5;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE GDP-mannose pyrophosphorylase.  
GN Name=manC;  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21135136; PubMed=11238967;  
RA Jensen S.O., Reeves P.R.;  
RT "Molecular evolution of the GDP-mannose pathway genes (manB and manC) in Salmonella enterica."  
RL Microbiology 147:599-610(2001).  
DR EMBL; AY012189; AAC41753.1; -, Genomic\_DNA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0008928; F:mannose-1-phosphate guanylyltransferase (GD. .); IEA.  
DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.  
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.  
DR GO; GO:0005976; P:polysaccharide metabolism; IEA.  
DR InterPro; IPR007113; Cupin region.  
DR InterPro; IPR006375; GMP PMI.  
DR InterPro; IPR001538; Man6P isomerase.  
DR InterPro; IPR005835; NTP transferase.  
DR Pfam; PF01050; MannoseP\_isomer; 1.  
DR Pfam; PF00483; NTP transferase; 1.  
DR ProDom; PD002664; Man6P isomerase; 1.  
DR TIGRFAMs; TIGR01479; GMP PMI; 1.  
SQ SEQUENCE 467 AA; 52570 MW; 41359274844CDAD3 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 467;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
Db 187 GGYLWN 192

RESULT 2  
Q31278\_ACXY  
ID Q31278\_ACXY PRELIMINARY; PRT; 492 AA.  
AC Q31278;  
DT 01-JAN-1998 (Tremblrel. 05, Created)  
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Mannose-6-phosphate isomerase (EC 5.3.1.8).  
GN Name=aceF;  
OS Acetobacter xylinus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
OC Acetobacteraceae; Gluconacetobacter.  
OX NCBI\_TaxID=28448;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C1;  
RX MEDLINE=97457201; PubMed=9311139; DOI=10.1016/S0378-1097(97)00358-3;  
RA Griffin A.M., Poelwick E., Morris V.J., Gasson M.J.;  
RT "Cloning of the aceF gene encoding the phosphomannose isomerase and  
RT GDP-mannose pyrophosphorylase activities involved in acetan  
RT biosynthesis in Acetobacter xylinum.";  
RL FEMS Microbiol. Lett. 154:389-396(1997).  
DR EMBL; Y11554; CAA72316.1; -; Genomic DNA.  
DR GO; GO:0016853; F:isomerase activity; IEA.  
DR GO; GO:0008928; F:mannose-1-phosphate isomerase activity; IEA.  
DR GO; GO:0004476; F:mannose-6-phosphate isomerase activity; IEA.  
DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.  
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.  
DR GO; GO:0005976; P:polysaccharide metabolism; IEA.  
DR InterPro; IPR007113; Cupin\_region.  
DR InterPro; IPR006375; GMP\_PMI.  
DR InterPro; IPR001538; Man6P\_isomerII.  
DR Pfam; PF01050; MannoseP\_isomer; 1.  
DR Pfam; PF00483; NTP\_transferase; 1.  
DR ProDom; PD002664; Man6P\_isomerII; 1.  
DR TIGRFAMs; TIGR01479; GMP\_PMI; 1.  
KW Isomerase.  
SQ SEQUENCE 492 AA; 54811 MW; 9FBA45F1F0257A5F CRC64;  
Query Match 100.0%; Score 40; DB 2; Length 492;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGYLWN 6  
|||||  
DB 211 GGYLWN 216  
RESULT 3  
Q8RR87 ACXY PRELIMINARY; PRT; 492 AA.  
AC Q8RR87; 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mannose-6-phosphate isomerase.  
GN Name=aceF;  
OS Acetobacter xylinus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
OC Acetobacteraceae; Gluconacetobacter.  
OX NCBI\_TaxID=28448;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BPR2001;  
RX MEDLINE=22145717; PubMed=12150936; DOI=10.1016/S0006-291X(02)00663-0;  
RA Ishida T., Sugano Y., Shoda M.;  
RT "Novel glycosyltransferase genes involved in the acetan biosynthesis  
RT of Acetobacter xylinum.";  
RL Biochem. Biophys. Res. Commun. 295:230-235(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BPR2001;  
RX MEDLINE=22240619; PubMed=12353627; DOI=10.1271/bbb.66.1677;  
RA Ishida T., Sugano Y., Nakai T., Shoda M.;  
RT "Effects of acetan on production of bacterial cellulose by Acetobacter  
RT xylinum.";  
RL Biosci. Biotechnol. Biochem. 66:1677-1681(2002).  
DR EMBL; AB059427; BAB88842.1; -; Genomic DNA.

DR GO; GO:0016853; F:isomerase activity; IEA.  
DR GO; GO:0008928; F:mannose-1-phosphate isomerase activity; IEA.  
DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.  
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.  
DR GO; GO:0005976; P:polysaccharide metabolism; IEA.  
DR InterPro; IPR007113; Cupin\_region.  
DR InterPro; IPR006375; GMP\_PMI.  
DR InterPro; IPR001538; Man6P\_isomerII.  
DR Pfam; PF01050; MannoseP\_isomer; 1.  
DR Pfam; PF00483; NTP\_transferase; 1.  
DR ProDom; PD002664; Man6P\_isomerII; 1.  
DR TIGRFAMs; TIGR01479; GMP\_PMI; 1.  
KW Isomerase.  
SQ SEQUENCE 492 AA; 54684 MW; 3ACCC80CBEF4317C CRC64;  
Query Match 100.0%; Score 40; DB 2; Length 492;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGYLWN 6  
|||||  
DB 211 GGYLWN 216  
RESULT 4  
Q55VE7 CRYNE PRELIMINARY; PRT; 560 AA.  
AC Q55VE7; 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=CNB5380;  
OS Cryptococcus neoformans var. neoformans B-3501A.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
OX NCBI\_TaxID=283643;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B-3501A;  
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
RA Wickes B.L., Fu J., Davis R.W.;  
RT "Cryptococcus neoformans serotype D sequencing.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL; AA001000015; EAL21837.1; -; Genomic DNA.  
DR EMBL; AA001000015; EAL21837.1; -; Genomic DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 560 AA; 62193 MW; 9BD25DC23AE3B652 CRC64;  
Query Match 100.0%; Score 40; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGYLWN 6  
|||||  
DB 498 GGYLWN 503  
RESULT 5  
Q5KKT9 CRYNE PRELIMINARY; PRT; 560 AA.  
AC Q5KKT9; 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Eukaryotic translation initiation factor 3 62 kDa subunit,  
DE putative.  
GN ORFNames=CNB01870;  
OS Cryptococcus neoformans var. neoformans JEC21.



OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=214684;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=JEC21;  
 RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,  
 RA Van Aken S., Fraser C.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RP STRAIN=JEC21;  
 RC STRAIN=JEC21;  
 RX PubMed=15653466; DOI=10.1126/science.1103773;  
 RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,  
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,  
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,  
 RA Mathewson C.A., Mitchell T.G., Pertea R., Riggs F.R., Salzberg S.L.,  
 RA Schein J.E., Shvartebeyn A., Shin H., Shumway M., Specht C.A.,  
 RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,  
 RA Fraser C.M., Hyman R.W.;  
 RT "The genome of the basidiomycetous yeast and human pathogen  
 RT Cryptococcus neoformans";  
 RL Science 307:1321-1324(2005).  
 DR EMBL: AE017343; AAW42248.1; -; Genomic DNA.  
 DR GO: GO:0003743; P:translation initiation factor activity; IEA.  
 DR GO: GO:0006446; P:regulation of translational initiation; IEA.  
 DR InterPro: IPR007316; ERF3\_gamma.  
 DR Pfam: PF04189; Gcd10p; 1.  
 KW Complete proteome; Initiation factor.  
 SQ SEQUENCE 560 AA; 62193 MW; 9BD25DC23AE3B652 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 560;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 Db 498 GGYLWN 503  
 |||||

RESULT 6  
 Q4PIK9\_USTMA PRELIMINARY; PRT; 368 AA.  
 ID Q4PIK9\_USTMA PRELIMINARY; PRT; 368 AA.  
 AC Q4PIK9;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=UM00054.1;  
 OS Ustilago maydis 521.  
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
 OX NCBI\_TaxID=237631;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=521;  
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
 RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
 RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,  
 RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,  
 RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,  
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,  
 RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gierin G., Gnerre S.,  
 RA Gnrke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,  
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,

RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kanvasselis M., Karlsson E.,  
 RA Kells C., Kieu A., Kiener P., Kodira C., Kulbokas E., Labutti K.,  
 RA Lana D., Landers T., Leger J., Levine S., Lewis D., Lewis T., O.,  
 RA Lindblad-coh K., Liu X., Lokitsang T., Lokitsang Y., Lucien J., O.,  
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,  
 RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,  
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,  
 RA Mesirov J., Mihalev A., Mihova T., Mikkelson T., Mlenga V., Moru K.,  
 RA Mezes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,  
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,  
 RA O'neil K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,  
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,  
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,  
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,  
 RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,  
 RA Towey S., Teamlia T., Tsomo N., Vallee D., Vassiliev H.,  
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadvav S.,  
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
 RA Zimmer A., Zody M., Lander E.;  
 RT "The genome sequence of Ustilago maydis";  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL: AACF01000002; EAK81439.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 368 AA; 40022 MW; 2B992BDCFA44362 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 368;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 Db 177 GGYVWN 182  
 |||||

RESULT 7  
 Q6EVV9\_YERPS PRELIMINARY; PRT; 425 AA.  
 ID Q6EVV9\_YERPS PRELIMINARY; PRT; 425 AA.  
 AC Q6EVV9;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Secondary type IV prepilin.  
 GN Name=piLV;  
 OS Yersinia pseudotuberculosis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=633;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=32777;  
 RX MEDLINE=22267116; PubMed=12379698;  
 RX DOI=10.1128/IAI.70.11.6196-6205.2002;  
 RA Marceau M.,  
 RA "Yersinia pseudotuberculosis harbors a type IV pilus gene cluster that  
 RT contributes to pathogenicity";  
 RN Infect. Immun. 70:6196-6205(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=32777;  
 RA Collyn F., Billault A., Mullet C., Simonet M., Marceau M.;  
 RT "YAPI, a new Yersinia pseudotuberculosis pathogenicity island";  
 RL Infect. Immun. 72:4784-4790(2004).  
 DR EMBL: AJ627388; CAP28494.1; -; Genomic\_DNA.  
 DR InterPro: IPR007001; Shufflon\_N.

DR Pfam; PF04917; Shufflon N; 1.  
SQ SEQUENCE 425 AA; 45880 MW; 74021D2C2807F57B CRC64;

Query Match 92.5%; Score 37; DB 2; Length 425;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
|||:|  
Db 148 GGYVWN 153

RESULT 8  
Q9VA99 DROME PRELIMINARY; PRT; 1097 AA.

AC Q9VA99;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE CG31028-PA, isoform A.  
GN Names=CG31028; ORFNames=CG31028;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA April J.F., Agbayani A., An H.-J., Andrews-Franckoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischmann W.,  
RA Roeler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.C., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,

RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX Berkeley Drosophila Genome Project;  
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacieb J., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AS003772; AAF57015.4; -; Genomic\_DNA.  
DR HSSP; P07505; ISRD.  
DR Ensembl; CG31028; Drosophila melanogaster.  
DR FlyBase; Fggn0051028; CG31028.  
DR FlyBase; Fggn0051030; CG31030.  
DR GO; GO:0016209; F:antioxidant activity; IEA.  
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.  
DR GO; GO:0046872; F:metal ion binding; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006801; P:superoxide metabolism; IEA.  
DR InterPro; IPR001424; SOD\_CU\_ZN.  
DR Pfam; PF00080; Sod\_Cu; 1.  
DR SEQUENCE 1097 AA; 123028 MW; 66A6B5BD00E9C667 CRC64;  
SQ

Query Match 92.5%; Score 37; DB 2; Length 1097;  
Best Local Similarity 83.3%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
|||:|  
Db 917 GGYVWN 922

RESULT 9  
Q8IM19 DROME PRELIMINARY; PRT; 1109 AA.  
ID Q8IM19;  
AC Q8IM19;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE CG31028-PB, isoform B.  
DE Names=CG31028; ORFNames=CG31028;  
GN Drosophila melanogaster (Fruit fly).  
OS

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,  
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Meunt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclele J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RA "The genome sequence of *Drosophila melanogaster*."  
RT Science 287:2185-2195(2000).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan R., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Paclele J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence."  
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirkas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celnik S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomics perspective."  
RN Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review."  
RN Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RN NUCLEOTIDE SEQUENCE.  
RX Berkeley *Drosophila* Genome Project;  
RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Paclele J., Park S., Svirkas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence."  
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RN NUCLEOTIDE SEQUENCE.  
RX FlyBase;  
RG Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB003772; AAN14221.1; -; Genomic\_DNA.  
DR HSP; P07505; ISRD  
DR Ensembl; CG31028; *Drosophila melanogaster*.  
DR FlyBase; FBGN0051028; CG31028.  
DR GO; GO:0016209; F:antioxidant activity; IEA.  
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.  
DR GO; GO:0046872; F:metal ion binding; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006801; P:superoxide metabolism; IEA.  
DR InterPro; IPR001424; SOD\_CU\_ZN.  
DR Pfam; PF00080; SOD\_Cu; 1-  
SQ SEQUENCE 1109 AA; 124552 MW; 5D020EF2910000A6 CRC64;  
Query Match 92.5%; Score 37; DB 2; Length 1109;  
Best Local Similarity 83.3%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGYLWN 6  
Db 929 GGYVMN 934  
RESULT 10  
QID QGNP40\_DROME PRELIMINARY; PRT; 1199 AA.  
AC QGNP40;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE R50384p (Fragment).  
GN Names:CG31028;  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; *Drosophila*.  
OX NCBI\_TaxID=7227;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=Berkley;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe R., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Paclele J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celnik S.;  
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BT011091; AAR82757.1; -; mRNA.  
DR HSP; P00445; IB4L.  
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.  
DR GO; GO:0020037; F:heme binding; IEA.  
DR GO; GO:0046872; F:metal ion binding; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0006801; P:superoxide metabolism; IEA.  
DR InterPro; IPR012282; Cytochrome\_c\_r.  
DR InterPro; IPR001424; SOD\_CU\_ZN.

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DR Pfam: PF00080; Sod_Cu; 1.
FT NON_TER 1
SQ SEQUENCE 1199 AA; 134574 MW; 55EOA00A85DA0FCB CRC64;

  Query Match      92.5%; Score 37; DB 2; Length 1199;
  Best Local Similarity 83.3%; Pred. No. 5.7e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
Db 962 GGYVWN 967
|||||

RESULT 11
Q522J8_MAGGR PRELIMINARY; PRT; 1279 AA.
AC Q522J8_MAGGR
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG04852.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nussbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnikre A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvysseilis M., Karlsson E.,
RA Kells C., Kieu A., Kiener P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasany U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutnan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tefaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=70-15;
RC Dean R., Mitchell T., Brown D., Pan H., Thon M.;

  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
  [3]
  RN NUCLEOTIDE SEQUENCE.
  RP STRAIN=70-15;
  RA Zhu H., Blackmon B.;
  RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
  CC -!- CAUTION: The sequence shown here is derived from an
  CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  CC preliminary data.
  CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
  CC -!- SIMILARITY: Belongs to the cation transport ATPase (P-type)
  CC family.
  DR EMBL; AACU01000757; EAA52160.1; -; Genomic_DNA.
  DR InterPro; IPR001757; ATPase_E1-E2.
  DR InterPro; IPR005834; Dehal_like_hydro.
  DR InterPro; IPR006539; Flippase.
  DR Pfam; PF00702; Hydrolase; 1.
  DR PRINTS; PR00119; CATATPASE.
  DR TIGRFAMs; TIGR01652; ATPase-Plipid; 1.
  DR TIGRFAMs; TIGR01494; ATPase_P-type; 2.
  DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN 1.
  KW ATP-binding; Hydrolase; Hypothetical protein; Nucleotide-binding;
  KW Transmembrane.
  SQ SEQUENCE 1279 AA; 143438 MW; 1A3E021D4AA1E99C CRC64;

  Query Match      92.5%; Score 37; DB 2; Length 1279;
  Best Local Similarity 83.3%; Pred. No. 6.1e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
Db 536 GGYVWN 541
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RESULT 12
MSGM_STRMU
ID MSGM_STRMU STANDARD; PRT; 277 AA.
AC Q00751;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Multiple sugar-binding transport system permease protein msgm.
GN Name=msgm; OrderedLocustNames=SMO.880;
OC Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ingbritt;
RX MEDLINE=92165821; PubMed=1537846;
RA Russell R.R.B., Aduse-Opoku J., Sutcliffe I.C., Tao L., Ferretti J.J.;
RT "A binding protein-dependent transport system in Streptococcus mutans
  responsible for multiple sugar metabolism.";
RL J. Biol. Chem. 267:4631-4637(1992).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carlson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najaf F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
  pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -!- FUNCTION: Involved in a binding protein-dependent transport system
  responsible for the uptake of melibiose, raffinose and
  isomaltotriose.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
  system permease family. MalFG subfamily.
CC -!- SIMILARITY: Contains 1 ABC transmembrane type-1 domain.

```

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 removed.  
 -----

EMBL; M77351; AAA26936.1; -; Genomic DNA.  
 EMBL; AE014929; AAN58595.1; -; Genomic DNA.  
 PIR; D42400; D42400.  
 InterPro; IPR000515; BPD\_transp.  
 Pfam; PF00528; BPD\_transp\_1; 1.  
 PROSITE; PS0928; ABC\_TM1; 1.  
 Complete proteome; Membrane; Sugar transport; Transmembrane;  
 Transport.  
 TRANSMEM 13 33 Potential.  
 TRANSMEM 74 94 Potential.  
 TRANSMEM 110 130 Potential.  
 TRANSMEM 141 161 Potential.  
 TRANSMEM 198 218 Potential.  
 TRANSMEM 243 263 Potential.  
 DOMAIN 69 263  
 SEQ SEQUENCE 277 AA; 31654 MW; C6B6D5C2F805B61A CRC64;

Query Match 90.0%; Score 36; DB 1; Length 277;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
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 Db 66 GGYFWN 71

## RESULT 13

Q4K7T4\_PSEF5  
 ID Q4K7T4\_PSEF5 PRELIMINARY; PRT; 281 AA.  
 AC Q4K7T4;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Sugar ABC transporter, permease protein.  
 GN ORFNames=PFL\_4615;  
 OS Pseudomonas fluorescens (strain Pf-5).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=220664;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PF-5;  
 RX PubMed=15980861; DOI=10.1038/nbt1110;  
 RA Paulsen I.I., Press C., Ravel J., Kobayashi D., Myers G.S.,  
 Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,  
 Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,  
 Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,  
 Khouri H.M., Pierson E., Pierson L. III, Thomasow L., Loper J.;  
 RT "Complete genome sequence of the plant commensal Pseudomonas  
 fluorescens Pf-5.";  
 RL Nat. Biotechnol. 23:873-878 (2005).  
 DR EMBL; CP000076; AAY93862.1; -; Genomic DNA.  
 SQ SEQUENCE 281 AA; 30668 MW; B2EF2A87BA2E4D5D CRC64;

Query Match 90.0%; Score 36; DB 2; Length 281;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 |||||  
 Db 71 GGYFWN 76

## RESULT 14

Q4IPC3\_GIBZE  
 ID Q4IPC3\_GIBZE PRELIMINARY; PRT; 370 AA.

Q4IPC3;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=FG00935.1;  
 OS Gibberella zeae PH-1.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
 OX NCBI\_TaxID=229533;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PH-1;  
 RA Birren B., Nusbaum C., Abouelheil A., Allen N., Anderson S.,  
 Arachchi H.M., Barna M., Bastien V., Bloom T., Boguslavskiy L.,  
 Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,  
 Choepel Y., Collymore A., Cooke A., Cooke P., Corum B., DeArelano K.,  
 Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,  
 Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,  
 Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,  
 Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,  
 Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,  
 Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
 Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,  
 Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,  
 Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
 Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,  
 Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
 Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,  
 Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,  
 Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
 Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,  
 Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
 Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
 Lander E.;  
 RT "Fusarium graminearum genome sequence.";  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; AACM01000045; EAA67712.1; -; Genomic DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 370 AA; 41068 MW; 32B07413C046F7D4 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 370;  
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
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 Db 269 GGFLWN 274

## RESULT 15

Q6WN42\_9PSED  
 ID Q6WN42\_9PSED PRELIMINARY; PRT; 430 AA.  
 AC Q6WN42;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase  
 (Fragment).  
 DE Name=alga;  
 GN Pseudomonas sp. QDA.  
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=211594;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

Query Match 90.0%; Score 36; DB 2; Length 281;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## RESULT 14

Q4IPC3\_GIBZE  
 ID Q4IPC3\_GIBZE PRELIMINARY; PRT; 370 AA.

DR GO; GO:0008928; F:mannose-1-phosphate guanylyltransferase (GD. . .; IEA.  
 DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0009058; P:biosynthesis; IEA.  
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.  
 DR GO; GO:0005976; P:polysaccharide metabolism; IEA.  
 DR InterPro; IPR006375; GMP\_FMI.  
 DR InterPro; IPR001538; Man6P\_isomerase.  
 DR InterPro; IPR005835; NTP\_transferase.  
 DR Pfam; PF01050; Mannosep\_isomerase; 1.  
 DR Pfam; PF00483; NTP\_transferase; 1.  
 DR ProDom; PD02864; Man6P\_isomerase; 1.  
 DR TIGRfam; TIGR01479; GMP\_FMI; 1.  
 KW Isomerase; Nucleotidyltransferase; Transferase.  
 FT NON\_TER 430 430  
 SQ SEQUENCE 430 AA; 47847 MW; 249A1E894633E807 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 430;  
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
 Db 189 GGYFWN 194

Search completed: December 30, 2005, 13:33:29  
 Job time : 57 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 13.4516 Seconds  
(without alignments)  
36.877 Million cell updates/sec

Title: US-10-735-916A-8  
Perfect score: 40  
Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCUTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	480	2	US-09-252-991A-19202
2	35	87.5	275	2	US-09-489-039A-12128
3	35	87.5	277	2	US-09-583-110-2944
4	35	87.5	278	2	US-09-769-787-19
5	35	87.5	290	2	US-09-107-433-4262
6	35	87.5	550	2	US-09-252-991A-17547
7	35	87.5	739	2	US-09-540-236-3594
8	34	85.0	144	1	US-09-108-051-2
9	34	85.0	144	2	US-09-440-833-2
10	34	85.0	180	2	US-08-913-159-13
11	34	85.0	301	2	US-09-328-352-7439
12	34	85.0	326	2	US-09-489-039A-9700
13	34	85.0	349	2	US-09-270-767-45401
14	34	85.0	516	2	US-09-489-039A-12893
15	34	85.0	609	2	US-09-949-016-6846
16	34	85.0	984	2	US-09-171-461-14
17	34	85.0	984	2	US-09-970-711-14
18	34	85.0	1091	2	US-09-328-352-5758
19	33	82.5	324	2	US-09-549-848B-34
20	33	82.5	324	2	US-09-688-069-34
21	33	82.5	347	2	US-09-902-540-13914
22	33	82.5	601	2	US-09-902-540-12462
23	32	80.0	114	1	US-08-741-437-3
24	32	80.0	114	1	US-09-134-593-3
25	32	80.0	143	2	US-09-270-767-33503
26	32	80.0	143	2	US-09-270-767-48720
27	32	80.0	289	1	US-08-741-437-1

28	32	80.0	289	1	US-08-741-437-4	Sequence 4, Appli
29	32	80.0	289	1	US-09-134-593-1	Sequence 1, Appli
30	32	80.0	289	1	US-09-134-593-4	Sequence 4, Appli
31	32	80.0	289	2	US-09-538-092-1335	Sequence 1335, Ap
32	32	80.0	339	2	US-09-583-110-3067	Sequence 3067, Ap
33	32	80.0	348	2	US-09-107-433-2966	Sequence 2966, Ap
34	32	80.0	411	2	US-09-540-236-3549	Sequence 3549, Ap
35	32	80.0	533	2	US-09-252-991A-25841	Sequence 25841, A
36	32	80.0	545	2	US-08-976-063E-10	Sequence 10, Appl
37	32	80.0	613	1	US-08-484-101B-46	Sequence 46, Appl
38	32	80.0	613	1	US-08-484-101B-48	Sequence 48, Appl
39	32	80.0	613	2	US-08-714-524D-46	Sequence 46, Appl
40	32	80.0	613	2	US-08-714-524D-48	Sequence 48, Appl
41	32	80.0	738	2	US-09-328-352-4315	Sequence 4315, Ap
42	32	80.0	886	2	US-09-769-787-126	Sequence 126, App
43	32	80.0	2504	2	US-09-328-352-5821	Sequence 5821, Ap
44	31	77.5	94	2	US-09-543-681A-7919	Sequence 7919, Ap
45	31	77.5	120	2	US-09-991-181-199	Sequence 199, App

#### ALIGNMENTS

RESULT 1  
US-09-252-991A-19202  
; Sequence 19202, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19202  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19202

Query Match 90.0%; Score 36; DB 2; Length 480;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
DB 194 GGYLWN 199  
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RESULT 2  
US-09-489-039A-12128  
; Sequence 12128, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 12128  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12128

Query Match 87.5%; Score 35; DB 2; Length 275;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 103 GGYTWN 108

RESULT 3  
US-09-583-110-2944  
; Sequence 2944, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 2944  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-2944

Query Match 87.5%; Score 35; DB 2; Length 277;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 66 GGYTWN 71

RESULT 4  
US-09-769-787-19  
; Sequence 19, Application US/09769787  
; Patent No. 6936252  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCES: FWC/F21129WO  
; CURRENT APPLICATION NUMBER: US/09/769,787  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-769-787-19

Query Match 87.5%; Score 35; DB 2; Length 278;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 66 GGYTWN 71

Db 67 GGYTWN 72  
RESULT 5  
US-09-107-433-4262  
; Sequence 4262, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
; THERAPEUTICS

NUMBER OF SEQUENCES: 5206  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: <Unknown>  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: <Unknown>  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,433  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/ 085131  
FILING DATE: May 12, 1998  
APPLICATION NUMBER: 60/051553  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 4262:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 290 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...290  
SEQUENCE DESCRIPTION: SEQ ID NO: 4262:  
US-09-107-433-4262

Query Match 87.5%; Score 35; DB 2; Length 290;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 79 GGYTWN 84

RESULT 6  
US-09-252-991A-17547  
; Sequence 17547, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136



; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17547  
; LENGTH: 550  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17547

Query Match 87.5%; Score 35; DB 2; Length 550;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 257 GGYWN 262

RESULT 7  
US-09-540-236-3594  
; Sequence 3594, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 3594  
; LENGTH: 739  
; TYPE: PRT  
; ORGANISM: M.catarrhalis  
US-09-540-236-3594

Query Match 87.5%; Score 35; DB 2; Length 739;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 339 GGYLWN 344

RESULT 8  
US-09-108-051-2  
; Sequence 2, Application US/09108051  
; Patent No. 5985576  
; GENERAL INFORMATION:  
; APPLICANT: Ellingson, Jay L.E.  
; APPLICANT: Stabel, Judith R.  
; TITLE OF INVENTION: Species-Specific Genetic Identification  
; TITLE OF INVENTION: of Mycobacterium Paratuberculosis  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis P. Ribando  
; STREET: 1815 N. University Street  
; CITY: Peoria  
; STATE: IL  
; COUNTRY: US  
; ZIP: 61604  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/108,051

; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ribando, Curtis P.  
; REGISTRATION NUMBER: 27,976  
; REFERENCE/DOCKET NUMBER: 0229.97  
; TELEPHONE: 309/681-6513  
; TELEFAX: 309/681-6688  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 144 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-108-051-2

Query Match 85.0%; Score 34; DB 1; Length 144;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLWN 6  
Db 30 GYLWN 34

RESULT 9  
US-09-440-833-2  
; Sequence 2, Application US/09440833  
; Patent No. 6277580  
; GENERAL INFORMATION:  
; APPLICANT: Ellingson, Jay L.E.  
; APPLICANT: Stabel, Judith R.  
; TITLE OF INVENTION: Species-Specific Genetic Identification  
; TITLE OF INVENTION: of Mycobacterium Paratuberculosis  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis P. Ribando  
; STREET: 1815 N. University Street  
; CITY: Peoria  
; STATE: IL  
; COUNTRY: US  
; ZIP: 61604  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/440,833  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/108,051  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ribando, Curtis P.  
; REGISTRATION NUMBER: 27,976  
; REFERENCE/DOCKET NUMBER: 0229.97  
; TELEPHONE: 309/681-6513  
; TELEFAX: 309/681-6688  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 144 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-440-833-2

Query Match 85.0%; Score 34; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9700
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9700

Query Match      85.0%; Score 34; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
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Db      240 GYLWN 244

RESULT 13
US-09-270-767-45401
; Sequence 45401, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 45401
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45401

Query Match      85.0%; Score 34; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLW 5
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Db      57 GGYLW 61

RESULT 14
US-09-489-039A-12893
; Sequence 12893, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12893
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12893

; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9700
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9700

Query Match      85.0%; Score 34; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
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Db      215 GYLWN 219

RESULT 12
US-09-489-039A-9700
; Sequence 9700, Application US/09489039A
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Query Match 85.0%; Score 34; DB 2; Length 516;  
Best Local Similarity 100.0%; Pred.No. 2.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYLW 5  
Db 491 GYLW 495

RESULT 15  
US-09-949-016-6846  
; Sequence 6846, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6846  
; LENGTH: 609  
; TYPE: PRT  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(609)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-949-016-6846

Query Match 85.0%; Score 34; DB 2; Length 609;  
Best Local Similarity 100.0%; Pred.No. 3.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLW 6  
Db 294 GYLW 298

Search completed: December 30, 2005, 13:37:18  
Job time : 14.4516 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 44.6129 Seconds  
(without alignments)  
56.194 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	5	US-10-735-916A-8
2	40	100.0	87	4	US-10-425-115-201562
3	40	100.0	117	5	US-10-735-916A-69
4	40	100.0	117	5	US-10-735-916A-75
5	40	100.0	117	5	US-10-735-916A-79
6	40	100.0	117	5	US-10-735-916A-83
7	40	100.0	127	5	US-10-735-916A-52
8	40	100.0	135	5	US-10-735-916A-77
9	40	100.0	135	5	US-10-735-916A-81
10	40	100.0	135	5	US-10-735-916A-85
11	40	100.0	544	4	US-10-320-797-3242
12	37	92.5	1471	6	US-11-097-143-3009
13	35	87.5	75	4	US-10-424-599-232932
14	35	87.5	83	4	US-10-080-170-414
15	35	87.5	83	4	US-10-080-170-414
16	35	87.5	83	4	US-10-468-356-414
17	35	87.5	86	4	US-10-425-115-192203
18	35	87.5	121	4	US-10-308-817-137
19	35	87.5	121	4	US-10-453-698-137
20	35	87.5	125	4	US-10-309-762-8
21	35	87.5	125	4	US-10-309-762-16
22	35	87.5	256	4	US-10-424-599-151457
23	35	87.5	278	3	US-09-769-787-19
24	35	87.5	285	5	US-10-472-928-3940
25	35	87.5	290	5	US-10-617-320-4262
26	35	87.5	400	4	US-10-017-161-2290
27	35	87.5	400	4	US-10-292-798-1936

28 34 85.0 50 4 US-10-424-599-232749 Sequence 232749,  
29 34 85.0 58 4 US-10-425-115-336772 Sequence 336772,  
30 34 85.0 72 4 US-10-106-698-4772 Sequence 4772, Ap  
31 34 85.0 73 4 US-10-425-115-328910 Sequence 328910,  
32 34 85.0 74 4 US-10-424-599-270959 Sequence 270959,  
33 34 85.0 79 4 US-10-437-963-141746 Sequence 141746,  
34 34 85.0 84 4 US-10-437-963-152064 Sequence 152064,  
35 34 85.0 109 4 US-10-074-024-293 Sequence 293, App  
36 34 85.0 115 4 US-10-425-115-364926 Sequence 364926,  
37 34 85.0 117 4 US-10-424-599-259100 Sequence 259100,  
38 34 85.0 137 6 US-11-097-143-3858 Sequence 3858, Ap  
39 34 85.0 139 3 US-09-864-408A-7378 Sequence 7378, Ap  
40 34 85.0 159 4 US-10-424-599-257904 Sequence 257904,  
41 34 85.0 168 4 US-10-767-701-32069 Sequence 32069, A  
42 34 85.0 170 4 US-10-424-599-163133 Sequence 163133,  
43 34 85.0 228 4 US-10-425-115-284834 Sequence 284834,  
44 34 85.0 230 4 US-10-767-701-51631 Sequence 51631, A  
45 34 85.0 240 6 US-11-097-143-22905 Sequence 22905, A

#### ALIGNMENTS

RESULT 1  
US-10-735-916A-8  
; Sequence 8, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOSTSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFIOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10735,916A  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-8

Query Match 100.0%; Score 40; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
Db 1 GGYLWN 6

RESULT 2  
US-10-425-115-201562  
; Sequence 201562, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 201562  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MR74577\_115409C.1.pcp  
US-10-425-115-201562

Query Match 100.0%; Score 40; DB 4; Length 87;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
| | | | |  
Db 62 GGYLWN 67

RESULT 3  
US-10-735-916A-69  
; Sequence 69, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 69  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-69

Query Match 100.0%; Score 40; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
| | | | |  
Db 31 GGYLWN 36

RESULT 4  
US-10-735-916A-75  
; Sequence 75, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie

; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 75  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-735-916A-75

Query Match 100.0%; Score 40; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
| | | | |  
Db 31 GGYLWN 36

RESULT 5  
US-10-735-916A-79  
; Sequence 79, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 79  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-735-916A-79

Query Match 100.0%; Score 40; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6

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Db          31 GGYLWN 36
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RESULT 6
US-10-735-916A-83
; Sequence 83, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83

Query Match          100.0%; Score 40; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GGYLWN 6
          |||||
Db          31 GGYLWN 36

RESULT 7
US-10-735-916A-52
; Sequence 52, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83

Query Match          100.0%; Score 40; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GGYLWN 6
          |||||
Db          31 GGYLWN 36

RESULT 8
US-10-735-916A-77
; Sequence 77, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-77

Query Match          100.0%; Score 40; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GGYLWN 6
          |||||
Db          49 GGYLWN 54

RESULT 9
US-10-735-916A-81
; Sequence 81, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
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; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-81
```

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Query Match          100.0%; Score 40; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GGYLWN 6
        |||||
Db       49 GGYLWN 54
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RESULT 10
US-10-735-916A-85
; Sequence 85, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-85
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Query Match          100.0%; Score 40; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GGYLWN 6
        |||||
Db       49 GGYLWN 54
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RESULT 11
US-10-320-797-3242
; Sequence 3242, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
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; APPLICANT: Broshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3242
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3242
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Query Match          100.0%; Score 40; DB 4; Length 544;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GGYLWN 6
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Db       467 GGYLWN 472
```

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RESULT 12
US-11-097-143-3009
; Sequence 3009, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3009
; LENGTH: 1471
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-3009
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Query Match          92.5%; Score 37; DB 6; Length 1471;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GGYLWN 6
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Db       871 GGYVWN 876
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RESULT 13



US-10-424-599-232932  
; Sequence 232932, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 232932  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_52362C.1.pap  
US-10-424-599-232932

Query Match 87.5%; Score 35; DB 4; Length 75;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
Db 69 GGYLWS 74

RESULT 14  
US-10-080-170-414  
; Sequence 414, Application US/10080170  
; Publication No. US20030129601A1  
; GENERAL INFORMATION:  
; APPLICANT: COLE, S.T.  
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR  
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR  
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES  
; FILE REFERENCE: 03495.0218  
; CURRENT APPLICATION NUMBER: US/10/080,170  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/270,123  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 652  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 414  
; LENGTH: 83  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
US-10-080-170-414

Query Match 87.5%; Score 35; DB 4; Length 83;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
Db 8 GGYLWS 13

RESULT 15  
US-10-080-170-414  
; Sequence 414, Application US/10080170  
; Publication No. US20040121322A9  
; GENERAL INFORMATION:  
; APPLICANT: COLE, S.T.  
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR  
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR  
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES  
; FILE REFERENCE: 03495.0218  
; CURRENT APPLICATION NUMBER: US/10/080,170

; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/270,123  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 652  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 414  
; LENGTH: 83  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
US-10-080-170-414  
Query Match 87.5%; Score 35; DB 4; Length 83;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGYLWN 6  
Db 8 GGYLWS 13  
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Job time : 45.6129 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 2.22581 Seconds  
(without alignments)  
20.187 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

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Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications\_AA\_New:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%	Query Match	Length	DB ID	Description
1	40	100.0	6	7	US-11-012-353-8	Sequence 8, Appli
2	40	100.0	117	7	US-11-012-353-69	Sequence 69, Appli
3	40	100.0	117	7	US-11-012-353-75	Sequence 75, Appli
4	40	100.0	117	7	US-11-012-353-79	Sequence 79, Appli
5	40	100.0	117	7	US-11-012-353-83	Sequence 83, Appli
6	40	100.0	127	7	US-11-012-353-52	Sequence 52, Appli
7	40	100.0	135	7	US-11-012-353-77	Sequence 77, Appli
8	40	100.0	135	7	US-11-012-353-81	Sequence 81, Appli
9	40	100.0	135	7	US-11-012-353-85	Sequence 85, Appli
10	35	87.5	278	6	US-10-873-528-19	Sequence 19, Appli
11	33	82.5	324	7	US-11-092-140-34	Sequence 34, Appli
12	32	80.0	289	6	US-10-821-234-1289	Sequence 1289, Ap
13	32	80.0	886	6	US-10-873-528-126	Sequence 126, App
14	32	80.0	1029	6	US-10-821-234-908	Sequence 908, App
15	32	80.0	1032	6	US-10-467-657-3278	Sequence 3278, Ap
16	31	77.5	120	6	US-10-131-826A-434	Sequence 434, App
17	30	75.0	99	7	US-11-054-669-36	Sequence 36, Appli
18	30	75.0	99	7	US-11-054-669-39	Sequence 39, Appli
19	30	75.0	99	7	US-11-084-554-50	Sequence 50, Appli
20	30	75.0	99	7	US-11-084-554-55	Sequence 55, Appli
21	30	75.0	253	7	US-11-054-515-1619	Sequence 1619, Ap
22	29	72.5	6	7	US-11-009-939-23	Sequence 23, Appli
23	29	72.5	90	6	US-10-467-657-3624	Sequence 3624, Ap
24	29	72.5	99	7	US-11-054-669-37	Sequence 37, Appli
25	29	72.5	118	7	US-11-012-353-70	Sequence 70, Appli

Sequence 22, Appli  
Sequence 3386, Ap  
Sequence 8, Appli  
Sequence 9, Appli  
Sequence 1546, Ap  
Sequence 1607, Ap  
Sequence 34, Appli  
Sequence 2234, Ap  
Sequence 71, Appli  
Sequence 624, App  
Sequence 49, Appli  
Sequence 244, App  
Sequence 10, Appli  
Sequence 132, App  
Sequence 38, Appli  
Sequence 26, Appli  
Sequence 464, App  
Sequence 5, Appli  
Sequence 5500, Ap  
Sequence 2730, Ap

#### ALIGNMENTS

##### RESULT 1

US-11-012-353-8  
; Sequence 8, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFILOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-8

Query Match 100.0%; Score 40; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.4e+04;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
|||||  
Db 1 GGYLWN 6

##### RESULT 2

US-11-012-353-69  
; Sequence 69, Application US/11012353

; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; PRIOR FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 69  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-69

Query Match 100.0%; Score 40; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.67; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 GGYLWN 6  
Db 31 GGYLWN 36

RESULT 3  
US-11-012-353-75  
; Sequence 75, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 75

; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-75

Query Match 100.0%; Score 40; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.67; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 GGYLWN 6  
Db 31 GGYLWN 36

RESULT 4  
US-11-012-353-79  
; Sequence 79, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 79  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-79

Query Match 100.0%; Score 40; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.67; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 GGYLWN 6  
Db 31 GGYLWN 36

RESULT 5  
US-11-012-353-83  
; Sequence 83, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198

; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 83  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-83

Query Match 100.0%; Score 40; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLMN 6  
|||||  
Db 31 GGYLMN 36

## RESULT 6

US-11-012-353-52  
; Sequence 52, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 52  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-52

Query Match 100.0%; Score 40; DB 7; Length 127;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLMN 6  
|||||

Db 41 GGYLMN 46

## RESULT 7

US-11-012-353-77  
; Sequence 77, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 77  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-77

Query Match 100.0%; Score 40; DB 7; Length 135;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLMN 6  
|||||  
Db 49 GGYLMN 54

## RESULT 8

US-11-012-353-81  
; Sequence 81, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653

;  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 81  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-81

Query Match 100.0%; Score 40; DB 7; Length 135;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
|||  
Db 49 GGYLWN 54

RESULT 9  
US-11-012-353-85  
; Sequence 85, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 85  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-85

Query Match 100.0%; Score 40; DB 7; Length 135;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
|||  
Db 49 GGYLWN 54

RESULT 10  
US-10-873-528-19  
; Sequence 19, Application US/10873528  
; Publication No. US20050276814A1  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M

;  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; CURRENT FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-19

Query Match 87.5%; Score 35; DB 6; Length 278;  
Best Local Similarity 83.3%; Pred. No. 10;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
|||  
Db 67 GGYLWN 72

RESULT 11  
US-11-092-140-34  
; Sequence 34, Application US/11092140  
; Publication No. US20050262590A1  
; GENERAL INFORMATION:  
; APPLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, Y  
; TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthe  
; FILE REFERENCE: 16515.054  
; CURRENT APPLICATION NUMBER: US/11/092,140  
; CURRENT FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: US/09/688,069  
; PRIOR FILING DATE: 2000-10-14  
; NUMBER OF SEQ ID NOS: 114  
; SEQ ID NO 34  
; LENGTH: 324  
; TYPE: PRT  
; ORGANISM: Synechocystis sp.  
US-11-092-140-34

Query Match 82.5%; Score 33; DB 7; Length 324;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
|||  
Db 58 GGYLWN 63

RESULT 12  
US-10-821-234-1289  
; Sequence 1289, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: Pt SEQ\_genes Version 1.0  
; SEQ ID NO 1289

; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1289

Query Match 80.0%; Score 32; DB 6; Length 289;  
Best Local Similarity 80.0%; Pred. No. 34;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLWN 6  
||:|  
Db 89 GYIWN 93

RESULT 13  
US-10-873-528-126  
; Sequence 126, Application US/10873528  
; Publication No. US20050276814A1  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hanebro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; PRIOR FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 398  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 126  
; LENGTH: 886  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-126

Query Match 80.0%; Score 32; DB 6; Length 886;  
Best Local Similarity 80.0%; Pred. No. 86;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLW 5  
|||:|  
Db 482 GGYIW 486

RESULT 14  
US-10-821-234-908  
; Sequence 908, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 908  
; LENGTH: 1029  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-908

Query Match 80.0%; Score 32; DB 6; Length 1029;

Best Local Similarity 80.0%; Pred. No. 97;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLWN 6  
||:|  
Db 124 GYIWN 128

RESULT 15  
US-10-467-657-3278  
; Sequence 3278, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 3278  
; LENGTH: 1032  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3278

Query Match 80.0%; Score 32; DB 6; Length 1032;  
Best Local Similarity 66.7%; Pred. No. 97;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
|||:|  
Db 302 GGYVWH 307

Search completed: December 30, 2005, 14:15:21  
Job time : 2.22581 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:23:43 ; Search time 181 Seconds  
(without alignments)  
14.565 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 41471

Minimum DB seq length: 6

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*  
1: Geneseqp1990s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	7	ADJ76842
2	40	100.0	6	9	ADZ67012
3	32	80.0	6	2	AAR05974
4	30	75.0	6	9	AEA40139
5	29	72.5	6	9	ADZ45406
6	29	72.5	6	9	ABE70898
7	27	67.5	6	8	ADP05843
8	27	67.5	6	8	ADP07180
9	26	65.0	6	8	ADP05839
10	26	65.0	6	8	ADP07176
11	26	65.0	6	8	ADP05872
12	23	57.5	6	2	AAR24717
13	23	57.5	6	2	AAW01150
14	23	57.5	6	2	AAR98564
15	23	57.5	6	2	AAW39848
16	23	57.5	6	2	AAW44173
17	23	57.5	6	2	AAW87989
18	23	57.5	6	7	ADM83262
19	23	57.5	6	8	ADL26967
20	23	57.5	6	8	ADS82610
21	23	57.5	6	9	ADZ45518
22	23	57.5	6	9	ADZ45310
23	23	57.5	6	9	ADZ45342
24	23	57.5	6	9	ADZ51223

25	23	57.5	6	9	ADZ51255	Amino aci
26	23	57.5	6	9	ADZ42129	Mouse ant
27	23	57.5	6	9	ADZ42097	Mouse ant
28	23	57.5	6	9	AEA88995	Hepatitis
29	23	57.5	6	9	AEC20779	M-CSF spe
30	22	55.0	6	2	AAR66826	Hexapepti
31	22	55.0	6	2	AAAY33848	G30 sub d
32	22	55.0	6	3	AAAY90100	Enhancer
33	22	55.0	6	3	AAAY50634	Alphal-pr
34	22	55.0	6	3	AAAY85089	HBV surfa
35	22	55.0	6	4	AAU06272	Anti-HIV
36	22	55.0	6	4	AAAB77005	Retrovira
37	22	55.0	6	4	ABBO3059	Viral cor
38	22	55.0	6	5	ABP67968	Human CD6
39	22	55.0	6	5	ABP67966	Human CD6
40	22	55.0	6	5	ABP67967	Human CD6
41	22	55.0	6	5	ABP67965	Human CD6
42	22	55.0	6	5	ABP67361	Human CD6
43	22	55.0	6	5	AAAM48304	Human CD4
44	22	55.0	6	5	ADE03081	Hybrid po
45	22	55.0	6	6	ADA19581	Carcinoem

#### ALIGNMENTS

##### RESULT 1

ID ADJ76842

XX ADJ76842 standard; peptide; 6 AA.

AC ADJ76842;

XX 06-MAY-2004 (first entry)

DT CDR sequence for anti-IGF-1R antibody.

XX cytotatic; antipsoriatic; antibody;

XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;

XX or epidermal growth factor receptor; EGFR; signal transduction pathway;

XX ligand; tumor; cancer; osteosarcoma; complementarity determining region;

XX CDR.

OS Mus musculus.

XX WO2003059951-A2.

PN 24-JUL-2003.

PD 20-JAN-2003; 2003WO-FR000178.

PF 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PA (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;

PI WPI; 2003-569653/53.

XX N-PSDB; ADJ76841.

XX New antibodies that bind to human insulin-like growth factor receptor,

XX useful for treatment, prevention and diagnosis of cancers.

PT Claim 1; SEQ ID NO 8; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional

XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-

XX IR) and optionally, (i) inhibit natural binding of insulin-like growth

XX factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

XX kinase activity of IGF-1R. Ab and its fragments are used to prevent or

XX treat diseases associated with overexpression and/or abnormal activity of

XX IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 40; DB 7; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6

Db 1 GGYLWN 6

RESULT 2

ID ADZ67012 standard; peptide; 6 AA.

XX ADZ67012;

AC ADZ67012;

DT 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:8.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;

KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;

KW musculoskeletal disease; respiratory disease; lung tumor;

KW endocrine disease; gynecology and obstetrics; breast tumor;

KW endometroid carcinoma; gastrointestinal disease; colon tumor;

KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

OS US2005084906-A1.

PN 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-0000653.

PR 18-JAN-2002; 2002FR-0000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFLOS A.

PA (HAUJ/) HAEUW J.

PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

PI WPI; 2005-321968/33.

XX N-PSDB; ADZ67011.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

PT antibody or its functional fragment, being capable of binding human IGF-

PT IR and specifically inhibiting tyrosine kinase activity of receptor,

PT useful for treating cancer.

XX Claim 1; SEQ ID NO 8; 125pp; English.

PS The invention relates to a novel isolated anti-insulin-like growth factor

XX I receptor (IGF-IR) antibody (I) or its functional fragment, being

CC capable of binding to human IGF-IR and, if necessary, capable of

CC

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 9; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6

Db 1 GGYLWN 6

RESULT 3

AAR05974

ID AAR05974 standard; protein; 6 AA.

XX AAR05974;

AC AAR05974;

XX 16-NOV-1990 (first entry)

DT Somatic immunoglobulin DH fragment DOB.

XX Immunoglobulin DH; cancer; lymphoid tumour; leukaemia; ds.

DE Homo sapiens.

XX WO9006998-A.

PN 28-JUN-1990.

XX 19-DEC-1988; 88JP-00319809.

PF 19-DEC-1988; 88JP-00319809.

PR (MITK ) MITSUI TOATSU CHEM INC.

XX (EDUC-) EDUCATIONAL FOUND FUJITA.

PA Kurosawa Y, Ichihara Y, Awaya K, Ishizuka Y;

XX WPI; 1990-224526/29.

XX

PT DNA fragments related to human immunoglobulin genes - in which are  
PT markers for diagnosis of lymphoid tumours by detection of B- and T-type  
XX tumour cells.

PS Disclosure; Page ?; -pp; Japanese.

CC DH immunoglobulin encoding sequences may be extracted as fragments and  
CC used in diagnosis of lymphoid tumours and leukaemias, detecting marker  
CC sequences from the VhDhJh gene cluster

XX Sequence 6 AA;

SQ Query Match 80.0%; Score 32; DB 2; Length 6;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYLNW 6  
||:|  
Db 1 GYIWN 5

RESULT 4  
AEA40139  
ID AEA40139 standard; peptide; 6 AA.

XX AC AEA40139;

XX DT 28-JUL-2005 (first entry)

XX DE TNF resistant monoclonal antibody VH region, F6VH CDR1.

XX KW tumor necrosis factor; TNF; monoclonal antibody; F6 mAb;  
XX light chain variable region; heavy chain variable region; F6VH.

XX OS Unidentified.

XX XX CN1544466-A.

XX PD 10-NOV-2004.

XX PF 13-NOV-2003; 2003CN-01105919.

XX PR 13-NOV-2003; 2003CN-01105919.

XX PA (UYFO-) UNIV FOURTH MILITARY MEDICAL.

XX PI Jin B, Liu X, Zhu C;

XX DR WPI; 2005-153078/17.

XX DR N-PSDB; AEA40138.

XX Variable region gene of high affinity monoclonal antibody of tumor  
PT necrosis factor and its preparation.

XX PS Claim 1; Page 3; 20pp; Chinese.

XX The invention relates to a method for preparing variable region genes of  
CC high affinity tumor necrosis factor (TNF) resistant monoclonal antibody  
CC (F6 mAb). The method comprises using recombinant human TNF immune BALB/c  
CC mouse to prepare mouse anti-TNF monoclonal antibody, screening high  
CC affinity F6 mAb using an indirect enzyme linked immunosorbent assay  
CC (ELISA). By cloning the monoclonal antibody light chain and heavy chain  
CC variable region (VL and VH respectively) genes, the monoclonal antibody  
CC light chain and heavy chain variable region gene sequence and amino acid  
CC sequence can be obtained, and the identity of the gene sequence and  
CC protein sequence can be confirmed. This sequence represents  
CC complementarity determining region, CDR1 of F6VH.

XX SQ Sequence 6 AA;

Query Match 75.0%; Score 30; DB 9; Length 6;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYLNW 6  
||:|  
Db 2 GYFWN 6

RESULT 5  
ADZ45406  
ID ADZ45406 standard; peptide; 6 AA.

XX AC ADZ45406;

XX DT 30-JUN-2005 (first entry)

XX DE Murine factor IX directed antibody CDR1 SEQ ID NO 110.

XX KW bispecific antibody; blood coagulation factor VIII; bleeding;  
XX fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;  
XX factor VIII deficiency; von Willebrand disease; hemostatic;  
XX immunostimulator; antibody engineering.

XX OS Mus musculus.

XX PN WO2005035756-A1.

XX PD 21-APR-2005.

XX PF 08-OCT-2004; 2004WO-JP014911.

XX PR 10-OCT-2003; 2003WO-JP013062.

XX PR 14-OCT-2003; 2003WO-JP013123.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Hattori K, Kojima T, Miyazaki T, Soeda T;

XX DR WPI; 2005-315563/32.

XX Novel bispecific antibody substituting for function of cofactor that  
PT enhances enzyme reaction, and recognizing both enzyme and substrates of  
PT enzyme, useful for treating hemophilia A.

XX PS Disclosure; SEQ ID NO 110; 69pp; Japanese.

XX This invention describes a novel bispecific antibody which can act as a  
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and  
CC the enzyme substrate. The antibody specifically binds to blood  
CC coagulation factor VIII. The invention also describes a composition  
CC comprising the antibody and a carrier, a kit useful in preventing and/or  
CC treating bleeding associated with a disorder or from a disease caused by  
CC bleeding. The composition includes blood coagulation factor VIII. The  
CC antibody of the invention can be a blood-coagulation fibrinolysis related  
CC factor including blood-coagulation factor VIII, blood coagulation factor  
CC X, or blood-coagulation factor IX. The antibody comprises a complementary  
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor  
CC antibody. The novel antibody or composition is useful for preventing  
CC and/or treating a disease accompanying bleeding, or the disease resulting  
CC from bleeding, where the disease accompanying bleeding or the disease  
CC resulting from bleeding develops and/or progresses by an active reduction  
CC or deletion of the blood coagulation factor VIII. The disease the  
CC develops and/or progresses by an active reduction or deletion of the  
CC blood coagulation factor VIII and/or activation blood coagulation factor  
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is  
CC an acquired hemophilia A. This sequence represents a fragment of the  
CC antibody described in the method of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 6 AA;

Query Match 72.5%; Score 29; DB 9; Length 6;  
Best Local Similarity 80.0%; Pred. No. 2e+06;





Query Match 65.0%; Score 26; DB 8; Length 6;  
Best Local Similarity 60.0%; Pred. NO. 2e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLWN 6  
|::||  
Db 1 GWVWN 5

RESULT 10  
ADP07176  
ID ADP07176 standard; peptide; 6 AA.  
XX AC ADP07176;  
XX 26-AUG-2004 (first entry)  
XX Trp-containing cell adhesion recognition (CAR) sequence #211.  
XX cell adhesion modulating agent;  
KW desmosomal cadherin-mediated cell adhesion;  
KW Trp-containing cell adhesion recognition sequence; CAR sequence;  
KW desmosomal cadherin molecule; cancer metastasis; angiogenesis;  
KW demyelinating neurological disorder; immune system modulation;  
KW pregnancy prevention; vasopermeability; synaptic stability;  
KW blood vessel regression; neurite outgrowth; spinal cord injury;  
KW angiogenesis; neovascularisation; psoriasis; diabetic retinopathy;  
KW dermatitis.  
XX Unidentified.  
OS WO2004048411-A2.  
XX PN 10-JUN-2004.  
XX PD 14-NOV-2003; 2003WO-IB006208.  
XX PF 14-NOV-2002; 2002US-0426551P.  
XX PR 14-NOV-2002; 2002US-0426689P.  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX PA Blaschuk OW, Michaud SD;  
XX PI WPI; 2004-450349/42.  
XX DR Cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion, useful for inhibiting cancer metastasis, comprises Trp-containing cell adhesion recognition sequence of desmosomal cadherin molecule.  
XX PT Claim 51; SEQ ID NO 1353; 507pp; English.  
XX PS The invention comprises a cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating agent comprises a Trp-containing cell adhesion recognition (CAR) sequence of a desmosomal cadherin molecule. The cell adhesion modulating agent of the invention is useful for: inhibiting cancer metastasis, inhibiting angiogenesis in a mammal, ameliorating a demyelinating neurological disorder in a mammal, modulating immune system of a mammal, preventing pregnancy in a mammal, increasing vasopermeability in a mammal, inhibiting synaptic stability in a mammal, stimulating blood vessel regression, increasing blood flow to a tumour in a mammal, disrupting neovasculature in a mammal, inhibiting endometriosis in a mammal, enhancing inhaled compound delivery in a mammal, enhancing adhesion of a foreign tissue implanted within a mammal, for enhancing/directing neurite outgrowth, and for ameliorating a spinal cord injury in a mammal. The cell adhesion modulating agent of the invention is useful for treating disease conditions that are dependent on angiogenesis and neovascularisation (e.g. psoriasis, diabetic retinopathy or dermatitis). The present amino acid sequence represents a Trp-containing CAR sequence of the invention.

SQ Sequence 6 AA;  
Query Match 65.0%; Score 26; DB 8; Length 6;  
Best Local Similarity 60.0%; Pred. NO. 2e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLWN 6  
|::||  
Db 1 GWVWN 5

RESULT 11  
ADP05872  
ID ADP05872 standard; peptide; 6 AA.  
XX AC ADP05872;  
XX 26-AUG-2004 (first entry)  
XX Trp-containing cell adhesion recognition (CAR) sequence #37.  
XX cell adhesion modulating agent;  
KW desmosomal cadherin-mediated cell adhesion;  
KW Trp-containing cell adhesion recognition sequence; CAR sequence;  
KW desmosomal cadherin molecule; cancer metastasis; angiogenesis;  
KW demyelinating neurological disorder; immune system modulation;  
KW pregnancy prevention; vasopermeability; synaptic stability;  
KW blood vessel regression; neurite outgrowth; spinal cord injury;  
KW angiogenesis; neovascularisation; psoriasis; diabetic retinopathy;  
KW dermatitis.  
XX Unidentified.  
OS WO2004048411-A2.  
XX PN 10-JUN-2004.  
XX PD 14-NOV-2003; 2003WO-IB006208.  
XX PF 14-NOV-2002; 2002US-0426551P.  
XX PR 14-NOV-2002; 2002US-0426689P.  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX PA Blaschuk OW, Michaud SD;  
XX PI WPI; 2004-450349/42.  
XX DR Cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion, useful for inhibiting cancer metastasis, comprises Trp-containing cell adhesion recognition sequence of desmosomal cadherin molecule.  
XX PS Disclosure; SEQ ID NO 49; 507pp; English.  
XX CC The invention comprises a cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating agent comprises a Trp-containing cell adhesion recognition (CAR) sequence of a desmosomal cadherin molecule. The cell adhesion modulating agent of the invention is useful for: inhibiting cancer metastasis, inhibiting angiogenesis in a mammal, ameliorating a demyelinating neurological disorder in a mammal, modulating immune system of a mammal, preventing pregnancy in a mammal, increasing vasopermeability in a mammal, inhibiting synaptic stability in a mammal, stimulating blood vessel regression, increasing blood flow to a tumour in a mammal, disrupting neovasculature in a mammal, inhibiting endometriosis in a mammal, enhancing inhaled compound delivery in a mammal, enhancing adhesion of a foreign tissue implanted within a mammal, for enhancing/directing neurite outgrowth, and for ameliorating a spinal cord injury in a mammal. The cell adhesion modulating agent of the invention is useful for treating disease conditions that are dependent on angiogenesis and neovascularisation (e.g. psoriasis, diabetic retinopathy or dermatitis). The present amino acid sequence represents a Trp-containing CAR sequence

CC of the invention.  
XX  
SQ Sequence 6 AA;

Query Match 65.0%; Score 26; DB 8; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLWN 6  
|:|  
Db 2 GWVWN 6

## RESULT 12

AAR24717  
ID AAR24717 standard; protein; 6 AA.

XX  
AC AAR24717;

XX 25-MAR-2003 (revised)  
DT 28-DEC-1992 (first entry)

XX Sequence of an anti-urokinase antibody heavy chain variable region chain  
DE designated 'J'.

XX Chimeric monoclonal antibody; anti-urokinase antibody;  
KW antithrombotic agent; myocardial infarction therapy.

XX Mus musculus.

XX EP491351-A2.

XX 24-JUN-1992.

XX 17-DEC-1991; 91EP-00121591.

XX 18-DEC-1990; 90JP-00413829.

XX 11-NOV-1991; 91JP-00294464.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Iwasa S, Tada H, Watanabe T;

XX WPI; 1992-209528/26.

XX Chimeric monoclonal antibodies - contain anti-human fibrin antibody light  
PT and heavy chain variable and constant for treating thrombotic conditions  
PT e.g. myocardial infarction.

XX Claim 21; Page 50; 87pp; English.

XX The inventors claim a chimeric monoclonal antibody which contains a  
CC urokinase-recognising antibody heavy chain variable region contg. at least  
CC one of the polypeptide chains G, H and I (AAR24717, R24718, AAR24719) and a  
CC human antibody heavy chain constant region. The chimeric Abs can be used  
CC both in vivo and in vitro and, since they have very low immunogenicity as  
CC compared with mouse Abs, they can be administered to humans for  
CC diagnostic and therapeutic purposes. They are also more stable and show a  
CC longer half-life in the blood as compared with the original mouse Abs.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 6 AA;

Query Match 57.5%; Score 23; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLWN 6  
|:|  
Db 3 YAWN 6

## RESULT 13

AAW01150

ID AAW01150 standard; peptide; 6 AA.

XX  
AC AAW01150;

XX 10-FEB-1997 (first entry)

XX MAb 1.4 heavy chain CDR (Mab binds type II phospholipase A2).

XX Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis;  
KW cerebral infarction; acute kidney failure; colitis; chronic rheumatism;  
KW adult respiratory distress syndrome; cardiac shock; treatment;  
KW preclinical testing; disease; hybridoma.

XX Mus musculus.

XX WO9620959-A1.

XX 11-JUL-1996.

XX 27-DEC-1995; 95WO-JP002714.

XX 29-DEC-1994; 94JP-00340006.

XX (YAMA ) YAMANOUCHI PHARM CO LTD.

XX Kawauchi Y, Takasaki J, Yasunaga T, Masuho Y;

XX WPI; 1996-333946/33.

XX Monoclonal antibody inhibiting type II phospholipase A2 activity - for  
PT treatment of myocardial and cerebral infarction.

XX Claim 7; Page 42; 69pp; Japanese.

XX Monoclonal antibodies which inhibit type II phospholipase A2 are useful  
CC in the treatment of myocardial infarction, cerebral infarction, acute  
CC kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult  
CC respiratory distress syndrome and colitis. The antibodies were generated  
CC by immunising Balb/C mice with recombinant human type II phospholipase  
CC A2. Spleen cells from the mice were fused with mouse myeloma P3U1  
CC (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase  
CC A2 inhibitory activity. Active clones were isolated including 12H5, 1.4  
CC and 10.1. These were cultured and the antibody isolated from the culture  
CC supernatant by precipitation with ammonium sulphate and purification on a  
CC column of protein A-Sepharose CL4B. Because the antibody acts on the  
CC primate and mouse forms of enzyme as well as human it is particularly  
CC suitable for preclinical testing. This peptide sequence corresponds to  
CC the first complementary determining region of the heavy chain of the  
CC monoclonal antibody isolated from the clone designated 1.4

XX Sequence 6 AA;

Query Match 57.5%; Score 23; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLWN 6  
|:|  
Db 3 YAWN 6

## RESULT 14

AAR98564

ID AAR98564 standard; peptide; 6 AA.

XX  
AC AAR98564;

XX 25-MAR-2003 (revised)

DT 06-NOV-1996 (first entry)

XX N-terminus of 6-SFT 49 kDa subunit.

XX





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:24:08 ; Search time 37 Seconds  
(without alignment)  
15.603 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 110

Minimum DB seq length: 6

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	40.0	6	PT0519	T-cell receptor be
2	15	37.5	6	B34835	dnaA protein - Pse
3	13	32.5	6	A61411	ameletin - rat
4	12	30.0	6	JU0355	lipopeptide WS1279
5	12	30.0	6	PT0514	T-cell receptor be
6	12	30.0	6	PT0512	T-cell receptor be
7	12	30.0	6	PT0720	T-cell receptor be
8	12	30.0	6	PT0560	T-cell receptor be
9	12	30.0	6	PT0723	T-cell receptor be
10	12	30.0	6	PT0727	T-cell receptor be
11	12	30.0	6	PT0730	T-cell receptor be
12	12	30.0	6	P41946	T-cell receptor ga
13	12	30.0	6	PT0605	T-cell receptor be
14	11	27.5	6	S66195	alcohol dehydrogen
15	11	27.5	6	B44510	hypothetical prote
16	11	27.5	6	A31263	dihydrofolate redu
17	11	27.5	6	B31263	dihydrofolate redu
18	11	27.5	6	B35640	carebollar degener
19	11	27.5	6	PT0629	T-cell receptor be
20	11	27.5	6	PT0532	T-cell receptor be
21	11	27.5	6	PT0637	T-cell receptor be
22	11	27.5	6	PT0641	T-cell receptor be
23	11	27.5	6	PT0726	T-cell receptor be
24	11	27.5	6	PD0028	pev-kinin 2 - pena
25	11	27.5	6	A61088	locustakinin - mig
26	11	27.5	6	I79564	hypothetical TCL3
27	10	25.0	6	JN0861	peptidyl-dipeptida
28	9	22.5	6	A41946	T-cell receptor ga
29	9	22.5	6	A43129	neuropeptide GNPFR

#### ALIGNMENTS

##### RESULT 1

PT0519

T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0519

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0519

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <PEE>

A;Cross-references: UNIPARC:UPI000017C7BE

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 40.0%; Score 16; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LWN 6

Db 4 LWD 6

##### RESULT 2

B34835

dnaA protein - Pseudomonas aeruginosa (fragment)

C;Species: Pseudomonas aeruginosa

C;Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 08-Oct-1999

C;Accession: B34835

R;Yee, T.W.; Smith, D.W.

Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990

A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from

A;Reference number: A34835; MUID:90160310; PMID:2106132

A;Accession: B34835

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-6 <VEE>

A;Cross-references: UNIPARC:UPI000011EAEC; GB:M30125; NID:G151419; PIDN:AAA25916.1; PIR

C;Keywords: DNA binding

Query Match 37.5%; Score 15; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5

Db 5 LW 6

sarcosine dehydrog  
collagen alpha 1(I  
hydrogensulfite re  
protamine P1 - gor  
laminin B1 - weste  
RNA-directed DNA p  
halo-toxin - Pseud  
phosphoglycerate t  
hydrogensulfite re  
mesquitecoidal toxi  
parasporal crystal  
jacalin beta-II ch  
angiotensin-conver  
variant surface gly  
antineoplastic gly  
H4 histone - Afric

30 8 20.0 6 2 A61419  
31 8 20.0 6 2 B56979  
32 7 17.5 6 2 S11556  
33 7 17.5 6 2 I37027  
34 7 17.5 6 2 I49421  
35 6 15.0 6 2 A35890  
36 6 15.0 6 2 A61049  
37 6 15.0 6 2 T11779  
38 6 15.0 6 2 S11024  
39 6 15.0 6 2 A44916  
40 6 15.0 6 2 S14159  
41 6 15.0 6 2 S29637  
42 6 15.0 6 2 PQ0008  
43 6 15.0 6 2 B61512  
44 6 15.0 6 2 A60494  
45 6 15.0 6 2 I51434

```

RESULT 3
A61411
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C;Accession: A61411
R;Burzynski, S.R.
Anal. Biochem. 70, 359-365, 1976
A;Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the
A;Reference number: A61411; MUID:76182447; PMID:1267130
A;Accession: A61411
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <BUR>
A;Cross-references: UNIPARC:UPI000017A501
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GY 3
  ||
Db 3 GY 4

RESULT 4
JU0355
Lipopeptide WS1279 [validated] - Streptomyces willmorei
C;Species: Streptomyces willmorei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: JU0355
R;Iwada, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A;Title: Structure and synthesis of an immunoactive lipopeptide, WS1279, of microbial or
A;Reference number: JU0355; MUID:91300586; PMID:2070441
A;Accession: JU0355
A;Molecule type: protein
A;Residues: 1-6 <TSU>
A;Cross-references: UNIPARC:UPI000017AB43
A;Note: the structure was confirmed by synthesis
C;Keywords: blocked amino end; lipoprotein
F;1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F;1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
  ||
Db 4 GG 5

RESULT 5
PT0514
T-cell receptor beta chain V-D-J region (100-4AC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0514
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0514
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <PEE>
A;Cross-references: UNIPARC:UPI000017C7B4
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
  ||
Db 5 GG 6

RESULT 6
PT0512
T-cell receptor beta chain V-D-J region (100-4D) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0512
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0512
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <PEE>
A;Cross-references: UNIPARC:UPI000017C7BF
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
  ||
Db 3 GG 4

RESULT 7
PT0720
T-cell receptor beta chain V-D-J region (126-1BB) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0548; PT0720
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0548
A;Accession: PT0548
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <PEE>
A;Cross-references: UNIPARC:UPI000017C809
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1BB
A;Accession: PT0720
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <PE2>
A;Cross-references: UNIPARC:UPI000017C809
A;Experimental source: newborn thymus, strain BALB/c, clone 140-2J
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
  ||
Db 5 GG 6

RESULT 8
PT0560
T-cell receptor beta chain V-D-J region (126-1CE) - mouse (fragment)

```

C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0560  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0560  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <PEE>  
A;Cross-references: UNIPARC:UPI000017C811  
A;Experimental source: day 18 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2  
||  
Db 5 GG 6

## RESULT 9

PT0723  
T-cell receptor beta chain V-D-J region (135-1AF) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0723  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0723

A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-6 <PEE>  
A;Cross-references: UNIPARC:UPI000017C819  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2  
||  
Db 5 GG 6

## RESULT 10

PT0727  
T-cell receptor beta chain V-D-J region (161-2F) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0727  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0727

A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-6 <PEE>  
A;Cross-references: UNIPARC:UPI000017C844  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2  
||  
Db 3 GG 4

## RESULT 11

PT0730  
T-cell receptor beta chain V-D-J region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0730; PT0594; PT0731  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0730

A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-6 <PEE>  
A;Cross-references: UNIPARC:UPI000017C850  
A;Experimental source: newborn thymus, strain BALB/c (clone 163-2C)  
A;Accession: PT0594

A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <PE2>  
A;Cross-references: UNIPARC:UPI000017C850  
A;Experimental source: day 19 fetal thymus, strain BALB/c (clone 159-2F)  
A;Accession: PT0731

A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-6 <PE3>  
A;Cross-references: UNIPARC:UPI000017C850  
A;Experimental source: newborn thymus, strain BALB/c (clone 165-3E)  
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2  
||  
Db 5 GG 6

## RESULT 12

F41946  
T-cell receptor gamma chain (1a.27) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C;Accession: F41946  
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma  
A;Reference number: A41946; MUID:92049316; PMID:1658619  
A;Accession: F41946

A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-6 <WHE>  
A;Cross-references: UNIPARC:UPI000017C862  
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 4 VW 5

## RESULT 13

PT0605  
T-cell receptor beta chain V-D-J region (120-1L) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C;Accession: PT0605  
R;Feeney, A.J.  
J;Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0605  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FEE>  
A;Cross-references: UNIPROT:O70586; UNIPARC:UPI000017C7DD  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2  
||  
DB 5 GG 6

RESULT 14

S66195  
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragment)  
C;Species: Gadus sp. (cod)  
C;Date: 13-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 12-Jun-1998  
C;Accession: S66195  
R;Hjeltnes, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.; FEBS Lett. 367, 237-240, 1995  
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M nzyme  
A;Reference number: S66191; MUID:95331382; PMID:7607314  
A;Accession: S66195  
A;Molecule type: protein  
A;Residues: 1-6 <HJE>  
A;Cross-references: UNIPARC:UPI0000171EA5  
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 27.5%; Score 11; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
DB 5 W 5

RESULT 15

B44510  
hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)  
C;Species: Lactococcus lactis  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 30-Sep-1993  
C;Accession: B44510  
R;Renault, P.; Gaillardin, C.; Heslot, H.  
J. Bacteriol. 171, 3108-3114, 1989  
A;Title: Product of the Lactococcus lactis gene required for malolactic fermentation is  
A;Reference number: A44510; MUID:89255069; PMID:2498286  
A;Accession: B44510  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-6 <REN>  
A;Cross-references: UNIPARC:UPI000017AC46; EMBL:M90762

Query Match 27.5%; Score 11; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4  
||

Db 5 YL 6

Search completed: December 30, 2005, 15:34:47  
Job time : 38 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:14:23 ; Search time 229 Seconds  
(without alignments)  
18.485 Million cell updates/sec

Title: US-10-735-916A-8  
Perfect score: 40  
Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 6  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	32.5	6	E101 LITRU	P82096 litoria rub
2	11	27.5	6	L0K1 LOCM1	P41491 locusta mig
3	9	22.5	6	FARP MONEX	P41966 moniezia ex
4	8	20.0	6	ASP2 LACSN	P82655 lactobacill
5	7	17.5	6	QVM LEPDE	P42985 leptinotars
6	6	15.0	6	CIP1 MYTED	P13736 mytilus edu
7	6	15.0	6	CIP2 MYTED	P13737 mytilus edu
8	6	15.0	6	SNAP SEPOF	P83569 sepiia offic
9	6	15.0	6	TMOF SARBH	P41495 sarcophaga
10	6	15.0	6	UN06 CLOPA	P81351 clostridium
11	6	15.0	6	VP19 HHV1K	P23210 human herpe
12	6	15.0	6	P83533 LACSN	P83533 lactobacill
13	4	10.0	6	ACPH RABIT	P25154 oryctolagus
14	4	10.0	6	TRPI PSERPU	P36414 pseudomonas
15	4	10.0	6	P82541 SPIOL	P82541 spinacia ol
16	3	7.5	6	PYF1 PENNO	P84005 penaeus mon
17	2	5.0	6	MAF SCHWA	P84575 schistosoma
18	2	5.0	6	P82181 SPIOL	P82181 spinacia ol
19	2	5.0	6	P82182 SPIOL	P82182 spinacia ol

## ALIGNMENTS

RESULT 1  
E101 LITRU  
ID E101 LITRU STANDARD; PRT; 6 AA.  
AC P82096;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)

Electrin-1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litoria electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC -----  
CC Amidation; Amphibian defense peptide; Direct protein sequencing.  
KW MOD\_RES 6  
FT Methylene amide.  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;  
  
Query Match 32.5%; Score 13; DB 1; Length 6;  
Best Local Similarity 50.0%; Pred. NO. 2.2e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 LW 5  
DB 4 IW 5  
  
RESULT 2  
L0K1 LOCM1  
ID L0K1 LOCM1 STANDARD; PRT; 6 AA.  
AC P41491;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Locustakinin I.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RE MEDLINE=92262851; PubMed=1585017; DOI=10.1016/0167-0115(92)90063-2;  
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,  
de Loof A.;  
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,  
isolation, primary structure and synthesis.";  
Regul. Pept. 37:49-57(1992).  
CC -1- FUNCTION: Myotropic peptide. May be important in the stimulation  
of ion transport and inhibition of diuretic activity in Malpighian  
tubules.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -----  
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the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC -----  
DR PIR; A61068; A61068.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 6  
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

```

Query Match      27.5%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
DB      5 W 5

RESULT 3
FARP_MONEX
ID FARP_MONEX STANDARD; PRT; 6 AA.
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuroptide GNFRF-amide.
OS Montezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Montezia.
OX NCBI_TaxID=28841;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRFamide: a novel FMRamide-immunoreactive peptide isolated from
the sheep tapeworm, Montezia expansa.";
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
CC -----
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CC -----
CC Query Match      22.5%; Score 9; DB 1; Length 6;
CC Best Local Similarity 33.3%; Pred. No. 2.2e+06;
CC Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGY 3
DB      1 GNF 3

RESULT 4
ASP2_LACSN
ID ASP2_LACSN STANDARD; PRT; 6 AA.
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis [Lactobacillus sanfrancisco].
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP PROTEIN SEQUENCE.
RX STRAIN=CB1;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Coconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.
CC -----
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CC removed.
CC -----
CC Query Match      20.0%; Score 8; DB 1; Length 6;
CC Best Local Similarity 50.0%; Pred. No. 2.2e+06;
CC Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 WN 6
DB      4 YN 5

RESULT 5
OVM_LPDDE
ID OVM_LPDDE STANDARD; PRT; 6 AA.
AC P42385;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Oviductal motility stimulating peptide (LeD-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
OC Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP PROTEIN SEQUENCE, AND SYNTHESIS.
RX TISSUS=Head;
RX MEDLINE=91271080; PubMed=2052497; DOI=10.1016/0196-9781(91)90162-I;
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
stimulating head peptide in the Colorado potato beetle, Leptinotarsa
decemlineata.";
RL Peptides 12:31-36(1991).
CC -!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
oviduct.
CC -----
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CC removed.
CC -----
CC Query Match      17.5%; Score 7; DB 1; Length 6;
CC Best Local Similarity 100.0%; Pred. No. 2.2e+06;
CC Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 Y 3
DB      3 Y 3

RESULT 6
CIP1_MYTED
ID CIP1_MYTED STANDARD; PRT; 6 AA.
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)

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DE Contraction-inhibiting peptide I (MIP I).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.  
 RN NCBI\_TaxID=6550;  
 [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RT "Structures and actions of Mytilus inhibitory peptides."  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -1- FUNCTION: Inhibitory action on contractions in several molluscan  
 CC muscles.  
 CC -1- SIMILARITY: To M.edulis MIP II.  
 CC -----  
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 CC removed.  
 CC -----  
 CC PIR; A27696; A27696.  
 DR Amidation; Direct protein sequencing; Hormone.  
 KW MOD RES 6 6 Valine amide.  
 FT SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;  
 SQ  
 Query Match 15.0%; Score 6; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 G 1  
 Db |  
 1 G 1

RESULT 7  
 CIP2 MYTED  
 ID CIP2 MYTED STANDARD; PRT; 6 AA.  
 AC PL3737;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-2005 (Rel. 46, Last annotation update)  
 DE Contraction-inhibiting peptide II (MIP II).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.  
 RN NCBI\_TaxID=6550;  
 [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RT "Structures and actions of Mytilus inhibitory peptides."  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -1- FUNCTION: Inhibitory action on contractions in several molluscan  
 CC muscles.  
 CC -1- SIMILARITY: To M.edulis MIP I.  
 CC -----  
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 CC removed.  
 CC -----  
 CC PIR; B27696; B27696.  
 DR Amidation; Direct protein sequencing; Hormone.  
 KW MOD RES 6 6 Valine amide.  
 FT SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;  
 SQ  
 Query Match 15.0%; Score 6; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1  
 Db |  
 1 G 1

RESULT 8  
 SAPP SEPOF  
 ID SAPP SEPOF STANDARD; PRT; 6 AA.  
 AC P33569;  
 DT 23-MAR-2004 (Rel. 43, Created)  
 DT 23-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Sperm attracting peptide SepSAP.  
 OS Sepia officinalis (Common cuttlefish).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Decapodiformes; Sepioidae; Sepiidae; Sepia.  
 RN NCBI\_TaxID=6610;  
 [1]  
 RP PROTEIN SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY,  
 RP AND AMIDATION.  
 RC TISSUE=Egg;  
 RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;  
 RA Zatylny C., Marvin L., Gagnon J., Henry J.;  
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-  
 RT attracting peptide."  
 RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).  
 CC -1- FUNCTION: Attracts sperm increasing the chances of gamete  
 CC collision.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DEVELOPMENTAL STAGE: First appears in the ovarian follicles during  
 CC vitellogenesis. Accumulates in the oocytes before being secreted  
 CC during fertilization. Expression continues in the embedded oocyte.  
 CC Accumulates in the egg capsule after fertilization.  
 CC -1- MASS SPECTROMETRY: MW=596.6; METHOD=MALDI; RANGE=1-6; NOTE=Ref. 1.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC KW Amidation; Direct protein sequencing.  
 FT MOD RES 6 6 Valine amide.  
 SQ SEQUENCE 6 AA; 597 MW; 72C8676AA0470000 CRC64;  
 Query Match 15.0%; Score 6; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 G 1  
 Db |  
 5 G 5

RESULT 9  
 TMOP SARB  
 ID TMOP SARB STANDARD; PRT; 6 AA.  
 AC P41495;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Trypsin-modulating oostatic factor (TMOF).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga; Neobellieria.  
 RN NCBI\_TaxID=7385;  
 [1]  
 RP PROTEIN SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Ovary;  
 RX MEDLINE=94211930; PubMed=8159807; DOI=10.1016/0167-0115(94)90192-9;  
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,

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RA de Loof A.;
RT "Sequencing and characterization of trypsin modulating oostatic factor
RT (TMOF) from the ovaries of the grey fleshfly, Neobellieria
RT (Sarcophaga) bullata.";
RL Regul. Pept. 50:61-72(1994).
CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
CC in the midgut which indirectly reduces the vitellogenin
CC concentration in the hemolymph resulting in inhibition of oocyte
CC development.
CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
CC epithelium after a blood meal.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Direct protein sequencing; Hormone.
SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 15.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 N 6
Db 1 N 1

RESULT 10
UN06_CLOPA STANDARD; PRT; 6 AA.
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein CP 6 from 2D-PAGE (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=W5;
RX Flengrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 75.9 kDa.
CC -----
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CC -----
KW Direct protein sequencing.
FT NON_TER 6
SQ SEQUENCE 6 AA; 658 MW; 605B1DC1A45A8000 CRC64;

Query Match 15.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 N 6
Db 2 N 2

RESULT 11

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VP19_HHV1K
ID VP19_HHV1K STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Capsid assembly and DNA maturation protein (Varion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN Name=UL38;
OS Human herpesvirus 1 (strain KOS) (HHV-1) (Human herpes simplex virus
OS 1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: Component of the basal layer in which the capsids are
CC embedded. Binds DNA.
CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
CC -----
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CC -----
DR EMBL; M57646; AAA45830.1; -; Genomic DNA.
KW Capsid protein; DNA packaging; DNA-binding; Structural protein.
FT NON_TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 15.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 N 6
Db 4 N 4

RESULT 12
P83533_LACSN
ID P83533_LACSN PRELIMINARY; PRT; 6 AA.
AC P83533;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RX DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
CC NON_TER 1
CC NON_TER 1
FT NON_TER 6
SQ SEQUENCE 6 AA; 590 MW; 6DDDD452D1AAC000 CRC64;

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Query Match 15.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 N 6  
DB 4 N 4

RESULT 13  
ACPH\_RABIT STANDARD; PRT; 6 AA.  
AC P25154;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-FEB-2005 (Rel. 46, Last annotation update)  
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide  
hydrolyase) (APH) (Acylaminoacyl-peptidase) (Fragment).  
GN Names=APRH;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;  
OC Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC TISSUE=Muscle;  
RX MEDLINE=92222120; PubMed=1807161;  
RA Krishna R.G., Chin C.C.Q., Wolf F.;  
RT "N-terminal sequence analysis of N alpha-acetylated proteins after  
unblocking with N-acetylaminoacyl-peptide hydrolase.";  
RL Anal. Biochem. 199;45:50(1991).  
CC -I- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal  
peptide bond of an N-acetylated peptide to generate an N-  
acetylated amino acid and a peptide with a free N-terminus. It  
preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.  
CC -I- CATALYTIC ACTIVITY: Cleavage of an N-acetyl or N-formyl amino acid  
from the N-terminus of a polypeptide.  
CC -I- SUBUNIT: Homotetramer.  
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -I- SIMILARITY: Belongs to the peptidase S9C family.

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CC PIR; A49792; A49792.  
DR InterPro; IPR002471; Pept S9 AS.  
DR PROSITE; PS00708; PRO\_ENDOPEP\_SER; PARTIAL.  
KW Acetylation; Direct protein sequencing; Hydrolase.  
FT MOD\_RES 1 1 N-acetylmethionine.  
FT NON\_TER 6 6  
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 10.0%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
DB 6 L 6

RESULT 14  
TRPI\_PSEPU STANDARD; PRT; 6 AA.  
AC P36414;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE HTH-type transcriptional regulator trpi (TrpBA operon transcriptional

activator) (Fragment).  
GN Name=trpi;  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=PPG1 C18;  
RX MEDLINE=89335826; PubMed=2503057; DOI=10.1016/0300-9084(89)90183-1;  
RA Eberly L., Crawford I.P.;  
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas  
putida.";  
RL Biochimie 71:521-531(1989).  
CC -I- FUNCTION: Activates the expression of the trpBA genes encoding the  
two tryptophan synthase subunits. In the absence of the inducer  
(indoleglycerol phosphate), trpi binds upstream of the trpAB  
operon, overlapping its own promoter region.  
CC -I- SIMILARITY: Contains 1 HTH lyser-type DNA-binding domain.

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CC EMBL; X13299; CAA31660.1; -: Genomic\_DNA.  
DR InterPro; IPR000847; HTH\_Lyser.  
DR PROSITE; PS05931; HTH\_Lyser; PARTIAL.  
KW Activator; Amino-acid biosynthesis; Aromatic amino acid biosynthesis;  
DNA-binding; Transcription; Transcription regulation;  
KW Tryptophan biosynthesis.  
FT NON\_TER 6 6  
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 10.0%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
DB 5 L 5

RESULT 15  
P82541\_SPIOL PRELIMINARY; PRT; 6 AA.  
AC P82541;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).  
OS Spinacia oleracea (Spinach).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC Caryophyllales; Amaranthaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP PROTEIN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC STRAIN=cv. ALWARO; TISSUE=Leaf;  
RX MEDLINE=20435797; PubMed=10874039; DOI=10.1074/jbc.M004350200;  
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;  
RT "The plastid ribosomal proteins. Identification of all the proteins in  
the 30S subunit of an organelle ribosome (chloroplast).";  
RL J. Biol. Chem. 275:28455-28465(2000).  
CC -I- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.  
CC -I- SUBCELLULAR LOCATION: CHLOROPLAST.  
CC -I- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC -I- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.  
CC -I- MASS SPECTROMETRY: MW=10495; METHOD=WALDI.  
CC -I- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA  
FORM IS THE MINOR BASIC FORM.

CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 kDa.  
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0019843; F:rRNA binding; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR InterPro; IPR002222; Ribosomal\_S19.  
DR PROSITE; PS00323; RIBOSOMAL\_S19; PARTIAL.  
KW Chloroplast; Ribosomal protein; rRNA-binding.  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;  
  
Query Match 10.0%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 L 4  
Db 4 L 4  
  
Search completed: December 30, 2005, 15:30:57  
Job time : 230 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:26:49 ; Search time 45 Seconds  
(without alignments)  
11.023 Million cell updates/sec

Title: US-10-735-916A-8  
Perfect score: 40  
Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 19666

Minimum DB seq length: 6  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pdp:\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pdp:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pdp:\*  
4: /cgn2\_6/ptodata/1/iaa/PTCUS COMB.pdp:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pdp:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	57.5	6	1	US-08-672-345C-52
2	23	57.5	6	2	US-09-214-095D-52
3	23	57.5	6	2	US-09-940-727B-52
4	22	55.0	6	1	US-08-089-994A-2
5	22	55.0	6	1	US-09-127-574-14
6	22	55.0	6	2	US-09-315-304B-1588
7	22	55.0	6	2	US-09-350-325-48
8	22	55.0	6	2	US-09-350-641C-1588
9	22	55.0	6	4	PCT-US94-07605-2
10	21	52.5	6	1	US-08-073-028-45
11	21	52.5	6	1	US-08-785-571-9
12	21	52.5	6	2	US-08-336-553A-32
13	21	52.5	6	2	US-08-554-616-45
14	21	52.5	6	2	US-08-439-157-32
15	21	52.5	6	2	US-09-437-895-32
16	21	52.5	6	2	US-09-515-965A-1658
17	21	52.5	6	2	US-09-350-841A-1688
18	21	52.5	6	2	US-09-211-715-99
19	21	52.5	6	2	US-09-211-715-155
20	21	52.5	6	2	US-09-578-063-65
21	21	52.5	6	2	US-10-005-305-37
22	21	52.5	6	2	US-10-005-305-94
23	21	52.5	6	4	PCT-US93-06734-9
24	20	50.0	6	1	US-08-024-253-11
25	20	50.0	6	1	US-08-482-228-186
26	20	50.0	6	2	US-08-482-528-186
27	20	50.0	6	2	US-09-620-091-470

28	20	50.0	6	2	US-09-620-091-471
29	19	47.5	6	1	US-07-822-924-9
30	19	47.5	6	1	US-07-805-727-3
31	19	47.5	6	1	US-07-805-727-7
32	19	47.5	6	1	US-07-718-577-5
33	19	47.5	6	1	US-07-969-307A-11
34	19	47.5	6	1	US-08-390-272-7
35	19	47.5	6	1	US-07-973-235A-10
36	19	47.5	6	1	US-07-802-667-33
37	19	47.5	6	1	US-08-351-058A-9
38	19	47.5	6	1	US-07-943-709-11
39	19	47.5	6	1	US-07-943-709-12
40	19	47.5	6	1	US-07-943-709-17
41	19	47.5	6	1	US-08-227-184A-4
42	19	47.5	6	1	US-08-487-890A-82
43	19	47.5	6	1	US-08-209-747-56
44	19	47.5	6	1	US-08-388-321-7
45	19	47.5	6	1	US-08-466-632-7

ALIGNMENTS

RESULT 1  
US-08-672-345C-52  
; Sequence 52, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-52

Query Match 57.5%; Score 23; DB 1; Length 6;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YLWN 6  
| | |  
Db 3 YAWN 6

RESULT 2

US-09-214-095D-52  
; Sequence 52, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 52  
; TYPE: PRT  
; LENGTH: 6  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-52  
  
Query Match 57.5%; Score 23; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 YLWN 6  
| | |  
DB 3 YAWN 6  
  
RESULT 3  
US-09-940-727B-52  
; Sequence 52, Application US/09940727B  
; Patent No. 6913917  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-52  
  
Query Match 57.5%; Score 23; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 YLWN 6  
| | |  
DB 3 YAWN 6  
  
RESULT 4  
US-08-089-994A-2  
; Sequence 2, Application US/08089994A  
; Patent No. 5380668  
; GENERAL INFORMATION:  
; APPLICANT: Herron, James N.  
; TITLE OF INVENTION: Compounds Having the Antigenicity of  
; FILE REFERENCE: hCG  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: University of Utah Technology  
; ADDRESSEE: Transfer Office  
; STREET: 421 Wakara Way, Suite 170  
; CITY: Salt Lake City

STATE: UT  
COUNTRY: USA  
ZIP: 84108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 144Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/089,994A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Turner, Allen C.  
REGISTRATION NUMBER: 33,041  
REFERENCE/DOCKET NUMBER: 2224  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 801/532-1922  
TELEFAX: 801/531-9168  
TELEX: 388961 1PM04UT  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-089-994A-2  
  
Query Match 55.0%; Score 22; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 YLW 5  
| | |  
DB 4 YLW 6  
  
RESULT 5  
US-09-127-574-14  
; Sequence 14, Application US/09127574  
; Patent No. 5985836  
; GENERAL INFORMATION:  
; APPLICANT: Basteck, Patrick  
; APPLICANT: Lang, John M.  
; APPLICANT: Baumbach, George A.  
; APPLICANT: Carbonell, Ruben G.  
; TITLE OF INVENTION: Alpha-1 Proteinase Inhibitor Binding Peptides  
; FILE REFERENCE: MSB-7248  
; CURRENT APPLICATION NUMBER: US/09/127,574  
; CURRENT FILING DATE: 1998-07-31  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-127-574-14  
  
Query Match 55.0%; Score 22; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 YLW 5  
| | |  
DB 4 YLW 6  
  
RESULT 6  
US-09-315-304B-1588

; Sequence 1588, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1588  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1588

Query Match 55.0%; Score 22; DB 2; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLW 5  
||:|  
Db 1 GGWNW 5

## RESULT 7

US-09-350-325-48  
; Sequence 48, Application US/09350325  
; Patent No. 6541020  
; GENERAL INFORMATION:  
; APPLICANT: Ding, S.  
; APPLICANT: Kang, M.  
; APPLICANT: Venetta, T.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF  
; TITLE OF INVENTION: THERAPEUTIC REAGENTS  
; FILE REFERENCE: 7872-062  
; CURRENT APPLICATION NUMBER: US/09/350,325  
; CURRENT FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 48  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: enhancer peptide  
US-09-350-325-48

Query Match 55.0%; Score 22; DB 2; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLW 5  
||:|  
Db 1 GGWNW 5

## RESULT 8

US-09-350-641C-1588  
; Sequence 1588, Application US/09350641C  
; Patent No. 6656906  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.

; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-067  
; CURRENT APPLICATION NUMBER: US/09/350,641C  
; CURRENT FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/315,304  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1757  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1588  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-350-641C-1588

Query Match 55.0%; Score 22; DB 2; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLW 5  
||:|  
Db 1 GGWNW 5

## RESULT 9

PCT-US94-07605-2  
; Sequence 2, Application PC/TUS9407605  
; GENERAL INFORMATION:  
; APPLICANT: Herron, James N.  
; TITLE OF INVENTION: Compounds Having the Antigenicity of  
; TITLE OF INVENTION: hCG  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: University of Utah Technology  
; ADDRESSEE: Transfer Office  
; STREET: 421 Wakara Way, Suite 170  
; CITY: Salt Lake City  
; STATE: UT  
; COUNTRY: USA  
; ZIP: 84108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07605  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/089,994  
; FILING DATE: 6 Jul 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Turner, Allen C.  
; REGISTRATION NUMBER: 33,041  
; REFERENCE/DOCKET NUMBER: 2224  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 801/532-1922  
; TELEFAX: 801/531-9168  
; TELEX: 388961 1PM04UT  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
PCT-US94-07605-2

Query Match 55.0%; Score 22; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLW 5  
DB 4 YLW 6

RESULT 10  
US-08-073-028-45  
; Sequence 45, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-073-028-45

Query Match 52.5%; Score 21; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LWN 6  
DB 2 LWN 4

RESULT 11  
US-08-785-571-9  
; Sequence 9, Application US/08785571  
; Patent No. 5854070  
; GENERAL INFORMATION:  
; APPLICANT: Rose, Lynn M.  
; TITLE OF INVENTION: Alleviation of Symptoms Associated with  
; TITLE OF INVENTION: Inflammatory Disease States  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/785,571  
; FILING DATE: 21-JAN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/396,089  
; FILING DATE:  
; APPLICATION NUMBER: US/08/094,535  
; FILING DATE:  
; APPLICATION NUMBER: US 08/060,699  
; FILING DATE: 10-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/915,068  
; FILING DATE: 16-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 31574  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-785-571-9

Query Match 52.5%; Score 21; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LWN 6  
DB 4 LWN 6

RESULT 12  
US-08-336-553A-32  
; Sequence 32, Application US/08336553A  
; Patent No. 6054264  
; GENERAL INFORMATION:  
; APPLICANT: CHIEN, DAVID Y.  
; APPLICANT: KOO, GEORGE  
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND  
; TITLE OF INVENTION: REAGENTS FOR USE THEREIN  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/336,553A

; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,400  
; FILING DATE: 10-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 22300-20947.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-336-553A-32

Query Match 52.5%; Score 21; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYLW 5  
DB 2 GYPW 5

RESULT 13  
US-08-554-616-45  
; Sequence 45, Application US/08554616  
; Patent No. 6133418  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/554,616  
; FILING DATE: 06-NOV-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/073,028  
; FILING DATE: 07-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown

; MOLECULE TYPE: peptide  
; US-08-554-616-45

Query Match 52.5%; Score 21; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LWN 6  
DB 2 LWN 4

RESULT 14  
US-08-439-157-32  
; Sequence 32, Application US/08439157  
; Patent No. 6416944  
; GENERAL INFORMATION:  
; APPLICANT: CHIEN, DAVID Y.  
; KUO, GEORGE  
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND  
; REAGENTS FOR USE THEREIN  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,157  
; FILING DATE: 11-MAY-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/336,553A  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/060,400  
; FILING DATE: 10-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 22300-20947.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
; US-08-439-157-32

Query Match 52.5%; Score 21; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYLW 5  
DB 2 GYPW 5

RESULT 15  
US-09-437-895-32  
; Sequence 32, Application US/09437895  
; Patent No. 6416946

GENERAL INFORMATION:  
APPLICANT: CHIEN, DAVID Y.  
          KUO, GEORGE  
TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND  
                    REAGENTS FOR USE THEREIN  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/437,895  
FILING DATE: 09-No. 6416946-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,553  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/060,400  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 22300-20947.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-437-895-32

Query Match          52.5%; Score 21; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYLW 5  
          |||  
Db      2 GYPW 5

Search completed: December 30, 2005, 15:35:38  
Job time : 46 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:34:14 ; Search time 161 Seconds  
(without alignments)  
15.571 Million cell updates/sec

Title: US-10-735-916A-8  
Perfect score: 40  
Sequence: 1 GGYLMN 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 20794

Minimum DB seq length: 6  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	5	US-10-735-916A-8
2	29	72.5	6	3	US-09-791-551-77
3	27	67.5	6	4	US-10-714-564A-20
4	27	67.5	6	4	US-10-714-564A-1357
5	26	65.0	6	4	US-10-714-564A-16
6	26	65.0	6	4	US-10-714-564A-49
7	26	65.0	6	4	US-10-714-564A-1353
8	24	60.0	6	4	US-10-024-652-844
9	23	57.5	6	3	US-09-340-727B-52
10	23	57.5	6	5	US-10-798-380-68
11	22	55.0	6	4	US-10-347-562-48
12	22	55.0	6	4	US-10-351-641-1588
13	22	55.0	6	4	US-10-714-564A-413
14	22	55.0	6	6	US-11-041-199-1
15	22	55.0	6	6	US-11-041-199-9
16	22	55.0	6	6	US-11-041-199-10
17	22	55.0	6	6	US-11-041-199-11
18	21	52.5	6	3	US-09-759-1308-435
19	21	52.5	6	4	US-10-074-547-6
20	21	52.5	6	4	US-10-042-431-65
21	21	52.5	6	4	US-10-005-305-37
22	21	52.5	6	4	US-10-005-305-94
23	21	52.5	6	4	US-10-741-790-435
24	21	52.5	6	4	US-10-714-564A-17
25	21	52.5	6	4	US-10-714-564A-18
26	21	52.5	6	4	US-10-714-564A-65
27	21	52.5	6	4	US-10-714-564A-70

28	21	52.5	6	4	US-10-714-564A-86	Sequence 86, Appl
29	21	52.5	6	4	US-10-714-564A-91	Sequence 91, Appl
30	21	52.5	6	4	US-10-714-564A-229	Sequence 229, App
31	21	52.5	6	4	US-10-714-564A-236	Sequence 236, App
32	21	52.5	6	4	US-10-714-564A-243	Sequence 243, App
33	21	52.5	6	4	US-10-714-564A-388	Sequence 388, App
34	21	52.5	6	4	US-10-714-564A-399	Sequence 399, App
35	21	52.5	6	4	US-10-714-564A-406	Sequence 406, App
36	21	52.5	6	4	US-10-714-564A-552	Sequence 552, App
37	21	52.5	6	4	US-10-714-564A-555	Sequence 555, App
38	21	52.5	6	4	US-10-714-564A-562	Sequence 562, App
39	21	52.5	6	4	US-10-714-564A-569	Sequence 569, App
40	21	52.5	6	4	US-10-714-564A-707	Sequence 707, App
41	21	52.5	6	4	US-10-714-564A-714	Sequence 714, App
42	21	52.5	6	4	US-10-714-564A-721	Sequence 721, App
43	21	52.5	6	4	US-10-714-564A-873	Sequence 873, App
44	21	52.5	6	4	US-10-714-564A-880	Sequence 880, App
45	21	52.5	6	4	US-10-714-564A-1354	Sequence 1354, Ap

ALIGNMENTS

RESULT 1  
US-10-735-916A-8  
; Sequence 8, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-8

Query Match 100.0%; Score 40; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLMN 6  
|||  
Db 1 GGYLMN 6

RESULT 2  
US-09-791-551-77  
; Sequence 77, Application US/09791551  
; Publication No. US20030235584A1  
; GENERAL INFORMATION:  
; APPLICANT: KLOETZER, WILLIAM S.  
; APPLICANT: HANNA, NABIL  
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES

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; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-77

Query Match 72.5%; Score 29; DB 3; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYLMN 6
Db 2 GYWMN 6

RESULT 3
US-10-714-564A-20
; Sequence 20, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative atypical cadherin Trp-containing
; OTHER INFORMATION: CAR sequence
US-10-714-564A-20

Query Match 67.5%; Score 27; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLMN 6
Db 1 GWMWN 5

RESULT 4
US-10-714-564A-1357
; Sequence 1357, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1357
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Trp-containing CAR sequences for
; OTHER INFORMATION: atypical cadherins
US-10-714-564A-49

Query Match 65.0%; Score 26; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLMN 6
Db 1 GWMWN 5

RESULT 5
US-10-714-564A-16
; Sequence 16, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative atypical cadherin Trp-containing
; OTHER INFORMATION: CAR sequence
US-10-714-564A-16

Query Match 65.0%; Score 26; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLMN 6
Db 1 GWMWN 5

RESULT 6
US-10-714-564A-49
; Sequence 49, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Trp-containing CAR sequences for
; OTHER INFORMATION: atypical cadherins
US-10-714-564A-49

Query Match 65.0%; Score 26; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 GYLWN 6  
|:|  
Db 2 GWVWN 6

## RESULT 7

US-10-714-564A-1353  
; Sequence 1353, Application US/10714564A  
; Publication No. US20040175361A1

; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS  
; FILE REFERENCE: 100086.418  
; CURRENT APPLICATION NUMBER: US/10/714.564A  
; CURRENT FILING DATE: 2003-11-14  
; NUMBER OF SEQ ID NOS: 1402  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1353  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Trp-containing cell adhesion recognition sequence  
US-10-714-564A-1353

Query Match 65.0%; Score 26; DB 4; Length 6;  
Best Local Similarity 60.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYLWN 6  
|:|  
Db 1 GWVWN 5

## RESULT 8

US-10-024-652-844  
; Sequence 844, Application US/10024652  
; Publication No. US20030219738A1

; GENERAL INFORMATION:  
; APPLICANT: Agensys, Inc  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Faris, Mary  
; APPLICANT: Afar, Daniel E.H.  
; APPLICANT: Hubert, Rene S. Chappell  
; APPLICANT: Mitchell, Steve  
; APPLICANT: Levin, Elana  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc  
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and  
; TITLE OF INVENTION: Detection of Cancer  
; FILE REFERENCE: 51158-20025.00  
; CURRENT APPLICATION NUMBER: US/10/024.652  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/256,210  
; PRIOR FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 2598  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 844  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: homo sapien

US-10-024-652-844

Query Match 60.0%; Score 24; DB 4; Length 6;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6  
|:|:|

Db 1 GGYIAN 6

## RESULT 9

US-09-940-727B-52  
; Sequence 52, Application US/09940727B  
; Publication No. US2003007793A1

; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940.727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: mouse

US-09-940-727B-52

Query Match 57.5%; Score 23; DB 3; Length 6;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YLWN 6  
|:|  
Db 3 YAWN 6

## RESULT 10

US-10-798-380-68  
; Sequence 68, Application US/10798380  
; Publication No. US20040265960A1

; GENERAL INFORMATION:  
; APPLICANT: YOUNG, DEBORAH A.  
; APPLICANT: WHITTERS, MATTHEW J.  
; APPLICANT: VALGE-ARCHER, VIIA  
; APPLICANT: COLLINS, MARY  
; APPLICANT: WILLIAMS, ANDREW JAMES  
; APPLICANT: WITEK, JOANNE  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-21 RECEPTOR AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 08702.0137-00000  
; CURRENT APPLICATION NUMBER: US/10/798,380  
; CURRENT FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: 60/454,336  
; PRIOR FILING DATE: 2003-03-14  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 68  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-798-380-68

Query Match 57.5%; Score 23; DB 5; Length 6;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYLW 5  
|:|  
Db 2 GYTW 5

RESULT 11  
US-10-347-562-48

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; Sequence 48, Application US/10347562
; Publication No. US2003016555A1
; GENERAL INFORMATION:
; APPLICANT: Ding, S.
; APPLICANT: Kang, M.
; APPLICANT: Venetta, T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF
; TITLE OF INVENTION: THERAPEUTIC REAGENTS
; FILE REFERENCE: 7872-104
; CURRENT APPLICATION NUMBER: US/10/347,562
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: enhancer peptide
US-10-347-562-48

Query Match          55.0%; Score 22; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGYLW 5
      ||:|
Db      1 GGWNW 5

RESULT 12
US-10-351-641-1588
; Sequence 1588, Application US/10351641
; Publication No. US2003018687A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1588
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1588

Query Match          55.0%; Score 22; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGYLW 5
      ||:|
Db      1 GGWNW 5

RESULT 13
US-10-714-564A-413
; Sequence 413, Application US/10714564A

; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Michaud, Stephanie D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 10086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary cyclic peptide
US-10-714-564A-413

Query Match          55.0%; Score 22; DB 4; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      ||:|
Db      2 GWNWD 6

RESULT 14
US-11-041-199-1
; Sequence 1, Application US/11041199
; Publication No. US20050153375A1
; GENERAL INFORMATION:
; APPLICANT: STANNERS, Clifford P.
; APPLICANT: ILANTZIS, Christian
; APPLICANT: ORDONEZ-GARCIA, Cosme
; APPLICANT: TAHERI, Maryam
; APPLICANT: SCREATOR, Robert A.
; APPLICANT: FUKS, Abraham
; APPLICANT: SARAGOVIT, H. Uri
; TITLE OF INVENTION: CEA/NCA-BASED DIFFERENTIATION CANCER THERAPY
; FILE REFERENCE: 14952
; CURRENT APPLICATION NUMBER: US/11/041,199
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 09/637,530
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: CA99/00119
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: CA 2,224,129
; PRIOR FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-041-199-1

Query Match          55.0%; Score 22; DB 6; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYLW 5
      ||:|
Db      1 GYSW 4

RESULT 15
US-11-041-199-9
; Sequence 9, Application US/11041199
; Publication No. US20050153375A1
; GENERAL INFORMATION:
; APPLICANT: STANNERS, Clifford P.
```

; APPLICANT: ILANTZIS, Christian  
; APPLICANT: ORDONEZ-GARCIA, Cosme  
; APPLICANT: TAHERI, Maryam  
; APPLICANT: SREANTON, Robert A.  
; APPLICANT: FUKS, Abraham  
; APPLICANT: SARAGOV, H. Uri  
; TITLE OF INVENTION: CEA/NCA-BASED DIFFERENTIATION CANCER THERAPY  
; FILE REFERENCE: 14952  
; CURRENT APPLICATION NUMBER: US/11/041,199  
; PRIOR FILING DATE: 2005-01-25  
; PRIOR APPLICATION NUMBER: 09/637,530  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: CA99/00119  
; PRIOR FILING DATE: 1999-02-11  
; PRIOR APPLICATION NUMBER: CA 2,224,129  
; PRIOR FILING DATE: 1998-02-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-041-199-9

Query Match 55.0%; Score 22; DB 6; Length 6;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYLW 5  
| |  
Db 1 GYSW 4

Search completed: December 30, 2005, 15:48:02  
Job time : 162 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:34:55 ; Search time 12 Seconds  
(without alignments)  
3.744 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 568

Minimum DB seq length: 6

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP:\*\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP:\*\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP:\*\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB\_PEP:\*\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US03\_NEW\_PUB\_PEP:\*\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP:\*\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB\_PEP:\*\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	40	100.0	6	7	US-11-012-353-8
2	29	72.5	6	7	US-11-009-939-23
3	20	50.0	6	6	US-10-929-988-470
4	20	50.0	6	6	US-10-929-988-471
5	18	45.0	6	7	US-11-054-515-3210
6	15	37.5	6	6	US-10-929-988-122
7	15	37.5	6	6	US-10-485-788A-288
8	15	37.5	6	7	US-11-090-497-18
9	14	35.0	6	6	US-10-485-788A-243
10	14	35.0	6	7	US-11-119-098-9
11	13	32.5	6	6	US-10-494-781-13
12	13	32.5	6	6	US-10-494-781-15
13	13	32.5	6	6	US-10-613-744-15
14	13	32.5	6	6	US-10-485-788A-138
15	13	32.5	6	7	US-11-079-969-1
16	13	32.5	6	7	US-11-113-224-58
17	13	32.5	6	7	US-11-113-224-60
18	13	32.5	6	7	US-11-108-185-64
19	13	32.5	6	7	US-11-022-341-63
20	13	32.5	6	7	US-11-102-743-8
21	12	30.0	6	7	US-11-195-197-1
22	12	30.0	6	6	US-10-966-648-19
23	12	30.0	6	6	US-10-467-657-9110
24	12	30.0	6	6	US-10-846-188C-7
25	12	30.0	6	6	US-10-522-398-2

26	12	30.0	6	6	US-10-925-366A-88	Sequence 88, Appl
27	12	30.0	6	6	US-10-485-788A-228	Sequence 228, App
28	12	30.0	6	6	US-10-485-788A-448	Sequence 448, App
29	12	30.0	6	7	US-11-057-058-3	Sequence 3, Appli
30	12	30.0	6	7	US-11-052-168A-41	Sequence 41, Appl
31	12	30.0	6	7	US-11-054-515-2193	Sequence 2193, Ap
32	12	30.0	6	7	US-11-113-224-78	Sequence 78, Appl
33	12	30.0	6	7	US-11-097-864-737	Sequence 737, App
34	12	30.0	6	7	US-11-097-912-737	Sequence 737, App
35	12	30.0	6	7	US-11-062-186-160	Sequence 160, App
36	12	30.0	6	7	US-11-093-808-3	Sequence 3, Appli
37	12	30.0	6	7	US-11-093-808-5	Sequence 5, Appli
38	12	30.0	6	7	US-11-112-882-43	Sequence 43, Appl
39	12	30.0	6	7	US-11-127-677-94	Sequence 94, Appl
40	12	30.0	6	7	US-11-192-449-7	Sequence 7, Appli
41	12	30.0	6	7	US-11-192-449-8	Sequence 8, Appli
42	11	27.5	6	6	US-10-939-890-9	Sequence 9, Appli
43	11	27.5	6	6	US-10-966-648-18	Sequence 18, Appl
44	11	27.5	6	6	US-10-467-657-958	Sequence 958, App
45	11	27.5	6	6	US-10-522-398-1	Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-11-012-353-8  
; Sequence 8, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUM, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-8

Query Match 100.0%; Score 40; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.4e+04;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6  
|||||  
Db 1 GGYLWN 6

RESULT 2  
US-11-009-939-23  
; Sequence 23, Application US/11009939

```
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-23

Query Match 72.5%; Score 29; DB 7; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.4e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
Db 1 GGYSWH 6

RESULT 3
US-10-929-988-470
; Sequence 470, Application US/10929988
; Publication No. US2005027588A1
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/929,988
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 470
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-929-988-470

Query Match 50.0%; Score 20; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLW 5
Db 3 GWVW 6

RESULT 4
US-10-929-988-471
; Sequence 471, Application US/10929988
; Publication No. US2005027588A1
```

```
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/929,988
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 471
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-929-988-471

Query Match 50.0%; Score 20; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLW 5
Db 3 GWVW 6

RESULT 5
US-11-054-515-3210
; Sequence 3210, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3210
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3210
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Query Match 45.0%; Score 18; DB 7; Length 6;  
Best Local Similarity 75.0%; Pred. No. 4.4e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYL 4  
|||  
Db 1 GGWL 4

## RESULT 6

US-10-929-988-122  
; Sequence 122, Application US/10929988  
; Publication No. US20050277588A1  
; GENERAL INFORMATION:  
; APPLICANT: CWRILA, STEVEN E.  
; APPLICANT: BALU, PALANI  
; APPLICANT: DUFFIN, DAVID J.  
; APPLICANT: PIPLANI, SUNILA  
; APPLICANT: MERRILL, BARBARA MCEOWEN  
; APPLICANT: SCHATZ, PETER JOSEPH  
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY  
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED  
; TITLE OF INVENTION: USES  
; FILE REFERENCE: 0300-0014  
; CURRENT APPLICATION NUMBER: US/10/929,988  
; CURRENT FILING DATE: 2004-08-30  
; PRIOR APPLICATION NUMBER: US/09/620,091  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 122  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-929-988-122

Query Match 37.5%; Score 15; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
|||  
Db 3 LW 4

## RESULT 7

US-10-485-788A-288  
; Sequence 288, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schweizer, Johannes  
; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 288  
; LENGTH: 6  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-485-788A-288

Query Match 37.5%; Score 15; DB 6; Length 6;  
Best Local Similarity 50.0%; Pred. No. 4.4e+04;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWL 5  
|||  
Db 2 GQYW 5

## RESULT 8

US-11-090-497-18  
; Sequence 18, Application US/11090497  
; Publication No. US20050282263A1  
; GENERAL INFORMATION:  
; APPLICANT: Large Scale Biology Corporation  
; TITLE OF INVENTION: FLEXIBLE VACCINE ASSEMBLY AND VACCINE DELIVERY PLATFORM  
; FILE REFERENCE: N8630  
; CURRENT APPLICATION NUMBER: US/11/090,497  
; CURRENT FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: 60/386,921  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: 60/407,795  
; PRIOR FILING DATE: 2002-09-03  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: human laminin  
US-11-090-497-18

Query Match 37.5%; Score 15; DB 7; Length 6;  
Best Local Similarity 66.7%; Pred. No. 4.4e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYL 4  
|||  
Db 1 GYI 3

## RESULT 9

US-10-485-788A-243  
; Sequence 243, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schweizer, Johannes  
; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 243  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-788A-243

Query Match 35.0%; Score 14; DB 6; Length 6;  
Best Local Similarity 66.7%; Pred. No. 4.4e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYL 4  
Db 4 GIV 6

RESULT 10  
US-11-119-098-9  
; Sequence 9, Application US/11119098  
; Publication No. US20050267030A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsao, Philip S.  
; TITLE OF INVENTION: Use of deltaPKC Peptides for Modulation of Reactive Oxygen Specie  
; FILE REFERENCE: 58600-8213 US00  
; CURRENT APPLICATION NUMBER: US/11/119,098  
; CURRENT FILING DATE: 2005-04-29  
; PRIOR APPLICATION NUMBER: US 60/567,315  
; PRIOR FILING DATE: 2004-04-30  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: beta-PKC-selective activator peptide  
US-11-119-098-9

Query Match 35.0%; Score 14; DB 7; Length 6;  
Best Local Similarity 33.3%; Pred. No. 4.4e+04;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LWN 6  
Db 4 IWD 6

RESULT 11  
US-10-494-781-13  
; Sequence 13, Application US/10494781  
; Publication No. US20050244895A1  
; GENERAL INFORMATION:  
; APPLICANT: King's College London  
; TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease  
; FILE REFERENCE: IT/KE/N13246  
; CURRENT APPLICATION NUMBER: US/10/494,781  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: GB 0127000.8  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: GB 0202562.5  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Bovine  
US-10-494-781-13

Query Match 32.5%; Score 13; DB 6; Length 6;  
Best Local Similarity 33.3%; Pred. No. 4.4e+04;  
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLW 5  
Db 2 FAW 4

RESULT 12  
US-10-494-781-15  
; Sequence 15, Application US/10494781

; Publication No. US20050244895A1  
; GENERAL INFORMATION:  
; APPLICANT: King's College London  
; TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease  
; FILE REFERENCE: IT/KE/N13246  
; CURRENT APPLICATION NUMBER: US/10/494,781  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: GB 0127000.8  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: GB 0202562.5  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Bovine  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: any amino acid  
; NAME/KEY: MISC FEATURE  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: any amino acid  
US-10-494-781-15

Query Match 32.5%; Score 13; DB 6; Length 6;  
Best Local Similarity 33.3%; Pred. No. 4.4e+04;  
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLW 5  
Db 2 FXW 4

RESULT 13  
US-10-613-744-15  
; Sequence 15, Application US/10613744  
; Publication No. US20050272093A1  
; GENERAL INFORMATION:  
; APPLICANT: MacKinnon, Roderick  
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With  
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation  
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof  
; FILE REFERENCE: 018512-002901US  
; CURRENT APPLICATION NUMBER: US/10/613,744  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: US/09/275,252  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: US 09/045,529  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: US 09/054,347  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307  
; PRIOR FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:channel protein  
; OTHER INFORMATION: central pore signature sequence  
US-10-613-744-15

Query Match 32.5%; Score 13; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GY 3

Db 3 GY 4  
||  
Query Match 32.5%; Score 13; DB 7; Length 6;  
Best Local Similarity 50.0%; Pred. No. 4.4e+04;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
US-10-485-788A-138  
; Sequence 138, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schweizer, Johannes  
; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 138  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-788A-138

Query Match 32.5%; Score 13; DB 6; Length 6;  
Best Local Similarity 50.0%; Pred. No. 4.4e+04;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
:|  
Db 2 IW 3

RESULT 15  
US-11-079-969-1  
; Sequence 1, Application US/11079969  
; Publication No. US20050244899A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, David S.F.  
; APPLICANT: Warner, Andrea  
; APPLICANT: Kelleher, Michelle  
; APPLICANT: McConkey, Fortunata  
; APPLICANT: Hahn, Susan E.  
; TITLE OF INVENTION: Laminin Receptor 1 Precursor Protein (37LRP) Epitope Delineated B  
; TITLE OF INVENTION: Hepatocellular Carcinoma Specific Antibody  
; FILE REFERENCE: 2056.049  
; CURRENT APPLICATION NUMBER: US/11/079,969  
; CURRENT FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 10/810,163  
; PRIOR FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: US 09/415,278  
; PRIOR FILING DATE: 1999-10-08  
; PRIOR APPLICATION NUMBER: US 09/727,361  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 10/713,642  
; PRIOR FILING DATE: 2003-11-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: peptide G, a synthetic peptide derived from the sequence of 37LRP  
US-11-079-969-1

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 142.194 Seconds  
(without alignments)  
49.440 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	16	7	ADJ76844 CDR seque
2	89	100.0	16	9	ADZ67014 Murine in
3	89	100.0	117	7	ADJ76903 Anti-IGF-
4	89	100.0	117	7	ADJ76909 Anti-IGF-
5	89	100.0	117	7	ADJ76917 Anti-IGF-
6	89	100.0	117	7	ADJ76913 Anti-IGF-
7	89	100.0	117	9	ADZ67083 Human ant
8	89	100.0	117	9	ADZ67087 Human ant
9	89	100.0	117	9	ADZ67073 Murine im
10	89	100.0	117	9	ADZ67079 Human ant
11	89	100.0	127	7	ADJ76886 Anti-IGF-
12	89	100.0	127	9	ADZ67056 Murine im
13	89	100.0	135	7	ADJ76911 Anti-IGF-
14	89	100.0	135	7	ADJ76919 Anti-IGF-
15	89	100.0	135	7	ADJ76915 Anti-IGF-
16	89	100.0	135	9	ADZ67089 Human ant
17	89	100.0	135	9	ADZ67081 Human ant
18	89	100.0	135	9	ADZ67085 Human ant
19	75	84.3	16	9	Aea40141 TNF resis
20	75	84.3	114	9	Aea40137 TNF resis
21	75	84.3	118	2	Aaw00829 Variable
22	75	84.3	118	2	Aaw19015 Anti-huma
23	75	84.3	136	3	Aay94391 Mouse VH
24	73	82.0	16	9	ADZ45407 Murine fa

25	73	82.0	119	9	ADZ45405	Adz45405 Murine fa
26	73	82.0	369	4	AAB73388	Aab73388 Anti-VHSV
27	72	80.9	16	9	ADZ45343	Adz45343 Murine fa
28	72	80.9	16	9	ADZ51256	Adz51256 Amino aci
29	72	80.9	16	9	ADZ42130	Adz42130 Mouse ant
30	72	80.9	65	6	ABU56867	Abu56867 BONT/A Hc
31	72	80.9	114	9	AEA40153	Aea40153 Mouse Igh
32	72	80.9	116	9	ADZ45341	Adz45341 Murine fa
33	72	80.9	116	9	ADZ51254	Adz51254 Amino aci
34	72	80.9	116	9	ADZ42128	Adz42128 Mouse ant
35	72	80.9	119	6	ABB98908	Abb98908 Variable
36	72	80.9	121	8	ADR38665	Adr38665 Mouse hea
37	71	79.8	118	7	ADJ76904	Adj76904 Anti-IGF-
38	71	79.8	118	9	ADZ67074	Adz67074 Mouse ant
39	70	78.7	16	9	ADZ45520	Adz45520 Murine fa
40	70	78.7	16	9	ADZ45311	Adz45311 Murine fa
41	70	78.7	16	9	ADZ51224	Adz51224 Amino aci
42	70	78.7	16	9	ADZ42098	Adz42098 Mouse ant
43	70	78.7	116	9	ADZ45309	Adz45309 Murine fa
44	70	78.7	116	9	ADZ51222	Adz51222 Amino aci
45	70	78.7	116	9	ADZ42096	Adz42096 Mouse ant

## ALIGNMENTS

## RESULT 1

ADJ76844	
ID	ADJ76844 standard; peptide; 16 AA.
XX	
AC	ADJ76844;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	CDR sequence for anti-IGF-1R antibody.
XX	
KW	cytostatic; antipneumatic; antibody;
KW	insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW	or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW	ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW	CDR.
OS	Mus musculus.
XX	
PN	WC2003059951-A2.
XX	
PD	24-JUL-2003.
XX	
PF	20-JAN-2003; 2003WO-FR000178.
XX	
PR	18-JAN-2002; 2002FR-00000653.
PR	18-JAN-2002; 2002FR-00000654.
PR	07-MAY-2002; 2002FR-00005753.
XX	
PA	(FABR ) FABRE MEDICAMENT SA PIERRE.
XX	
PI	Goetsch L, Corvaia N, Leger O;
XX	
DR	WPI; 2003-569653/53.
DR	N-PSDB; ADJ76843.
XX	
PT	New antibodies that bind to human insulin-like growth factor receptor,
PT	useful for treatment, prevention and diagnosis of cancers.
XX	
PS	Claim 1; SEQ ID NO 10; 164pp; French.
XX	
CC	The invention relates to an isolated antibody (Ab), and its
CC	fragments, that bind to human insulin-like growth factor-1,
CC	IR) and optionally: (i) inhibit natural binding of insulin;
CC	factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically
CC	kinase activity of IGF-1R. Ab and its fragments are used to
CC	treat diseases associated with overexpression and/or abnorm
CC	IGF-1R and/or epidermal growth factor receptor (EGFR) and/c

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 89; DB 7; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 |||||  
 Db 1 YISYDGTNNYKPSLKD 16

RESULT 2  
 ADZ67014  
 ID ADZ67014 standard; peptide; 16 AA.

XX AC ADZ67014;

XX DT 30-JUN-2005 (first entry)

XX DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:10.

XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX OS Mus musculus.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOET/) GOETSCH L.

XX PA (CORV/) CORVAIA N.

XX PA (LEGE/) LEGER O.

XX PA (DUFLO/) DUFLOS A.

XX PA (HAEU/) HAEUW J.

XX PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX DR WPI; 2005-321968/33.

XX DR N-PSDB; ADZ67013.

XX PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

XX PT antibody or its functional fragment, being capable of binding human IGF-

XX PT IR and specifically inhibiting tyrosine kinase activity of receptor,

XX PT useful for treating cancer.

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 89; DB 9; Length 16;

Best Local Similarity 100.0%; Pred. No. 6.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16

Db 1 YISYDGTNNYKPSLKD 16

RESULT 3

ADJ76903

ID ADJ76903 standard; protein; 117 AA.

XX AC ADJ76903;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-IR related protein #16.

XX KW cytostatic; antipsoriatic; antibody;

XX KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;

XX KW or epidermal growth factor receptor; EGFR; signal transduction pathway;

XX KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;

XX CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;  
 XX WPI; 2003-569653/53.  
 XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.  
 XX Disclosure; SEQ ID NO 69; 164pp; French.  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX SQ Sequence 117 AA;  
 Query Match 100.0%; Score 89; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 DB 51 YISYDGTNNYKPSLKD 66  
 RESULT 4  
 ID ADJ76909 standard; protein; 117 AA.  
 AC ADJ76909;  
 DT 06-MAY-2004 (first entry)  
 DE Anti-IGF-1R related protein #22.  
 KW cytostatic; antiproliferative; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 CDR.  
 XX Homo sapiens.  
 OS WO2003059951-A2.  
 PN 24-JUL-2003.  
 PD 20-JAN-2003; 2003WO-FR000178.  
 PF 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA Goetsch L, Corvaia N, Leger O;  
 PI WPI; 2003-569653/53.  
 XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.  
 XX Disclosure; SEQ ID NO 83; 164pp; French.  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX SQ Sequence 117 AA;  
 Query Match 100.0%; Score 89; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 DB 51 YISYDGTNNYKPSLKD 66  
 RESULT 5  
 ID ADJ76917 standard; protein; 117 AA.  
 AC ADJ76917;  
 DT 06-MAY-2004 (first entry)  
 DE Anti-IGF-1R related protein #26.  
 KW cytostatic; antiproliferative; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 CDR.  
 XX Homo sapiens.  
 OS WO2003059951-A2.  
 PN 24-JUL-2003.  
 PD 20-JAN-2003; 2003WO-FR000178.  
 PF 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA Goetsch L, Corvaia N, Leger O;  
 PI WPI; 2003-569653/53.  
 XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.  
 XX Disclosure; SEQ ID NO 83; 164pp; French.  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX SQ Sequence 117 AA;  
 Query Match 100.0%; Score 89; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 DB 51 YISYDGTNNYKPSLKD 66  
 RESULT 5  
 ID ADJ76917 standard; protein; 117 AA.  
 AC ADJ76917;  
 DT 06-MAY-2004 (first entry)  
 DE Anti-IGF-1R related protein #26.  
 KW cytostatic; antiproliferative; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 CDR.  
 XX Homo sapiens.  
 OS WO2003059951-A2.  
 PN 24-JUL-2003.  
 PD 20-JAN-2003; 2003WO-FR000178.  
 PF 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA Goetsch L, Corvaia N, Leger O;  
 PI WPI; 2003-569653/53.  
 XX New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

XX  
 SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 DB 51 YISYDGTNNYKPSLKD 66

RESULT 6  
 ADJ76913  
 ID ADJ76913 standard; protein; 117 AA.

XX AC ADJ76913;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Anti-IGF-1R related protein #24.  
 XX KW cytostatic; antiproliferative; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX OS Homo sapiens.  
 XX PN WO2003059951-A2.  
 XX PD 24-JUL-2003.  
 XX PF 20-JAN-2003; 2003WO-FR000178.  
 XX PR 18-JAN-2002; 2002FR-00000653.  
 XX PR 18-JAN-2002; 2002FR-00000654.  
 XX PR 07-MAY-2002; 2002FR-00005753.  
 XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
 XX PI Goetsch L, Corvaia N, Leger O;  
 XX DR WPI; 2003-569653/53.

XX PT New antibodies that bind to human insulin-like growth factor receptor,  
 XX useful for treatment, prevention and diagnosis of cancers.  
 XX PS Disclosure; SEQ ID NO 79; 164pp; French.

XX CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally; (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2, and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the

CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 DB 51 YISYDGTNNYKPSLKD 66

RESULT 7  
 ADZ67083  
 ID ADZ67083 standard; protein; 117 AA.

XX AC ADZ67083;  
 XX DT 30-JUN-2005 (first entry)  
 XX DE Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.  
 XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
 KW antiproliferative; psoriasis; dermatological disease; immune disorder;  
 KW heavy chain variable region.

XX OS Homo sapiens.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOET/) GOETSCH L.

XX PA (CORV/) CORVAIA N.

XX PA (LEGE/) LEGER O.

XX PA (DUFL/) DUFLOS A.

XX PA (HAET/) HAEUW J.

XX PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX DR WPI; 2005-321968/33.

XX PT Novel isolated anti-insulin-like growth factor I receptor (IGF-1R)  
 XX antibody or its functional fragment, being capable of binding human IGF-  
 XX IR and specifically inhibiting tyrosine kinase activity of receptor,  
 XX useful for treating cancer.

XX PS Example 13; SEQ ID NO 79; 125pp; English.

XX CC The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-1R) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-1R and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in



CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGFR with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1- and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 9; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 |||||  
 DB 51 YISYDGTNNYKPSLKD 66

## RESULT 8

ID ADZ67087 standard; protein; 117 AA.

XX AC ADZ67087;

XX DT 30-JUN-2005 (first entry)

XX DE Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.

XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antiproliferative; psoriasis; dermatological disease; immune disorder;  
 KW heavy chain variable region.

XX OS Homo sapiens.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOETSC) GOETSCH L.

PA (CORV/) CORVAIA N.  
 PA (LEGE/) LEGER O.  
 PA (DUFEL/) DUFLOS A.  
 PA (HAEU/) HAEUW J.  
 PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WI; 2005-321968/33.

XX PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.

XX PS Example 13; SEQ ID NO 83; 125pp; English.

XX CC The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor.  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGFR with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1- and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 9; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 |||||  
 DB 51 YISYDGTNNYKPSLKD 66

## RESULT 9

ID ADZ67073 standard; protein; 117 AA.

XX AC ADZ67073;

XX DT 30-JUN-2005 (first entry)

XX DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW immunoglobulin; heavy chain variable region.  
 XX Mus musculus.  
 XX US2005084906-A1.  
 XX 21-APR-2005.  
 XX 16-DEC-2003; 2003US-00735916.  
 XX 18-JAN-2002; 2002FR-00000653.  
 XX 18-JAN-2002; 2002FR-00000654.  
 XX 07-MAY-2002; 2002FR-00005753.  
 XX 20-JAN-2003; 2003WO-FR000178.  
 XX 11-JUL-2003; 2003FR-00008538.  
 XX (GOET/) GOETSCH L.  
 XX (CORV/) CORVAIA N.  
 XX (LEGE/) LEGER O.  
 XX (DUFL/) DUFLOS A.  
 XX (HAEU/) HAEUW J.  
 XX (BECK/) BECK A.  
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 PI WPI; 2005-321968/33.  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX Example 13; SEQ ID NO 69; 125pp; English.  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-

CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX Sequence 117 AA;  
 Query Match 100.0%; Score 89; DB 9; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 DB 51 YISYDGTNNYKPSLKD 66  
 RESULT 10  
 ADZ67079  
 ID ADZ67079 standard; protein; 117 AA.  
 XX AC ADZ67079;  
 XX 30-JUN-2005 (first entry)  
 XX Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.  
 XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW heavy chain variable region.  
 XX Homo sapiens.  
 XX US2005084906-A1.  
 XX 21-APR-2005.  
 XX 16-DEC-2003; 2003US-00735916.  
 XX 18-JAN-2002; 2002FR-00000653.  
 XX 18-JAN-2002; 2002FR-00000654.  
 XX 07-MAY-2002; 2002FR-00005753.  
 XX 20-JAN-2003; 2003WO-FR000178.  
 XX 11-JUL-2003; 2003FR-00008538.  
 XX (GOET/) GOETSCH L.  
 XX (CORV/) CORVAIA N.  
 XX (LEGE/) LEGER O.  
 XX (DUFL/) DUFLOS A.  
 XX (HAEU/) HAEUW J.  
 XX (BECK/) BECK A.  
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 PI WPI; 2005-321968/33.  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX Example 13; SEQ ID NO 75; 125pp; English.  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment

CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-1R and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-1R and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-1R and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-1R and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC 1R and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 9; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
 |||||  
 Db 51 YISYDGTNNYKPSLKD 66

RESULT 11

ADJ76886  
 ID ADJ76886 standard; protein; 127 AA.

AC ADJ76886;

DT 06-MAY-2004 (first entry)

DE Anti-IGF-1R related protein #4.

KW cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.

XX Mus musculus.

XX WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

PT New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.

PS Disclosure; SEQ ID NO 52; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

XX Sequence 127 AA;

Query Match 100.0%; Score 89; DB 7; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
 |||||  
 Db 61 YISYDGTNNYKPSLKD 76

RESULT 12

ADZ67056

ID ADZ67056 standard; protein; 127 AA.

AC ADZ67056;

DT 30-JUN-2005 (first entry)

DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.

KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
 KW immunoglobulin; heavy chain variable region.

XX Mus musculus.

XX Key Location/Qualifiers  
 FH Peptide 1..10  
 FT /note= "leader peptide"

FT Region 41..46  
 FT /note= "CDR1"

FT Region 61..76  
 FT /note= "CDR2"

FT Region 109..116  
 FT /note= "CDR3"

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.  
 PA (CORV/) CORVAIA N.  
 PA (LEGE/) LEGER O.  
 PA (DUFL/) DUFLOS A.  
 PA (HAU/) HAEUW J.  
 PA (BECK/) BECK A.  
 XX  
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 XX WPI; 2005-321968/33.  
 XX N-PSDB; ADZ67055.  
 XX  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX  
 XX Example 8; SEQ ID NO 52; 125pp; English.  
 XX  
 XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX  
 XX Sequence 127 AA;  
 XX  
 XX Query Match 100.0%; Score 89; DB 9; Length 127;  
 XX Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 Db |||||  
 61 YISYDGTNNYKPSLKD 76  
 RESULT 13  
 ID ADJ76911 standard; protein; 135 AA.  
 XX  
 XX ADJ76911;  
 AC  
 XX

DT 06-MAY-2004 (first entry)  
 XX Anti-IGF-IR related protein #23.  
 DE  
 XX  
 XX cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003059951-A2.  
 PN  
 XX 24-JUL-2003.  
 PD  
 XX  
 PF 20-JAN-2003; 2003WO-FR000178.  
 PR 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX  
 PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
 XX  
 PI Goetsch L, Corvaia N, Leger O;  
 DR WPI; 2003-569653/53.  
 XX  
 PT New antibodies that bind to human insulin-like growth factor receptor,  
 PT useful for treatment, prevention and diagnosis of cancers.  
 XX  
 PS Disclosure; SEQ ID NO 77; 164pp; French.  
 XX  
 CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 XX Sequence 135 AA;  
 XX  
 XX Query Match 100.0%; Score 89; DB 7; Length 135;  
 XX Best Local Similarity 100.0%; Pred. No. 5.9e-06;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 Db |||||  
 69 YISYDGTNNYKPSLKD 84  
 RESULT 14  
 ID ADJ76919 standard; protein; 135 AA.  
 XX  
 XX ADJ76919;  
 AC  
 XX  
 XX 06-MAY-2004 (first entry)  
 DT  
 XX Anti-IGF-IR related protein #27.  
 DE  
 XX cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW

KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003059951-A2.  
 XX  
 XX  
 PD 24-JUL-2003.  
 XX  
 XX 20-JAN-2003; 2003WO-FR000178.  
 XX  
 XX 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA  
 XX Goetsch L, Corvaia N, Leger O;  
 PI WPI; 2003-569653/53.  
 XX  
 DR New antibodies that bind to human insulin-like growth factor receptor,  
 XX useful for treatment, prevention and diagnosis of cancers.  
 PT  
 PS Disclosure; SEQ ID NO 85; 164pp; French.  
 XX  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 135 AA;  
 Query Match 100.0%; Score 89; DB 7; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 DB 69 YISYDGTNNYKPSLKD 84  
 RESULT 15  
 ADJ76915  
 ID ADJ76915 standard; protein; 135 AA.  
 XX  
 AC ADJ76915;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-IGF-1R related protein #25.  
 XX  
 XX cytosolic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2003059951-A2.  
 PN  
 XX

PD 24-JUL-2003.  
 XX  
 PF 20-JAN-2003; 2003WO-FR000178.  
 XX  
 XX 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA  
 XX Goetsch L, Corvaia N, Leger O;  
 PI WPI; 2003-569653/53.  
 XX  
 DR New antibodies that bind to human insulin-like growth factor receptor,  
 XX useful for treatment, prevention and diagnosis of cancers.  
 PT  
 PS Disclosure; SEQ ID NO 81; 164pp; French.  
 XX  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 135 AA;  
 Query Match 100.0%; Score 89; DB 7; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 DB 69 YISYDGTNNYKPSLKD 84  
 Search completed: December 30, 2005, 13:24:01  
 Job time : 143.194 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 22.7097 Seconds  
(without alignments)  
67.789 Million cell updates/sec

Title: US-10-735-916A-10  
Perfect score: 89  
Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: Pirl:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	84.3	104	2 S26467	Ig heavy chain V r
2	75	84.3	116	1 HVMS31	Ig heavy chain pre
3	72	80.9	120	2 A25114	Ig heavy chain V r
4	70	78.7	119	2 B25114	Ig heavy chain V r
5	69	77.5	136	2 S07637	Ig heavy chain V r
6	68	76.4	121	2 S37200	Ig heavy chain V r
7	66	74.2	116	2 S38718	Ig heavy chain V r
8	65	73.0	115	2 F25114	Ig heavy chain V r
9	65	73.0	119	2 C25114	Ig heavy chain V r
10	61	68.5	117	2 I28195	Ig heavy chain V r
11	61	68.5	119	2 D25114	Ig heavy chain pre
12	61	68.5	137	1 AVMS35	Ig heavy chain V r
13	58	65.2	106	2 S59639	Ig heavy chain V r
14	57	64.0	106	2 S26454	Ig heavy chain V r
15	57	64.0	134	2 B24672	Ig heavy chain pre
16	56	62.9	97	2 S26906	Ig heavy chain V r
17	56	62.9	97	2 S12416	Ig heavy chain V r
18	56	62.9	99	2 S12412	Ig heavy chain V r
19	56	62.9	105	2 S44125	Ig lambda chain V
20	56	62.9	116	2 B26340	Ig heavy chain pre
21	56	62.9	118	2 A26340	Ig heavy chain pre
22	56	62.9	130	2 S31690	Ig heavy chain V r
23	56	62.9	140	2 I37782	Ig variable region
24	55	61.8	97	2 PH0876	Ig heavy chain V r
25	54	60.7	94	2 S26461	Ig heavy chain V r
26	54	60.7	100	2 S14485	Ig heavy chain V r
27	54	60.7	101	2 S14484	Ig heavy chain V r
28	54	60.7	102	2 S14486	Ig heavy chain V r
29	54	60.7	113	1 G2MS60	Ig heavy chain V r

30	54	60.7	115	2 S57464	Ig heavy chain V-J
31	54	60.7	115	2 D33932	Ig mu chain precu
32	53	59.6	114	2 T01262	Ig heavy chain V r
33	53	59.6	146	2 S09711	Ig heavy chain V r
34	51	57.3	102	2 S14487	Ig heavy chain V r
35	51	57.3	102	2 S14488	Ig heavy chain V r
36	51	57.3	116	1 HVMS1B	Ig heavy chain pre
37	51	57.3	135	2 PL0100	Ig heavy chain pre
38	49	55.1	123	2 S42771	Ig heavy chain - m
39	48	53.9	98	2 S12414	Ig heavy chain V r
40	48	53.9	98	2 S28903	Ig heavy chain V r
41	48	53.9	99	2 S28801	Ig heavy chain V r
42	48	53.9	99	2 S28802	Ig heavy chain V r
43	48	53.9	99	2 S28803	Ig heavy chain V r
44	48	53.9	116	2 S37456	Ig mu chain - huma
45	48	53.9	117	2 E34964	Ig heavy chain pre

ALIGNMENTS

RESULT 1

S26467  
Ig heavy chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S26467  
R;Kavaier, J.  
submitted to the EMBL Data Library, April 1991  
A;Reference number: S26459  
A;Accession: S26467  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-104 <XAV>  
A;Cross-references: UNIPARC:UPI0000115F5F; EMBL:X59105; NID:951939; PIDN:CAA41831.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;6-89/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 75; DB 2; Length 104;  
Best Local Similarity 81.2%; Pred. No. 5.2e-05;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
DB 42 YISYDGSNNYNPSLKN 57  
|||||:|||||:  
|||||:|||||:

RESULT 2

HVMS31  
Ig heavy chain precursor V region (M315) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: J0509  
R;Levy, N.S.; Malpietro, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary ir  
A;Reference number: J0501; MUID:89279149; PMID:2499654  
A;Accession: J0509  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-116 <LEV>  
A;Cross-references: UNIPROT:P18531; UNIPARC:UPI00000278E0  
A;Experimental source: strain BALB/cJ  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;13-116/Product: Ig heavy chain V region (M315) #status predicted <MAT>  
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 75; DB 1; Length 116;  
Best Local Similarity 81.2%; Pred. No. 5.8e-05;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
|||||:|||||:  
Db 69 YISYDGSNNYKPSLKN 84

RESULT 3  
S07614  
Ig heavy chain V region (HP22, HP27) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 21-Jul-2000  
C:Accession: A25114  
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.  
EMBO J. 4, 3681-3688, 1985  
A:Title: The idiotypic network and the internal image: possible regulation of a germ-lin  
A:Reference number: A91028; MUID:86136012; PMID:3937730  
A:Accession: A25114  
A:Molecule type: mRNA  
A:Residues: 1-120 <OLL>  
A:Cross-references: UNIPARC:UPI0000115D15; GB:X03374; NID:g51983; PIDN:CAA27071.1; PID:g  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 72; DB 2; Length 120;  
Best Local Similarity 75.0%; Pred. No. 0.00018;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
|||||:|||||:  
Db 51 YINYDGSNNYKPSLKN 66

RESULT 4  
E25114  
Ig heavy chain V region (HP25) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 20-Jun-2000  
C:Accession: E25114  
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.  
EMBO J. 4, 3681-3688, 1985  
A:Title: The idiotypic network and the internal image: possible regulation of a germ-lin  
A:Reference number: A91028; MUID:86136012; PMID:3937730  
A:Accession: E25114  
A:Molecule type: mRNA  
A:Residues: 1-119 <OLL>  
A:Cross-references: UNIPARC:UPI0000115D24; GB:X03378; NID:g52007; PIDN:CAA27095.1; PID:g  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 70; DB 2; Length 119;  
Best Local Similarity 75.0%; Pred. No. 0.00039;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
|||||:|||||:  
Db 51 YISYDGSNNYKPSLKN 66

RESULT 5  
S07637  
Ig heavy chain V region (PTF.02) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 23-Jul-1999  
C:Accession: S07637  
R;Urakov, D.N.; Deev, S.M.; Polyanovsky, O.I.  
Nucleic Acids Res. 17, 9481, 1989  
A:Title: The structure of the expressible VH gene from a hybridoma producing monoclonal  
A:Reference number: S07637; MUID:90067954; PMID:2587273  
A:Accession: S07637  
A:Molecule type: DNA  
A:Residues: 1-136 <URA>

A:Cross-references: UNIPARC:UPI0000115E36; EMBL:X16740; NID:g52099; PIDN:CAA34714.1; PID:  
A:Note: the authors translated the codon TAT for residue 112 as Ile, TAC for residue 113  
C:Genetics:  
A:Introns: 15/3  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 69; DB 2; Length 136;  
Best Local Similarity 75.0%; Pred. No. 0.00065;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
|||||:|||||:  
Db 69 YISYDGSNNYKPSLKN 84

RESULT 6  
S37200  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S37200  
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.  
submitted to the EMBL Data Library, August 1993  
A:Description: Production and cloning of TMV-specific monoclonal antibodies.  
A:Reference number: S37200  
A:Accession: S37200  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-121 <FIS>  
A:Cross-references: UNIPARC:UPI00001161AC; EMBL:X74587; NID:g402640  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 121;  
Best Local Similarity 75.0%; Pred. No. 0.00083;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
|||||:|||||:  
Db 51 YISYDGRNDYNPSLKN 66

RESULT 7  
S38718  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S38718  
R;Cimani, A.Y.  
submitted to the EMBL Data Library, November 1993  
A:Reference number: S38713  
A:Accession: S38718  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-116 <CIM>  
A:Cross-references: UNIPARC:UPI0000117542; EMBL:X76018; NID:g416102; PIDN:CAA53605.1; PI:  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 116;  
Best Local Similarity 80.0%; Pred. No. 0.0017;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15  
|||||:|||||:  
Db 51 YISYSGTTNNYKPSLK 65

RESULT 8  
F25114



Ig heavy chain V region (HP12) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 20-Jun-2000  
 C;Accession: F25114  
 R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.  
 EMBO J. 4, 3681-3688, 1985  
 A;Title: The idiotypic network and the internal image: possible regulation of a germ-line  
 A;Reference number: A91028; MUID:86136012; PMID:3937730  
 A;Accession: F25114  
 A;Molecule type: mRNA  
 A;Residues: 1-115 <OLL>  
 A;Cross-references: UNIPARC:UPI0000115D28; GB:X03379; NID:G52013; PIDN:CAA27101.1; PID:G  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 115;  
 Best Local Similarity 73.3%; Pred. No. 0.0024;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15  
 : ||||| : |||||  
 Db 51 FIRYDGSNNYPSLK 65

RESULT 9  
 C25114  
 Ig heavy chain V region (HP20) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 20-Jun-2000  
 C;Accession: C25114  
 R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.  
 EMBO J. 4, 3681-3688, 1985  
 A;Title: The idiotypic network and the internal image: possible regulation of a germ-line  
 A;Reference number: A91028; MUID:86136012; PMID:3937730  
 A;Accession: C25114  
 A;Molecule type: mRNA  
 A;Residues: 1-119 <OLL>  
 A;Cross-references: UNIPARC:UPI0000115D1A; GB:X03376; NID:G51995; PIDN:CAA27083.1; PID:G  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 119;  
 Best Local Similarity 68.8%; Pred. No. 0.0025;  
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 16  
 : ||||| : |||||  
 Db 51 YIKYDGSNNYPSLK 66

RESULT 10  
 I28195  
 Ig heavy chain V region (anti-haloperidol antibody D) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 23-Jul-1999  
 C;Accession: I28195  
 R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
 J. Biol. Chem. 263, 4059-4063, 1988  
 A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s  
 A;Reference number: A28195; MUID:88153717; PMID:3267217  
 A;Accession: I28195  
 A;Molecule type: mRNA  
 A;Residues: 1-117 <SH>  
 A;Cross-references: UNIPARC:UPI0000114D72; GB:M19775; NID:G195526; PIDN:AAA38343.1; PID:  
 A;Note: the authors translated the codon AAC for residue 61 as Thr, and did not transla  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 61; DB 2; Length 117;  
 Best Local Similarity 73.3%; Pred. No. 0.011;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15  
 : ||||| : |||||  
 Db 51 YISYGTTSYNPSLK 65

RESULT 11  
 D25114  
 Ig heavy chain V region (HP21) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 20-Jun-2000  
 C;Accession: D25114  
 R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.  
 EMBO J. 4, 3681-3688, 1985  
 A;Title: The idiotypic network and the internal image: possible regulation of a germ-line  
 A;Reference number: A91028; MUID:86136012; PMID:3937730  
 A;Accession: D25114  
 A;Molecule type: mRNA  
 A;Residues: 1-119 <OLL>  
 A;Cross-references: UNIPARC:UPI0000115D1F; GB:X03377; NID:G52001; PIDN:CAA27089.1; PID:G  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 61; DB 2; Length 119;  
 Best Local Similarity 68.8%; Pred. No. 0.011;  
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 16  
 : ||||| : |||||  
 Db 51 YISFDGNNYPSLK 66

RESULT 12  
 AVMS35  
 Ig heavy chain precursor V region (MOPC 315) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 24-Apr-1984 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C;Accession: FLO102; S03262; A93814; A91462; A93787; S23599  
 R;Rinfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.  
 Mol. Immunol. 26, 431-434, 1989  
 A;Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment.  
 A;Reference number: FLO102; MUID:89238351; PMID:2497341  
 A;Accession: FLO102  
 A;Molecule type: mRNA  
 A;Residues: 1-137 <RIN>  
 A;Cross-references: UNIPROT:P01822; UNIPARC:UPI000002727B; GB:M27638; NID:G602706; PIDN:.  
 A;Experimental source: strain MOPC 315  
 R;Rinfret, A.; Dorrington, K.J.; Klein, M.  
 submitted to the EMBL Data Library, June 1988  
 A;Reference number: S03262  
 A;Accession: S03262  
 A;Molecule type: DNA  
 A;Residues: 1-15,'G',16-137 <RI2>  
 A;Cross-references: UNIPARC:UPI000016CE1C; EMBL:X07880; NID:G51760; PIDN:CAA30727.1; PID  
 R;Jilka, R.L.; Pecht, S.  
 Proc. Natl. Acad. Sci. U.S.A. 74, 5692-5696, 1977  
 A;Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin he  
 A;Reference number: A93814; MUID:78094475; PMID:414225  
 A;Accession: A93814  
 A;Molecule type: protein  
 A;Residues: 1-14,'H',16-31 <JIL>  
 A;Cross-references: UNIPARC:UPI000017373E  
 A;Note: the authors translated mRNA in vitro to obtain the precursor protein  
 R;Schechter, I.; Wolf, O.; Zemall, R.; Burstein, Y.  
 Fed. Proc. 38, 1839-1845, 1979  
 A;Title: Structure and function of immunoglobulin genes and precursors.  
 A;Reference number: A91462; MUID:79148758; PMID:428562  
 A;Accession: A91462  
 A;Molecule type: protein  
 A;Residues: 1,'X',3-11,'X',14-21 <SCH>  
 A;Cross-references: UNIPARC:UPI000017373F

A>Note: the authors translated mRNA in vitro to obtain the precursor protein  
R;Francis, S.H.; Leslie, R.G.O.; Hood, L.; Eisen, H.N.  
Proc. Natl. Acad. Sci. U.S.A. 71, 1123-1127, 1974  
A>Title: Amino-acid sequence of the variable region of the heavy (alpha) chain of a mouse  
A;Reference number: A93787; MUID:74170779; PMID:4524622  
A;Accession: A93787  
A:Molecule type: protein  
A;Residues: 19-52, 'K', 53-75, 'BYGB', 80-101, 'D', 103-106, '2B', 109-122, 124-137 <FRA>  
A;Cross-references: UNIPARC:UPI0000173740  
R;Hood, L.; Margolies, M.; Givol, D.; Zakut, R.  
unpublished results, cited by Padlan, E.A., Davies, D.R., Pecht, I., Givol, D., and Wigd  
A;Reference number: A94484  
A;Contents: annotation, revision to residue 53  
R;Chedle, C.; Hook, L.E.; Givol, D.; Ricca, G.A.  
Mol. Immunol. 29, 21-30, 1992  
A>Title: Cloning and expression of the variable regions of mouse myeloma protein MOPC315  
A;Reference number: S23599; MUID:92114886; PMID:1731188  
A;Accession: S23599  
A:Molecule type: mRNA  
A;Residues: 19-137 <CHE>  
A;Cross-references: UNIPARC:UPI0000113794; EMBL:X63972; NID:G53532; PIDN:CAA45384.1; PID  
C;Comment: This alpha chain was isolated from a myeloma protein that has anti-dinitrophen  
C;Genetics:  
A;Introns: 15/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;1-18/Domain: signal sequence #status experimental <SIG>  
F;19-136/Product: Ig heavy chain V region (MOPC 315) #status experimental <MAT>  
F;33-116/Domain: immunoglobulin homology <IMM>  
Query Match 68.5%; Score 61; DB 1; Length 137;  
Best Local Similarity 62.5%; Pred. No. 0.013;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 YISYDGTNNYKPSLKD 16  
DB 69 FIKYDGSNGYNPSLKN 84  
RESULT 13  
S59639  
Ig heavy chain V region N10 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 17-Mar-1999  
C;Accession: S59639  
R;Bossart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S.  
J. Mol. Biol. 253, 559-575, 1995  
A>Title: The crystal structure of the antibody N10-staphylococcal nuclease complex at 2.  
A;Reference number: S59639; MUID:96068846; PMID:7473734  
A;Accession: S59639  
A;Status: preliminary  
A:Molecule type: mRNA  
A;Residues: 1-106 <BOS>  
A;Cross-references: UNIPARC:UPI0000176905; EMBL:U25121  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;19-134/Product: Ig heavy chain V region VGAM3-2 #status predicted <MAT>  
F;8-91/Domain: immunoglobulin homology <IMM>  
Query Match 65.2%; Score 58; DB 2; Length 106;  
Best Local Similarity 66.7%; Pred. No. 0.03;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 YISYDGTNNYKPSLK 15  
DB 44 YITYSGTTSYNPSLK 58  
RESULT 14  
S26464  
Ig heavy chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S26464

R;Kavaler, J.  
submitted to the EMBL Data Library, April 1991  
A;Reference number: S26459  
A;Accession: S26464  
A;Status: preliminary  
A:Molecule type: mRNA  
A;Residues: 1-106 <NAV>  
A;Cross-references: UNIPARC:UPI0000115P68; EMBL:X59114; NID:G51926; PIDN:CAA41840.1; PID:  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;3-86/Domain: immunoglobulin homology <IMM>  
Query Match 64.0%; Score 57; DB 2; Length 106;  
Best Local Similarity 66.7%; Pred. No. 0.044;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 YISYDGTNNYKPSLK 15  
DB 39 YIYSGSGTSYNPSLK 53  
RESULT 15  
B24672  
Ig heavy chain precursor V region (VGAM3-2) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 18-Oct-1996  
C;Accession: B24672  
R;Winter, E.; Radbruch, A.; Krawinkel, U.  
EMBO J. 4, 2861-2867, 1985  
A;Reference number: A91022; MUID:86055722; PMID:2998759  
A;Accession: B24672  
A:Molecule type: DNA  
A;Residues: 1-134 <WIN>  
A;Cross-references: UNIPARC:UPI00001768F5  
A;Note: this sequence was determined from the differentiated gene  
C;Genetics:  
A;Introns: 15/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;19-134/Product: Ig heavy chain V region VGAM3-2 #status predicted <MAT>  
F;33-116/Domain: immunoglobulin homology <IMM>  
Query Match 64.0%; Score 57; DB 2; Length 134;  
Best Local Similarity 66.7%; Pred. No. 0.057;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 YISYDGTNNYKPSLK 15  
DB 69 YIHSYSGTSYNPSLK 83  
Search completed: December 30, 2005, 13:34:56  
Job time : 23.7097 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 144 Seconds  
(without alignments)  
78.392 Million cell updates/sec

Title: US-10-735-916A-10  
Perfect score: 89  
Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	84.3	116	1 HV60_MOUSE	P18531 mus musculu
2	72	80.9	98	2 Q53VR6_MOUSE	Q53vr6 mus musculu
3	72	80.9	120	2 Q53VR7_MOUSE	Q53vr7 mus musculu
4	72	80.9	479	2 Q99M22_MOUSE	Q99m22 mus musculu
5	70	78.7	98	2 Q53VQ4_MOUSE	Q53vq4 mus musculu
6	70	78.7	119	2 Q53VQ5_MOUSE	Q53vq5 mus musculu
7	69	77.5	136	2 Q53VQ6_MOUSE	Q53vq6 mus musculu
8	68	76.4	483	2 Q53VQ7_MOUSE	Q53vq7 mus musculu
9	65	73.0	98	2 Q53VQ8_MOUSE	Q53vq8 mus musculu
10	65	73.0	115	2 Q53VQ9_MOUSE	Q53vq9 mus musculu
11	65	73.0	119	2 Q53VQ0_MOUSE	Q53vq0 mus musculu
12	65	73.0	119	2 Q53VQ1_MOUSE	Q53vq1 mus musculu
13	61	68.5	98	2 Q53VQ2_MOUSE	Q53vq2 mus musculu
14	61	68.5	119	2 Q53VQ3_MOUSE	Q53vq3 mus musculu
15	61	68.5	137	1 HV46_MOUSE	P01822 mus musculu
16	56	62.9	139	2 Q86SX2_HUMAN	Q86sx2 homo sapien
17	55	61.8	119	2 Q53VQ4_MOUSE	Q53vq4 mus musculu
18	54	60.7	113	1 HV47_MOUSE	P01823 mus musculu
19	52	58.4	615	2 Q569B6_RAT	Q569b6 rattus norv
20	51	57.3	116	1 HV61_MOUSE	P18532 mus musculu
21	51	57.3	477	2 Q6GMX7_HUMAN	Q6gmx7 homo sapien
22	50	56.2	358	2 Q4JSK6_CORJK	Q4jsk6 corynebacte
23	49	55.1	262	2 Q65Z11_MOUSE	Q65z11 mus musculu
24	49	55.1	378	2 Q54891_DICDI	Q54891 dictyosteli
25	48	53.9	455	2 Q8CXP9_OCEIH	Q8cxp9 oceanobacil
26	48	53.9	476	2 Q569B8_RAT	Q569b8 rattus norv
27	47	52.8	590	2 Q6GMX1_HUMAN	Q6gmx1 homo sapien
28	47	52.8	116	2 Q723Y6_HUMAN	Q723y6 homo sapien
29	47	52.8	476	2 Q6MZX7_HUMAN	Q6mzx7 homo sapien
30	47	52.8	595	2 Q8WUX4_HUMAN	Q8wux4 homo sapien
31	47	52.8	597	2 Q9BU10_HUMAN	Q9bu10 homo sapien

32	47	52.8	597	2	Q6GMX5_HUMAN	Q6gmx5 homo sapien
33	47	52.8	625	2	Q96AA6_HUMAN	Q96aa6 homo sapien
34	47	52.8	1547	2	Q7QV96_GIALA	Q7qv96 giardia lam
35	46	51.7	102	2	Q5A937_CANAL	Q5a937 candida alb
36	46	51.7	119	1	HV40_MOUSE	P01810 mus musculu
37	46	51.7	179	2	Q4T5M8_TETNG	Q4t5m8 tetraodon n
38	46	51.7	321	2	Q8TZN1_PYRFU	Q8tzn1 pyrococcus
39	46	51.7	809	2	Q7SDN1_NEUPC	Q7sdn1 neurospora
40	46	51.7	952	2	Q51W19_MAGGR	Q51w19 magnaporthe
41	46	51.7	1055	2	Q55XG3_CRYNE	Q55xg3 cryptococcu
42	46	51.7	1055	2	Q55XG3_CRYNE	Q55xg3 cryptococcu
43	46	51.7	1174	2	Q7QCE8_ANOGA	Q7qce8 anopheles g
44	46	51.7	1533	2	Q54NW5_DICDI	Q54nw5 dictyosteli
45	45	50.6	454	2	Q5WAD9_BACSK	Q5wad9 bacillus cl

ALIGNMENTS

RESULT 1  
HV60\_MOUSE STANDARD; PRT; 116 AA.  
ID HV60\_MOUSE  
AC P18531;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DB Ig heavy chain V region M315 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BALE/cj;  
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;  
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response".  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC -----  
CC PIR; JT0509; HVMS31.  
DR PDB; 1EZV; X-ray; X=22-116.  
DR SMR; P18531; 19-116.  
DR Ensembl; ENSMUSG00000057048; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 116 Ig heavy chain V region M315.  
FT REGION 19 48 Framework-1.  
FT REGION 49 53 Complementarity-determining-1.  
FT REGION 54 67 Framework-2.  
FT REGION 68 84 Complementarity-determining-2.  
FT REGION 85 116 Framework-3.  
FT DISULFID 40 114 By similarity.  
FT NON TER 116  
SQ SEQUENCE 116 AA; 4562B03E53DC9E10 CRC64;  
Query Match 84.3%; Score 75; DB 1; Length 116;  
Best Local Similarity 81.2%; Pred. No. 0.0003;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
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Db 69 YISYDGSNNYPSLKN 84

# RESULT 2

Q53VR6 MOUSE  
ID Q53VR6\_MOUSE PRELIMINARY; PRT; 98 AA.  
AC Q53VR6;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE VH-region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86136012; PubMed=3937730;  
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;  
RT "The idiotypic network and the internal image: possible regulation of  
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
antibodies in the GAT system.";  
RL EMBO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RA Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X03375; CAA27078.1; -; mRNA.  
DR EMBL; X03374; CAA27072.1; -; mRNA.  
FT NON\_TER 1 1  
FT NON\_TER 98 98  
SQ SEQUENCE 98 AA; 11255 MW; EBC71AA2F8F5FD60 CRC64;

Query Match 80.9%; Score 72; DB 2; Length 98;  
Best Local Similarity 75.0%; Pred. No. 0.00077;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
||:|||||:  
Db 51 YINYDGSNNYPSLKN 66

# RESULT 3

Q53VR7 MOUSE  
ID Q53VR7\_MOUSE PRELIMINARY; PRT; 120 AA.  
AC Q53VR7;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE VH-D-JH region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86136012; PubMed=3937730;  
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;  
RT "The idiotypic network and the internal image: possible regulation of  
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
antibodies in the GAT system.";  
RL EMBO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RA Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X03375; CAA27077.1; -; mRNA.  
DR EMBL; X03374; CAA27071.1; -; mRNA.  
FT NON\_TER 1 1  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13892 MW; 013452306EBA33BE CRC64;

Query Match 80.9%; Score 72; DB 2; Length 120;  
Best Local Similarity 75.0%; Pred. No. 0.00097;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
||:|||||:  
Db 51 YINYDGSNNYPSLKN 66

# RESULT 4

Q99M22 MOUSE  
ID Q99M22\_MOUSE PRELIMINARY; PRT; 479 AA.  
AC Q99M22;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE LOC238447 protein.  
GN Name=LOC238447;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Mix FVB/N;  
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Strauss R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Huiyk S.W.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Mix FVB/N;  
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RG NIH MGC Project;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002091; AA02091.1; -; mRNA.  
DR HSSP; P01820; 1G7J.  
DR GO; GO:0003823; F:antigen binding; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; CI-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Immunoglobulin domain.  
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 80.9%; Score 72; DB 2; Length 479;  
Best Local Similarity 75.0%; Pred. No. 0.0045;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 YISYDGTNNYKPSLKD 16
Db 69 YIYDGSNNYPSLKN 84

RESULT 5
Q53VQ4_MOUSE
ID Q53VQ4_MOUSE PRELIMINARY; PRT; 98 AA.
AC Q53VQ4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigen encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688 (1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03378; CAA27096.1; -; mRNA.
FT NON_TER 1 98
FT TER 1 98
SQ SEQUENCE 98 AA; 11202 MW; 4049CF8C7EB8AAE0 CRC64;

Query Match 78.7%; Score 70; DB 2; Length 98;
Best Local Similarity 75.0%; Pred. No. 0.0016;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGSNNYPSLKN 66

RESULT 6
Q53VQ5_MOUSE
ID Q53VQ5_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53VQ5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigen encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688 (1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03378; CAA27095.1; -; mRNA.
FT NON_TER 1 119
FT TER 1 119
SQ SEQUENCE 119 AA; 13931 MW; 502E51A5213F056E CRC64;

Query Match 78.7%; Score 69; DB 2; Length 136;
Best Local Similarity 75.0%; Pred. No. 0.0035;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 69 YISYDGSNNYPSLKN 84

RESULT 8
Q5U413_MOUSE
ID Q5U413_MOUSE PRELIMINARY; PRT; 483 AA.
AC Q5U413;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE LOC544903 protein.
GN Name=LOC544903;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=FVB/N; TISSUE=Colon;
RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RG NIH MGC Project;  
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC085312; AAH85312.1; -; mRNA.  
 DR Ensembl; ENSMUSG0000054328; Mus musculus.  
 DR GO; GO:0003823; F:antigen binding; IEA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 2.  
 DR SMART; SM00409; IG; 3.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 SQ SEQUENCE 483 AA; 52714 MW; 7C272DA501A4A0D1 CRC64;

Query Match 76.4%; Score 68; DB 2; Length 483;  
 Best Local Similarity 80.0%; Pred. No. 0.021;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15  
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 DB 69 YISYSGSNYNPSLK 83

RESULT 9  
 Q53VQ0\_MOUSE  
 ID Q53VQ0\_MOUSE PRELIMINARY; PRT; 98 AA.  
 AC Q53VQ0;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE VH region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86136012; PubMed=3937730;  
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;  
 RT "The idiotypic network and the internal image; possible regulation of  
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
 RT antibodies in the GAT system.";  
 RL EMBO J. 4:3681-3688(1985).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE OF 28-29.  
 RA Fougereau M.;  
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X03379; CAA27102.1; -; mRNA.  
 FT NON\_TER

FT NON\_TER 98 98  
 SQ SEQUENCE 98 AA; 11191 MW; B3585BBE6F080616 CRC64;  
 Query Match 73.0%; Score 65; DB 2; Length 98;  
 Best Local Similarity 73.3%; Pred. No. 0.011;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15  
 :||||:|||||  
 DB 51 FIRYDGSNNYNPSLK 65

RESULT 10  
 Q53VR2\_MOUSE  
 ID Q53VR2\_MOUSE PRELIMINARY; PRT; 98 AA.  
 AC Q53VR2;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE VH region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86136012; PubMed=3937730;  
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;  
 RT "The idiotypic network and the internal image; possible regulation of  
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
 RT antibodies in the GAT system.";  
 RL EMBO J. 4:3681-3688(1985).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE OF 28-29.  
 RA Fougereau M.;  
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X03376; CAA27084.1; -; mRNA.  
 FT NON\_TER 1  
 FT NON\_TER 98 98  
 SQ SEQUENCE 98 AA; 11132 MW; 50878B9A4CF7298B CRC64;

Query Match 73.0%; Score 65; DB 2; Length 98;  
 Best Local Similarity 68.8%; Pred. No. 0.011;  
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 16  
 |||||:|||||  
 DB 51 YIKYDGNNSYNPSLK 66

RESULT 11  
 Q53VQ1\_MOUSE  
 ID Q53VQ1\_MOUSE PRELIMINARY; PRT; 115 AA.  
 AC Q53VQ1;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE VH-D-JH region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86136012; PubMed=3937730;  
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;  
 RT "The idiotypic network and the internal image; possible regulation of  
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
 RT antibodies in the GAT system.";  
 RL EMBO J. 4:3681-3688(1985).  
 RN [2]

RP NUCLEOTIDE SEQUENCE OF 28-29.  
RA Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X03379; CAA27101.1; -, mRNA.  
FT NON TER 1 1  
FT NON TER 115 115  
SQ SEQUENCE 115 AA; 13257 MW; D465A5854DF459A3 CRC64;  
  
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Best Local Similarity 73.3%; Pred. No. 0.013;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
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Db 51 FIRYDGNINYNPSLKN 65  
  
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Q53VR3 MOUSE  
ID Q53VR3\_MOUSE PRELIMINARY; PRT; 119 AA.  
AC Q53VR3;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE VH-D-JH region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86136012; PubMed=3937730;  
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;  
RT "The idiotypic network and the internal image: possible regulation of  
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
antibodies in the GAT system.";  
RL EMO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RA Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X03376; CAA27083.1; -, mRNA.  
FT NON TER 1 1  
FT NON TER 119 119  
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Query Match 73.0%; Score 65; DB 2; Length 119;  
Best Local Similarity 68.8%; Pred. No. 0.014;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 YISYDGTNNYKPSLK 16  
Db 51 YIKYDGNINYNPSLKN 66  
  
RESULT 13  
Q53VQ8 MOUSE  
ID Q53VQ8\_MOUSE PRELIMINARY; PRT; 98 AA.  
AC Q53VQ8;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE VH region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86136012; PubMed=3937730;  
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;

RT "The idiotypic network and the internal image: possible regulation of  
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
antibodies in the GAT system.";  
RL EMO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RA Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X03377; CAA27090.1; -, mRNA.  
FT NON TER 1 1  
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SQ SEQUENCE 98 AA; 11191 MW; 5B21146E5DA368C6 CRC64;  
  
Query Match 68.5%; Score 61; DB 2; Length 98;  
Best Local Similarity 68.8%; Pred. No. 0.05;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 YISYDGTNNYKPSLK 16  
Db 51 YISFDGNINYNPSLKN 66  
  
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AC Q53VQ9;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE VH-D-JH region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86136012; PubMed=3937730;  
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;  
RT "The idiotypic network and the internal image: possible regulation of  
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
antibodies in the GAT system.";  
RL EMO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RA Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X03377; CAA27089.1; -, mRNA.  
FT NON TER 1 1  
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Best Local Similarity 68.8%; Pred. No. 0.062;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
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Db 51 YISFDGNINYNPSLKN 66  
  
RESULT 15  
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ID HV46\_MOUSE STANDARD; PRT; 137 AA.  
AC P01822;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE 1g heavy chain V region MOPC 315 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.





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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 35.871 Seconds  
(without alignments)  
36.877 Million cell updates/sec

Title: US-10-735-916A-10

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Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	84.3	118	2	US-09-065-059-11
2	75	84.3	118	2	US-08-913-555-11
3	62	69.7	241	2	US-08-902-486-13
4	62	69.7	496	2	US-08-902-486-15
5	60	67.4	121	1	US-08-887-352B-2
6	60	67.4	121	2	US-08-109-207C-2
7	60	67.4	121	2	US-09-296-005-2
8	60	67.4	121	2	US-09-920-171-2
9	60	67.4	121	2	US-09-716-028-2
10	60	67.4	121	2	US-10-113-996-2
11	60	67.4	134	2	US-08-466-151-3
12	60	67.4	134	2	US-08-466-163B-3
13	60	67.4	134	2	US-09-802-096-3
14	60	67.4	134	2	US-09-802-077-3
15	60	67.4	134	2	US-09-925-179-3
16	58	65.2	451	2	US-09-925-179-66
17	57	64.0	16	2	US-09-170-769A-14
18	57	64.0	119	2	US-08-767-128-18
19	57	64.0	137	2	US-08-466-151-7
20	57	64.0	137	2	US-08-466-163B-7
21	57	64.0	137	2	US-09-802-096-7
22	57	64.0	137	2	US-09-802-077-7
23	57	64.0	137	2	US-09-925-179-7
24	57	64.0	213	2	US-09-170-769A-2
25	56	62.9	16	2	US-09-424-840B-110
26	56	62.9	21	2	US-08-918-148-45
27	56	62.9	21	2	US-09-138-091A-45

Sequence 22, Appl  
Sequence 35, Appl  
Sequence 101, Appl  
Sequence 42, Appl  
Sequence 52, Appl  
Sequence 53, Appl  
Sequence 41, Appl  
Sequence 49, Appl  
Sequence 69, Appl  
Sequence 43, Appl  
Sequence 23, Appl  
Sequence 23, Appl  
Sequence 140, Appl  
Sequence 140, Appl  
Sequence 13, Appl  
Sequence 48, Appl  
Sequence 142, Appl

#### ALIGNMENTS

RESULT 1  
US-09-065-059-11  
; Sequence 11, Application US/09065059  
; Patent No. 6068841  
; GENERAL INFORMATION:  
; APPLICANT: SEINO, Ken-ichiro  
; APPLICANT: KAVAGAKI, No. 6068841uhiko  
; APPLICANT: YAGITA, Hideo  
; APPLICANT: OKUMURA, Ko  
; APPLICANT: NAKATA, Motom1  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/065,059  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bucca Ph.D., Daniel  
; REGISTRATION NUMBER: P-42,368  
; REFERENCE/DOCKET NUMBER: 50356-151  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-518-5100  
; TELEFAX: 703-684-1124  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-065-059-11

Query Match 84.3%; Score 75; DB 2; Length 118;  
Best Local Similarity 81.2%; Pred. No. 9.4e-05;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
|||||:|||||

Db 50 YISYDGSNNYPSLKN 65

RESULT 2  
US-08-913-555-11  
; Sequence 11, Application US/08913555  
; Patent No. 6946255  
; GENERAL INFORMATION:  
; APPLICANT: KAYAGAKI, No. 6946255uhiko  
; APPLICANT: YAGITA, Kideo  
; APPLICANT: OKUMURA, Ko  
; APPLICANT: NAKATA, Motomi  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY  
; TITLE OF INVENTION: REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,555  
; FILING DATE: 19-SEP-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bucca Ph.D., Daniel  
; REGISTRATION NUMBER: 42,368  
; REFERENCE/DOCKET NUMBER: 50356-150  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-756-8690  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-913-555-11

Query Match 84.3%; Score 75; DB 2; Length 118;  
Best Local Similarity 81.2%; Pred. NO. 9.4e-05;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
|||||:|||||:  
Db 50 YISYDGSNNYPSLKN 65

RESULT 3  
US-08-902-486-13  
; Sequence 13, Application US/08902486  
; Patent No. 6140075  
; GENERAL INFORMATION:  
; APPLICANT: Russel, David R.  
; APPLICANT: Fuller, James T.  
; TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND  
; TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,486  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 670513.90261  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 496 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-902-486-13

Query Match 69.7%; Score 62; DB 2; Length 241;  
Best Local Similarity 68.8%; Pred. NO. 0.027;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
|||||:|||||:  
Db 180 YIRYDGTSEYTPSLKN 195

RESULT 4  
US-08-902-486-15  
; Sequence 15, Application US/08902486  
; Patent No. 6140075  
; GENERAL INFORMATION:  
; APPLICANT: Russel, David R.  
; APPLICANT: Fuller, James T.  
; TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND  
; TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,486  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J.  
; REGISTRATION NUMBER: 27386  
; REFERENCE/DOCKET NUMBER: 670513.90261  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-251-5000  
; TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 496 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-902-486-15



RESULT 9  
US-09-716-028-2  
; Sequence 2, Application US/09716028  
; Patent No. 6723833  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/716,028  
; CURRENT FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: US 09/109,207  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 2  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-716-028-2

Query Match 67.4%; Score 60; DB 2; Length 121;  
Best Local Similarity 66.7%; Pred. No. 0.027;  
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYKPSLKD 16  
|:||||:|||||  
Db 52 ITYDGSSNYPNSLKN 66

RESULT 10  
US-10-113-996-2  
; Sequence 2, Application US/10113996  
; Patent No. 6761889  
; GENERAL INFORMATION:  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Lowe, John  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies  
; FILE REFERENCE: P1123C3US  
; CURRENT APPLICATION NUMBER: US/10/113,996  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: US 08/887,352  
; PRIOR FILING DATE: 1997-07-02  
; PRIOR APPLICATION NUMBER: US 09/296,005  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: US 09/920,171  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 2  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-113-996-2

Query Match 67.4%; Score 60; DB 2; Length 121;  
Best Local Similarity 66.7%; Pred. No. 0.027;  
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYKPSLKD 16  
|:||||:|||||  
Db 52 ITYDGSSNYPNSLKN 66

RESULT 11  
US-08-466-151-3  
; Sequence 3, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.

; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 3  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-466-163B-3

Query Match 67.4%; Score 60; DB 2; Length 134;  
Best Local Similarity 66.7%; Pred. No. 0.03;  
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Cy 2 ISYDGTNNYKPSLKD 16  
|:||||:|||||  
Db 52 ITYDSSNYPNPSLKN 66

## RESULT 13

US-09-802-096-3  
; Sequence 3, Application US/09802096  
; Patent No. 6685939  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C3US  
; CURRENT APPLICATION NUMBER: US/09/802,096  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 3  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-802-096-3

Query Match 67.4%; Score 60; DB 2; Length 134;  
Best Local Similarity 66.7%; Pred. No. 0.03;  
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Cy 2 ISYDGTNNYKPSLKD 16  
|:||||:|||||  
Db 52 ITYDSSNYPNPSLKN 66

## RESULT 14

US-09-802-077-3  
; Sequence 3, Application US/09802077  
; Patent No. 6699472  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C2US  
; CURRENT APPLICATION NUMBER: US/09/802,077  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 3  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-802-077-3

Query Match 67.4%; Score 60; DB 2; Length 134;  
Best Local Similarity 66.7%; Pred. No. 0.03;  
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Cy 2 ISYDGTNNYKPSLKD 16  
|:||||:|||||  
Db 52 ITYDSSNYPNPSLKN 66

## RESULT 15

US-09-925-179-3  
; Sequence 3, Application US/09925179  
; Patent No. 6914129  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)  
; FILE REFERENCE: P0718P2C1D1C1US  
; CURRENT APPLICATION NUMBER: US/09/925,179  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 08/466,163  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 68  
; SEQ ID NO 3  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-925-179-3

Query Match 67.4%; Score 60; DB 2; Length 134;  
Best Local Similarity 66.7%; Pred. No. 0.03;  
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Cy 2 ISYDGTNNYKPSLKD 16  
|:||||:|||||  
Db 52 ITYDSSNYPNPSLKN 66

Search completed: December 30, 2005, 13:37:19  
Job time : 36.871 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 118.968 Seconds  
(without alignments)  
56.194 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main.\*

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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*

3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*

4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*

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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	16	5	US-10-735-916A-10
2	89	100.0	117	5	US-10-735-916A-69
3	89	100.0	117	5	US-10-735-916A-75
4	89	100.0	117	5	US-10-735-916A-79
5	89	100.0	117	5	US-10-735-916A-83
6	89	100.0	127	5	US-10-735-916A-52
7	89	100.0	135	5	US-10-735-916A-77
8	89	100.0	135	5	US-10-735-916A-81
9	89	100.0	135	5	US-10-735-916A-85
10	75	84.3	136	3	US-09-858-349-2
11	72	80.9	121	3	US-09-144-886-70
12	72	80.9	121	4	US-10-632-706-67
13	71	79.8	118	5	US-10-735-916A-70
14	70	78.7	118	4	US-10-372-481-17
15	70	78.7	118	4	US-10-371-797-17
16	66	74.2	116	6	US-11-003-819-4
17	65	73.0	120	4	US-10-383-447-2
18	65	73.0	120	4	US-10-383-447-22
19	65	73.0	120	4	US-10-383-447-24
20	65	73.0	120	4	US-10-383-447-26
21	65	73.0	120	4	US-10-383-447-28
22	60	67.4	116	5	US-10-822-306A-26
23	60	67.4	116	5	US-10-822-306A-14
24	60	67.4	121	3	US-09-920-171-2
25	60	67.4	121	4	US-10-113-996-2
26	60	67.4	121	5	US-10-791-619-2
27	60	67.4	134	3	US-09-802-077-3

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Sequence 21, Appli  
Sequence 23, Appli  
Sequence 9, Appli  
Sequence 11, Appli  
Sequence 66, Appli  
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Sequence 131, App  
Sequence 131, App  
Sequence 131, App  
Sequence 136, App  
Sequence 157, App  
Sequence 157, App  
Sequence 258, App  
Sequence 46, Appli  
Sequence 128, App

28 60 67.4 134 3 US-09-802-096-3  
29 60 67.4 134 3 US-09-925-179-3  
30 60 67.4 134 5 US-10-968-237-3  
31 58 65.2 16 5 US-10-822-306A-21  
32 58 65.2 16 5 US-10-822-306A-23  
33 58 65.2 116 5 US-10-822-306A-9  
34 58 65.2 116 5 US-10-822-306A-11  
35 58 65.2 451 3 US-09-925-179-66  
36 58 65.2 451 5 US-10-968-237-66  
37 57 64.0 115 4 US-10-308-817-131  
38 57 64.0 115 4 US-10-308-817-136  
39 57 64.0 115 4 US-10-453-698-131  
40 57 64.0 115 4 US-10-453-698-136  
41 57 64.0 116 4 US-10-308-817-157  
42 57 64.0 116 4 US-10-453-698-157  
43 57 64.0 119 4 US-10-207-655-258  
44 57 64.0 119 5 US-10-627-556-46  
45 57 64.0 120 4 US-10-309-762-128

#### ALIGNMENTS

##### RESULT 1

US-10-735-916A-10  
; Sequence 10, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFIOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: Patentin ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-10

Query Match 100.0%; Score 89; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
| | | | | | | | | | | | | | | |  
Db 1 YISYDGTNNYKPSLKD 16

##### RESULT 2

US-10-735-916A-69  
; Sequence 69, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier

```
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-69

Query Match      100.0%; Score 89; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YISYDGTNNYKPSLKD 16
       |||||
Db      51 YISYDGTNNYKPSLKD 66

RESULT 3
US-10-735-916A-75
; Sequence 75, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-75

Query Match      100.0%; Score 89; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YISYDGTNNYKPSLKD 16
       |||||
Db      51 YISYDGTNNYKPSLKD 66

RESULT 4
US-10-735-916A-79
; Sequence 79, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-79

Query Match      100.0%; Score 89; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YISYDGTNNYKPSLKD 16
       |||||
Db      51 YISYDGTNNYKPSLKD 66

RESULT 5
US-10-735-916A-83
; Sequence 83, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
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; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83

Query Match      100.0%; Score 89; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGTNNYKPSLKD 66

RESULT 6
US-10-735-916A-52
; Sequence 52, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52

Query Match      100.0%; Score 89; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 61 YISYDGTNNYKPSLKD 76

RESULT 7
US-10-735-916A-77
; Sequence 77, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52

Query Match      100.0%; Score 89; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 61 YISYDGTNNYKPSLKD 76

RESULT 7
US-10-735-916A-77
; Sequence 77, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-81

Query Match      100.0%; Score 89; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 69 YISYDGTNNYKPSLKD 84

RESULT 8
US-10-735-916A-81
; Sequence 81, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-81

Query Match      100.0%; Score 89; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 69 YISYDGTNNYKPSLKD 84

RESULT 9
US-10-735-916A-85
; Sequence 85, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
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; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-85
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Query Match 100.0%; Score 89; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 YISYDGTNNYKPSLKD 16
Db 69 YISYDGTNNYKPSLKD 84
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RESULT 10
US-09-858-349-2
; Sequence 2, Application US/09858349
; Patent No. US20020012909A1
; GENERAL INFORMATION:
; APPLICANT: ELAKSIN, Daniel
; TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
; FILE REFERENCE: 87534-2800
; CURRENT APPLICATION NUMBER: US/09/858,349
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 136
; TYPE: PRT
; ORGANISM: mouse hybridoma specific for H-2D + RGPGRFVTI peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (99)..(107)
; OTHER INFORMATION: variable
US-09-858-349-2
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Query Match 84.3%; Score 75; DB 3; Length 136;
Best Local Similarity 81.2%; Pred. No. 0.00047;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGSNNYNPSLKN 66
|||||
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RESULT 11
US-09-144-886-70
; Sequence 70, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
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; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 70
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 2B6 region VH epitope 3
US-09-144-886-70
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Query Match 80.9%; Score 72; DB 3; Length 121;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 1 YISYDGTNNYKPSLKD 16
Db 50 YINYDGSNNYNPSLKN 65
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RESULT 12
US-10-632-706-67
; Sequence 67, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 67
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-67
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Query Match 80.9%; Score 72; DB 4; Length 121;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 1 YISYDGTNNYKPSLKD 16
Db 50 YINYDGSNNYNPSLKN 65
|||
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RESULT 13
US-10-735-916A-70
; Sequence 70, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
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; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 70  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-70

Query Match 79.8%; Score 71; DB 5; Length 118;  
Best Local Similarity 75.0%; Pred. No. 0.0018;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
||:|||||:|||||:  
Db 51 YINYDGNNNYPSLKN 66

## RESULT 14

US-10-372-481-17  
; Sequence 17, Application US/10372481  
; Publication No. US20030202975A1  
; GENERAL INFORMATION:

; APPLICANT: Tedder, Thomas F.  
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES

; FILE REFERENCE: 5405.306  
; CURRENT APPLICATION NUMBER: US/10/372,481  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/US03/05549  
; PRIOR FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 60/420,472  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/359,419  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 17  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-372-481-17

Query Match 78.7%; Score 70; DB 4; Length 118;  
Best Local Similarity 75.0%; Pred. No. 0.0026;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
||:|||||:|||||:  
Db 51 YIRYDGSNNYPSLKN 66

## RESULT 15

US-10-371-797-17  
; Sequence 17, Application US/10371797  
; Publication No. US20040001828A1  
; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: TUSCANO, Joseph  
; APPLICANT: TEDDER, Thomas  
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22  
; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 39754-0951  
; CURRENT APPLICATION NUMBER: US/10/371,797  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 60/420,472  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/359,419  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-371-797-17

Query Match 78.7%; Score 70; DB 4; Length 118;  
Best Local Similarity 75.0%; Pred. No. 0.0026;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
||:|||||:|||||:  
Db 51 YIRYDGSNNYPSLKN 66

Search completed: December 30, 2005, 14:14:58  
Job time : 123.968 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 5.93548 Seconds  
(without alignments)  
20.187 Million cell updates/sec

Title: US-10-735-916a-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62

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Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /cgn2\_6/ptodata/1/pubaa/US08 NEW PUB pep.\*  
2: /cgn2\_6/ptodata/1/pubaa/US06 NEW PUB pep.\*  
3: /cgn2\_6/ptodata/1/pubaa/US07 NEW PUB pep.\*  
4: /cgn2\_6/ptodata/1/pubaa/PCT NEW PUB pep.\*  
5: /cgn2\_6/ptodata/1/pubaa/US03 NEW PUB pep.\*  
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7: /cgn2\_6/ptodata/1/pubaa/US11 NEW PUB pep.\*  
8: /cgn2\_6/ptodata/1/pubaa/US60 NEW PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	16	7 US-11-012-353-10	Sequence 10, Appl
2	89	100.0	117	7 US-11-012-353-69	Sequence 69, Appl
3	89	100.0	117	7 US-11-012-353-75	Sequence 75, Appl
4	89	100.0	117	7 US-11-012-353-79	Sequence 79, Appl
5	89	100.0	117	7 US-11-012-353-83	Sequence 83, Appl
6	89	100.0	127	7 US-11-012-353-52	Sequence 52, Appl
7	89	100.0	135	7 US-11-012-353-77	Sequence 77, Appl
8	89	100.0	135	7 US-11-012-353-81	Sequence 81, Appl
9	89	100.0	135	7 US-11-012-353-85	Sequence 85, Appl
10	71	79.8	118	7 US-11-012-353-70	Sequence 70, Appl
11	70	78.7	259	6 US-10-512-184-34	Sequence 34, Appl
12	70	78.7	371	6 US-10-512-184-71	Sequence 71, Appl
13	70	78.7	626	6 US-10-512-184-49	Sequence 49, Appl
14	56	62.9	97	7 US-11-144-248-36	Sequence 36, Appl
15	56	62.9	97	7 US-11-054-669-42	Sequence 42, Appl
16	56	62.9	97	7 US-11-054-669-52	Sequence 52, Appl
17	56	62.9	97	7 US-11-054-669-53	Sequence 53, Appl
18	56	62.9	97	7 US-11-084-554-54	Sequence 54, Appl
19	56	62.9	97	7 US-11-144-222-36	Sequence 36, Appl
20	56	62.9	99	7 US-11-054-669-43	Sequence 43, Appl
21	56	62.9	99	7 US-11-084-554-55	Sequence 55, Appl
22	56	62.9	113	7 US-11-144-248-20	Sequence 20, Appl
23	56	62.9	113	7 US-11-144-222-20	Sequence 20, Appl
24	55	61.8	98	7 US-11-084-554-10	Sequence 10, Appl
25	55	61.8	114	6 US-10-923-327-5	Sequence 5, Appl

26 55 61.8 229 6 US-10-923-327-13 Sequence 13, Appl  
27 55 61.8 233 6 US-10-923-327-18 Sequence 18, Appl  
28 55 61.8 248 6 US-10-923-327-15 Sequence 15, Appl  
29 55 61.8 451 6 US-10-923-327-7 Sequence 7, Appl  
30 55 61.8 451 6 US-10-923-327-9 Sequence 9, Appl  
31 54 60.7 118 7 US-11-012-353-71 Sequence 71, Appl  
32 53 59.6 249 7 US-11-054-515-1339 Sequence 2002, Ap  
33 53 59.6 253 7 US-11-054-515-1339 Sequence 1339, Ap  
34 51 57.3 102 7 US-11-185-615-4 Sequence 4, Appl  
35 51 57.3 246 7 US-11-054-515-1847 Sequence 1847, Ap  
36 51 57.3 247 7 US-11-054-515-1993 Sequence 1993, Ap  
37 48 53.9 98 7 US-11-054-669-35 Sequence 35, Appl  
38 48 53.9 98 7 US-11-084-554-49 Sequence 49, Appl  
39 48 53.9 99 7 US-11-054-669-36 Sequence 36, Appl  
40 48 53.9 99 7 US-11-054-669-38 Sequence 38, Appl  
41 48 53.9 99 7 US-11-054-669-39 Sequence 39, Appl  
42 48 53.9 99 7 US-11-084-554-50 Sequence 50, Appl  
43 48 53.9 247 7 US-11-054-515-1981 Sequence 1981, Ap  
44 48 53.9 251 7 US-11-054-515-1316 Sequence 1316, Ap  
45 48 53.9 253 7 US-11-054-515-1619 Sequence 1619, Ap

#### ALIGNMENTS

RESULT 1  
US-11-012-353-10  
; Sequence 10, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GORTSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HARUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 01753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 10  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-10

Query Match 100.0%; Score 89; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
Db 1 YISYDGTNNYKPSLKD 16

RESULT 2  
US-11-012-353-69  
; Sequence 69, Application US/11012353

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/ Publication No. US20050249730A1
/ GENERAL INFORMATION:
/ APPLICANT: GOETSCH, LILIANE
/ APPLICANT: CORVAIA, NATHALIE
/ APPLICANT: DUFLOS, ALAIN
/ APPLICANT: HAEUW, JEAN-FRANCOIS
/ APPLICANT: LEGER, OLIVIER
/ APPLICANT: BECK, ALAIN
/ TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
/ TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
/ FILE REFERENCE: 017753-198
/ CURRENT APPLICATION NUMBER: US/11/012,353
/ CURRENT FILING DATE: 2004-12-16
/ PRIOR APPLICATION NUMBER: 10/735,916
/ PRIOR FILING DATE: 2003-12-16
/ PRIOR APPLICATION NUMBER: FR 0308538
/ PRIOR FILING DATE: 2003-07-11
/ PRIOR APPLICATION NUMBER: PCT/FR03/00178
/ PRIOR FILING DATE: 2003-01-20
/ PRIOR APPLICATION NUMBER: FR 0205753
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: FR 0200653
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: FR 0200654
/ PRIOR FILING DATE: 2002-01-18
/ NUMBER OF SEQ ID NOS: 162
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 69
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-11-012-353-69

Query Match      100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGTNNYKPSLKD 66

RESULT 3
US-11-012-353-75
/ Sequence 75, Application US/11012353
/ Publication No. US20050249730A1
/ GENERAL INFORMATION:
/ APPLICANT: GOETSCH, LILIANE
/ APPLICANT: DUFLOS, ALAIN
/ APPLICANT: HAEUW, JEAN-FRANCOIS
/ APPLICANT: LEGER, OLIVIER
/ APPLICANT: BECK, ALAIN
/ TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
/ TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
/ FILE REFERENCE: 017753-198
/ CURRENT APPLICATION NUMBER: US/11/012,353
/ CURRENT FILING DATE: 2004-12-16
/ PRIOR APPLICATION NUMBER: 10/735,916
/ PRIOR FILING DATE: 2003-12-16
/ PRIOR APPLICATION NUMBER: FR 0308538
/ PRIOR FILING DATE: 2003-07-11
/ PRIOR APPLICATION NUMBER: PCT/FR03/00178
/ PRIOR FILING DATE: 2003-01-20
/ PRIOR APPLICATION NUMBER: FR 0205753
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: FR 0200653
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: FR 0200654
/ NUMBER OF SEQ ID NOS: 162
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 79
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-012-353-79

Query Match      100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGTNNYKPSLKD 66

RESULT 5
US-11-012-353-83
/ Sequence 83, Application US/11012353
/ Publication No. US20050249730A1
/ GENERAL INFORMATION:
/ APPLICANT: GOETSCH, LILIANE
/ APPLICANT: DUFLOS, ALAIN
/ APPLICANT: HAEUW, JEAN-FRANCOIS
/ APPLICANT: LEGER, OLIVIER
/ APPLICANT: BECK, ALAIN
/ TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
/ TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
/ FILE REFERENCE: 017753-198
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; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 83  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-83

Query Match 100.0%; Score 89; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
|||||

Db 51 YISYDGTNNYKPSLKD 66  
|||||

## RESULT 6

US-11-012-353-52  
; Sequence 52, Application US/11/012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 52  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-52

Query Match 100.0%; Score 89; DB 7; Length 127;  
Best Local Similarity 100.0%; Pred. No. 2.2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
|||||

Db 61 YISYDGTNNYKPSLKD 76

## RESULT 7

US-11-012-353-77  
; Sequence 77, Application US/11/012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 77  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-77

Query Match 100.0%; Score 89; DB 7; Length 135;  
Best Local Similarity 100.0%; Pred. No. 2.4e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
|||||

Db 69 YISYDGTNNYKPSLKD 84  
|||||

## RESULT 8

US-11-012-353-81  
; Sequence 81, Application US/11/012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 81  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-81

Query Match 100.0%; Score 89; DB 7; Length 127;  
Best Local Similarity 100.0%; Pred. No. 2.2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
|||||





Publication No. US20050244901A1  
GENERAL INFORMATION:  
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.  
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant  
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease  
TITLE OF INVENTION: resistance against fungi  
FILE REFERENCE: 3581.01US01  
CURRENT APPLICATION NUMBER: US/10/512,184  
CURRENT FILING DATE: 2004-10-22  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 71  
LENGTH: 371  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: precursor  
OTHER INFORMATION: fusion protein comprising ACE - linker -  
OTHER INFORMATION: scFv PL2.  
US-10-512-184-71  
Query Match 78.7%; Score 70; DB 6; Length 371;  
Best Local Similarity 81.2%; Pred. No. 0.00011;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YISYDGTNNYKPSLKD 16  
Db 165 YISYDGTNNNNPSLKN 180  
RESULT 13  
US-10-512-184-49  
Sequence 49, Application US/10512184  
Publication No. US20050244901A1  
GENERAL INFORMATION:  
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.  
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant  
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease  
TITLE OF INVENTION: resistance against fungi  
FILE REFERENCE: 3581.01US01  
CURRENT APPLICATION NUMBER: US/10/512,184  
CURRENT FILING DATE: 2004-10-22  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 49  
LENGTH: 626  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: fusion protein  
OTHER INFORMATION: comprising the leader peptide - chitinase- linker  
OTHER INFORMATION: - scFv PL2 - cmcy/His6.  
US-10-512-184-49  
Query Match 78.7%; Score 70; DB 6; Length 626;  
Best Local Similarity 81.2%; Pred. No. 0.00019;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YISYDGTNNYKPSLKD 16  
Db 394 YISYDGTNNNNPSLKN 409  
RESULT 14  
US-11-144-248-36  
Sequence 36, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Corvaian, Jose R.

APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PF2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 36  
LENGTH: 97  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-36  
Query Match 62.9%; Score 56; DB 7; Length 97;  
Best Local Similarity 66.7%; Pred. No. 0.0055;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 YISYDGTNNYKPSLK 15  
Db 50 YIYSGSTNNPSLK 64  
RESULT 15  
US-11-054-669-42  
Sequence 42, Application US/11054669  
Publication No. US20050261480A1  
GENERAL INFORMATION:  
APPLICANT: Foote, Jefferson  
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES  
FILE REFERENCE: 30219/US/3  
CURRENT APPLICATION NUMBER: US/11/054,669  
CURRENT FILING DATE: 2005-02-08  
PRIOR APPLICATION NUMBER: US 10/194,975  
PRIOR FILING DATE: 2002-07-12  
PRIOR APPLICATION NUMBER: US 60/305,111  
PRIOR FILING DATE: 2001-07-12  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 42  
LENGTH: 97  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-669-42  
Query Match 62.9%; Score 56; DB 7; Length 97;  
Best Local Similarity 66.7%; Pred. No. 0.0055;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 YISYDGTNNYKPSLK 15  
Db 50 YIYSGSTNNPSLK 64  
Search completed: December 30, 2005, 14:15:22  
Job time : 6.93548 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:37:27 ; Search time 132.5 Seconds  
(without alignments)  
53.057 Million cell updates/sec

Title: US-10-735-916A-10  
Perfect score: 89  
Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 19975

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	16	7	ADJ76844 CDR seque
2	89	100.0	16	9	ADZ67014 Murine in
3	75	84.3	16	9	Aea40141 TNF resis
4	73	82.0	16	9	ADZ45407 Murine fa
5	72	80.9	16	9	ADZ45343 Murine fa
6	72	80.9	16	9	ADZ51256 Amino aci
7	72	80.9	16	9	ADZ42130 Mouse ant
8	70	78.7	16	9	ADZ45520 Murine fa
9	70	78.7	16	9	ADZ45311 Murine fa
10	70	78.7	16	9	ADZ51224 Amino aci
11	70	78.7	16	9	ADZ42098 Murine ant
12	68	76.4	16	9	ADZ45479 Murine fa
13	62	69.7	16	4	AB73650 Murine mo
14	58	65.2	16	2	AAR24718 Sequence
15	57	64.0	16	9	AEC20782 M-CSF spe
16	56	62.9	16	5	Aau81236 Human trk
17	56	62.9	16	8	ADO58086 S9 cell d
18	56	62.9	16	9	ADZ66143 VH CDR2 f
19	55	61.8	16	2	AAW90327 Human ant
20	55	61.8	16	9	ADX98335 Human ant
21	53	59.6	16	8	ADL26968 Murine de
22	51	57.3	16	2	AAW90297 Human ant
23	51	57.3	16	5	AQ017789 CDR2 regi
24	50	56.2	16	8	AUS19315 Heavy Cha

25	49	55.1	16	2	AAW01151 MAB 1.4 h
26	49	55.1	16	2	AAW24541 CDR #2 of
27	49	55.1	16	2	AAW44174 Monoclonal
28	49	55.1	16	9	AEB00995 Human IPI
29	48	53.9	16	4	AAE10502 Humanised
30	48	53.9	16	4	AAE10499 Humanised
31	48	53.9	16	4	AAE10527 Humanised
32	48	53.9	16	4	AAE10500 Humanised
33	48	53.9	16	4	AAU81239 Human trk
34	48	53.9	16	5	ABP66457 Human RSV
35	48	53.9	16	5	ABP66395 Human RSV
36	48	53.9	16	5	ABP66379 Human RSV
37	48	53.9	16	5	ABP66391 Human RSV
38	48	53.9	16	5	AAE28034 Human mod
39	48	53.9	16	5	AAE28046 Human mod
40	48	53.9	16	5	AAE28050 Human mod
41	48	53.9	16	6	ABU69320 Respirato
42	48	53.9	16	6	ABU69242 Respirato
43	48	53.9	16	6	ABU69254 Respirato
44	48	53.9	16	6	ABU69258 Respirato
45	48	53.9	16	7	ADE35749 SYNAGIS a

## ALIGNMENTS

RESULT 1  
ADJ76844  
ID ADJ76844 standard; peptide; 16 AA.  
XX AC ADJ76844;  
XX AC  
DT 06-MAY-2004 (first entry)  
XX  
DE CDR sequence for anti-IGF-1R antibody.

XX cytosolic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.

XX Mus musculus.  
XX WO2003059951-A2.  
XX PD 24-JUL-2003.  
XX PF 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000553.  
PR 18-JAN-2002; 2002FR-00000554.  
PR 07-MAY-2002; 2002FR-00005753.  
XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;  
FI WPI; 2003-569653/53.  
XX N-PSDB; ADJ76843.

XX New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.

XX Claim 1; SEQ ID NO 10; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC IR) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 89; DB 7; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 |||||  
 Db 1 YISYDGTNNYKPSLKD 16

RESULT 2  
 ADZ67014  
 ID ADZ67014 standard; peptide; 16 AA.

XX AC ADZ67014;

XX DT 30-JUN-2005 (first entry)

XX DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:10.

XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; androgen; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX OS Mus musculus.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOET/) GOETSCH L.

XX PA (CORV/) CORVAIA N.

XX PA (LEGE/) LEGER O.

XX PA (DUFL/) DUFLOS A.

XX PA (HAEU/) HAEUW J.

XX PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX DR N-PSDB; ADZ67013.

XX DR WPI; 2005-321968/33.

XX PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

XX PT antibody or its functional fragment, being capable of binding human IGF-IR

XX PT and specifically inhibiting tyrosine kinase activity of receptor,

XX PT useful for treating cancer.

XX PS Claim 1; SEQ ID NO 10; 125pp; English.

XX CC The invention relates to a novel isolated anti-insulin-like growth factor

XX CC I receptor (IGF-IR) antibody (I) or its functional fragment, being

XX CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HPR2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 89; DB 9; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 |||||  
 Db 1 YISYDGTNNYKPSLKD 16

RESULT 3

AEA40141

ID AEA40141 standard; peptide; 16 AA.

XX AC AEA40141;

XX DT 28-JUL-2005 (first entry)

XX DE TNF resistant monoclonal antibody VH region, F6VH CDR2.

XX KW tumor necrosis factor; TNF; monoclonal antibody; F6 mAb;  
 XX light chain variable region; heavy chain variable region; F6VH.

XX OS Unidentified.

XX PN CN1544466-A.

XX PD 10-NOV-2004.

XX PF 13-NOV-2003; 2003CN-01105919.

XX PR 13-NOV-2003; 2003CN-01105919.

XX PA (UYFO-) UNIV FOURTH MILITARY MEDICAL.

XX PI Jin B, Liu X, Zhu C;

XX DR WPI: 2005-153078/17.

XX DR N-PSDB; AEA40140.

XX Variable region gene of high affinity monoclonal antibody of tumor  
PT necrosis factor and its preparation.  
XX  
XX Claim 1; Page 3; 20pp; Chinese.  
XX  
CC The invention relates to a method for preparing variable region genes of  
CC high affinity tumor necrosis factor (TNF) resistant monoclonal antibody  
CC (F6 mAb). The method comprises using recombinant human TNF immune BALB/c  
CC mouse to prepare mouse anti-TNF monoclonal antibody, screening high  
CC affinity F6 mAb using an indirect enzyme linked immunosorbent assay  
CC (ELISA). By cloning the monoclonal antibody light chain and heavy chain  
CC variable region (VL and VH respectively) genes, the monoclonal antibody  
CC light chain and heavy chain variable region gene sequence and amino acid  
CC sequence can be obtained, and the identity of the gene sequence and  
CC protein sequence can be confirmed. This sequence represents  
CC complementarity determining region, CDR2 of F6VH.  
XX  
XX Sequence 16 AA;  
SQ

Query Match 84.3%; Score 75; DB 9; Length 16;  
Best Local Similarity 81.2%; Pred. No. 0.0001;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
| | | | | : | | | | |  
Db 1 YISYDGSNNYNPSLKN 16

RESULT 4  
ADZ45407  
ID ADZ45407 standard; peptide; 16 AA.  
XX  
AC ADZ45407;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Murine factor IX directed antibody CDR2 SEQ ID NO 111.  
XX  
KW bispecific antibody; blood coagulation factor VIII; bleeding;  
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;  
KW factor VIII deficiency; von Willebrand's disease; hemostatic;  
KW immunostimulator; antibody engineering.  
XX  
OS Mus musculus.  
XX  
XX WO2005035756-A1.  
XX  
XX 21-APR-2005.  
XX  
XX 08-OCT-2004; 2004WO-JP014911.  
XX  
XX 10-OCT-2003; 2003WO-JP013062.  
XX  
XX 14-OCT-2003; 2003WO-JP013123.  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX  
XX Hattori K, Kojima T, Miyazaki T, Soeda T;  
XX  
XX WPI; 2005-315563/32.  
XX

Novel bispecific antibody substituting for function of cofactor that  
PT enhances enzyme reaction, and recognizing both enzyme and substrates of  
PT enzyme, useful for treating hemophilia A.  
XX  
XX Disclosure; SEQ ID NO 111; 69pp; Japanese.

XX This invention describes a novel bispecific antibody which can act as a  
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and  
CC the enzyme substrate. The antibody specifically binds to blood  
CC coagulation factor VIII. The invention also describes a composition  
CC comprising the antibody and a carrier, a kit useful in preventing and/or  
CC treating bleeding associated with a disorder or from a disease caused by

CC bleeding. The composition includes blood coagulation factor VIII. The  
CC antibody of the invention can be a blood-coagulation fibrinolysis related  
CC factor including blood-coagulation factor VIII, blood coagulation factor  
CC X, or blood-coagulation factor IX. The antibody comprises a complementary  
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor  
CC antibody. The novel antibody or composition is useful for preventing  
CC and/or treating a disease accompanying bleeding, or the disease resulting  
CC from bleeding, where the disease accompanying bleeding or the disease  
CC resulting from bleeding develops and/or progresses by an active reduction  
CC or deletion of the blood coagulation factor VIII. The disease the  
CC develops and/or progresses by an active reduction or deletion of the  
CC blood coagulation factor VIII and/or activation blood coagulation factor  
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is  
CC an acquired hemophilia A. This sequence represents a fragment of the  
CC antibody described in the method of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 16 AA;  
SQ

Query Match 82.0%; Score 73; DB 9; Length 16;  
Best Local Similarity 81.2%; Pred. No. 0.00021;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16  
| | | | | : | | | | |  
Db 1 YISYDGTNNYNPSLKN 16

RESULT 5  
ADZ45343  
ID ADZ45343 standard; peptide; 16 AA.  
XX  
AC ADZ45343;  
XX

DT 30-JUN-2005 (first entry)  
XX  
DE Murine factor IX directed antibody CDR2 SEQ ID NO 47.  
XX

KW bispecific antibody; blood coagulation factor VIII; bleeding;  
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;  
KW factor VIII deficiency; von Willebrand's disease; hemostatic;  
KW immunostimulator; antibody engineering.  
XX  
OS Mus musculus.

XX WO2005035756-A1.  
XX  
XX 21-APR-2005.  
XX  
XX 08-OCT-2004; 2004WO-JP014911.  
XX  
XX 10-OCT-2003; 2003WO-JP013062.  
XX  
XX 14-OCT-2003; 2003WO-JP013123.  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX

XX Hattori K, Kojima T, Miyazaki T, Soeda T;  
XX  
XX WPI; 2005-315563/32.  
XX

Novel bispecific antibody substituting for function of cofactor that  
PT enhances enzyme reaction, and recognizing both enzyme and substrates of  
PT enzyme, useful for treating hemophilia A.  
XX  
XX Claim 5; SEQ ID NO 47; 69pp; Japanese.

XX This invention describes a novel bispecific antibody which can act as a  
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and  
CC the enzyme substrate. The antibody specifically binds to blood  
CC coagulation factor VIII. The invention also describes a composition  
CC comprising the antibody and a carrier, a kit useful in preventing and/or

CC treating bleeding associated with a disorder or from a disease caused by  
 CC bleeding. The composition includes blood coagulation factor VIII. The  
 CC antibody of the invention can be a blood-coagulation fibrinolysis related  
 CC factor including blood-coagulation factor VIII, blood coagulation factor  
 CC X, or blood-coagulation factor IX. The antibody comprises a complementary  
 CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor  
 CC antibody. The novel antibody or composition is useful for preventing  
 CC and/or treating a disease accompanying bleeding, or the disease resulting  
 CC from bleeding, where the disease accompanying bleeding or the disease  
 CC resulting from bleeding develops and/or progresses by an active reduction  
 CC or deletion of the blood coagulation factor VIII. The disease the  
 CC develops and/or progresses by an active reduction or deletion of the  
 CC blood coagulation factor VIII and/or activation blood coagulation factor  
 CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is  
 CC an acquired hemophilia A. This sequence represents a fragment of the  
 CC antibody described in the method of the invention. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 16 AA;

Query Match 80.9%; Score 72; DB 9; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 0.0003;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 ||:|||||  
 Db 1 YINYDGSNNYPSLKN 16

RESULT 6  
 ADZ51256  
 ID ADZ51256 standard; peptide; 16 AA.

AC ADZ51256;  
 XX  
 XX  
 DT 30-JUN-2005 (first entry)  
 DE Amino acid sequence of a variable heavy chain region CDR.

XX bispecific antibody; AR1 chain; AR2 chain; hemostatic; bleeding;  
 KW antibody therapy; blood coagulation factor VIII; factor VIII deficiency;  
 KW von willebrand's disease; heavy chain; complementarity determining region;  
 KW CDR.

XX Mus musculus.  
 XX  
 XX WO2005035753-A1.  
 XX

PD 21-APR-2005.

XX 10-OCT-2003; 2003WO-JP013062.

XX 10-OCT-2003; 2003WO-JP013062.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;  
 PI Kasutani K, Ishii S;

DR WPI; 2005-315560/32.

XX Novel bispecific antibody substituting for functional protein or  
 PT substituting for ligand for receptor comprising two types of molecules,  
 PT useful as pharmaceutical for treating or preventing diseases e.g.  
 PT bleeding.

XX Claim 18; SEQ ID NO 73; 143pp; Japanese.

XX The specification describes a bispecific antibody substituting for  
 CC functional protein or substituting for a ligand for a receptor comprising  
 CC two types of molecules. The antibody comprises AR1 and AR2 chains.

CC Bispecific antibodies of the invention are useful for preventing and  
 CC treating bleeding, diseases accompanying bleeding or diseases resulting  
 CC from bleeding. These diseases develop or progress by active reduction of  
 CC blood coagulation factor VIII/activated blood coagulation factor VIII,  
 CC e.g. hemophilia A, acquired hemophilia or von Willebrand disease. The  
 CC present sequence represents a complementarity determining region (CDR)  
 CC from a variable heavy chain region, which was used to construct  
 CC bispecific antibodies of the invention.  
 XX

SQ Sequence 16 AA;

Query Match 80.9%; Score 72; DB 9; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 0.0003;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 ||:|||||  
 Db 1 YINYDGSNNYPSLKN 16

RESULT 7  
 ADZ42130

ID ADZ42130 standard; peptide; 16 AA.

XX AC ADZ42130;

XX 30-JUN-2005 (first entry)

DE Mouse anti-s AR antibody heavy chain CDR 2 SEQ ID NO 73.

XX viral infection; neoplasm; immune disorder; bleeding; infection;  
 KW cardiovascular disease; Virucide; Hepatotropic; Antiinflammatory;  
 KW Neuroprotective; Hemostatic; Cytostatic; Immunotherapy; antibody.

OS Mus musculus.

XX WO2005035754-A1.

XX 21-APR-2005.

XX 14-OCT-2003; 2003WO-JP013123.

XX 14-OCT-2003; 2003WO-JP013123.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;  
 PI Kasutani K, Ishii S;

DR WPI; 2005-315561/32.

XX Novel bispecific antibody substituting for functional protein and having  
 PT ligand functional alternative activity to receptor containing  
 PT heteromolecule, useful for preventing/treating viral disease,  
 PT immunological disease or bleeding.

XX Claim 28; SEQ ID NO 73; 151pp; Japanese.

XX The invention relates to a bispecific antibody (I) substituting for: a  
 CC functional protein and having ligand functional alternative activity with  
 CC respect to receptor containing heteromolecule; or a functional cofactor  
 CC which enhances an enzyme reaction and recognizes both substrates of  
 CC enzyme. Also claimed are a composition (II) containing (I). (I) and (II)  
 CC are useful for preventing and/or treating viral disease, neoplasm, or  
 CC immunological disease, or bleeding or disease resulting from bleeding.  
 CC The viral disease is a hepatitis C virus or hepatitis B virus infection  
 CC such as an acute or chronic liver cirrhosis or hepatic carcinoma. The  
 CC neoplasms are chronic myeloid leukemia, malignant melanoma, multiple  
 CC myeloma, renal carcinoma, glioblastoma, medulloblastoma, astrocytoma,  
 CC hairy cell leukemia, AIDS-related Kaposi's sarcoma, skin T cell lymphoma  
 CC or non-Hodgkin's lymphoma. The immunological disease is multiple  
 CC sclerosis. The bleeding disease is the disease resulting from the active  
 CC reduction or a defect of blood coagulation factor VIII such as hemophilia

CC or von Willebrand disease. (II) is useful for manufacturing (I). (I) has  
CC high stability and low antigenicity in blood. The present sequence  
CC represents a mouse anti-AR antibody CDR.  
XX  
SQ Sequence 16 AA;  
Query Match 80.9%; Score 72; DB 9; Length 16;  
Best Local Similarity 75.0%; Pred. No. 0.0003;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YISYDGTNNYKPSLKD 16  
| | | | | | | | | | | | | | | |  
Db 1 YINYDGSNNYNPSLKN 16  
| | | | | | | | | | | | | | | |  
RESULT 8  
ADZ45520  
ID ADZ45520 standard; peptide; 16 AA.  
XX  
AC ADZ45520;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Murine factor IX directed antibody CDR2 SEQ ID NO 224.  
XX  
KW bispecific antibody; blood coagulation factor VIII; bleeding;  
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;  
KW factor VIII deficiency; von Willebrand's disease; hemostatic;  
KW immunostimulator; antibody engineering; ds; gene.  
XX  
OS Mus musculus.  
XX  
FN WO2005035756-A1.  
XX  
PD 21-APR-2005.  
XX  
PF 08-OCT-2004; 2004WO-JP014911.  
XX  
PR 10-OCT-2003; 2003WO-JP013062.  
PR 14-OCT-2003; 2003WO-JP013123.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Hattori K, Kojima T, Miyazaki T, Soeda T;  
XX  
DR N-PSDB; ADZ45519.  
XX  
PT Novel bispecific antibody substituting for function of cofactor that  
PT enhances enzyme reaction, and recognizing both enzyme and substrates of  
PT enzyme, useful for treating hemophilia A.  
XX  
PS Disclosure; SEQ ID NO 224; 69pp; Japanese.  
XX  
CC This invention describes a novel bispecific antibody which can act as a  
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and  
CC the enzyme substrate. The antibody specifically binds to blood  
CC coagulation factor VIII. The invention also describes a composition  
CC comprising the antibody and a carrier, a kit useful in preventing and/or  
CC treating bleeding associated with a disorder or from a disease caused by  
CC bleeding. The composition includes blood coagulation factor VIII. The  
CC antibody of the invention can be a blood-coagulation fibrinolysis related  
CC factor including blood-coagulation factor VIII, blood coagulation factor  
CC X, or blood-coagulation factor IX. The antibody comprises a complementary  
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor  
CC antibody. The novel antibody or composition is useful for preventing  
CC and/or treating a disease accompanying bleeding, or the disease resulting  
CC from bleeding, where the disease accompanying bleeding or the disease  
CC resulting from bleeding develops and/or progresses by an active reduction  
CC or deletion of the blood coagulation factor VIII. The disease the  
CC develops and/or progresses by an active reduction or deletion of the  
CC blood coagulation factor VIII and/or activation blood coagulation factor  
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is

CC an acquired hemophilia A. This sequence encodes a fragment of the  
CC antibody described in the method of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 16 AA;  
Query Match 78.7%; Score 70; DB 9; Length 16;  
Best Local Similarity 75.0%; Pred. No. 0.00061;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YISYDGTNNYKPSLKD 16  
| | | | | | | | | | | | | | | |  
Db 1 YISFDGTNDYNPSLKN 16  
| | | | | | | | | | | | | | | |  
RESULT 9  
ADZ45311  
ID ADZ45311 standard; peptide; 16 AA.  
XX  
AC ADZ45311;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Murine factor IX directed antibody CDR2 SEQ ID NO 15.  
XX  
KW bispecific antibody; blood coagulation factor VIII; bleeding;  
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;  
KW factor VIII deficiency; von Willebrand's disease; hemostatic;  
KW immunostimulator; antibody engineering.  
XX  
OS Mus musculus.  
XX  
FN WO2005035756-A1.  
XX  
PD 21-APR-2005.  
XX  
PF 08-OCT-2004; 2004WO-JP014911.  
XX  
PR 10-OCT-2003; 2003WO-JP013062.  
PR 14-OCT-2003; 2003WO-JP013123.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Hattori K, Kojima T, Miyazaki T, Soeda T;  
XX  
DR WPI; 2005-315563/32.  
XX  
PT Novel bispecific antibody substituting for function of cofactor that  
PT enhances enzyme reaction, and recognizing both enzyme and substrates of  
PT enzyme, useful for treating hemophilia A.  
XX  
PS Claim 5; SEQ ID NO 15; 69pp; Japanese.  
XX  
CC This invention describes a novel bispecific antibody which can act as a  
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and  
CC the enzyme substrate. The antibody specifically binds to blood  
CC coagulation factor VIII. The invention also describes a composition  
CC comprising the antibody and a carrier, a kit useful in preventing and/or  
CC treating bleeding associated with a disorder or from a disease caused by  
CC bleeding. The composition includes blood coagulation factor VIII. The  
CC antibody of the invention can be a blood-coagulation fibrinolysis related  
CC factor including blood-coagulation factor VIII, blood coagulation factor  
CC X, or blood-coagulation factor IX. The antibody comprises a complementary  
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor  
CC antibody. The novel antibody or composition is useful for preventing  
CC and/or treating a disease accompanying bleeding, or the disease resulting  
CC from bleeding, where the disease accompanying bleeding or the disease  
CC resulting from bleeding develops and/or progresses by an active reduction  
CC or deletion of the blood coagulation factor VIII. The disease the  
CC develops and/or progresses by an active reduction or deletion of the  
CC blood coagulation factor VIII and/or activation blood coagulation factor  
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is

CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is  
 CC an acquired hemophilia A. This sequence represents a fragment of the  
 CC antibody described in the method of the invention. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 16 AA;

Query Match 78.7%; Score 70; DB 9; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 0.00061;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
 |||:||||:||||:  
 Db 1 YISFDGTNDYNPSLKN 16

RESULT 10

ADZ51224  
 ID ADZ51224 standard; peptide; 16 AA.

XX AC ADZ51224;

XX DT 30-JUN-2005 (first entry)

XX DE Amino acid sequence of a variable heavy chain region CDR.

XX KW bispecific antibody; AR1 chain; AR2 chain; hemostatic; bleeding;  
 KW antibody therapy; blood coagulation factor VIII; factor VIII deficiency;  
 KW von Willebrand disease; heavy chain; complementarity determining region;  
 KW CDR.

XX OS Mus musculus.

XX PN WO2005035753-A1.

XX PD 21-APR-2005.

XX PF 10-OCT-2003; 2003WO-JP013062.

XX PR 10-OCT-2003; 2003WO-JP013062.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;  
 PI Kasutani K, Ishii S;

XX DR WPI; 2005-315560/32.

XX PT Novel bispecific antibody substituting for functional protein or  
 PT substituting for ligand for receptor comprising two types of molecules,  
 PT useful as pharmaceutical for treating or preventing diseases e.g.  
 PT bleeding.

XX PS Claim 18; SEQ ID NO 41; 143pp; Japanese.

XX CC The specification describes a bispecific antibody substituting for  
 CC functional protein or substituting for a ligand for a receptor comprising  
 CC two types of molecules. The antibody comprises AR1 and AR2 chains.  
 CC Bispecific antibodies of the invention are useful for preventing and  
 CC treating bleeding, diseases accompanying bleeding or diseases resulting  
 CC from bleeding. These diseases develop or progress by active reduction of  
 CC blood coagulation factor VIII/activated blood coagulation factor VIII,  
 CC e.g. hemophilia A, acquired hemophilia or von Willebrand disease. The  
 CC present sequence represents a complementarity determining region (CDR)  
 CC from a variable heavy chain region, which was used to construct  
 CC bispecific antibodies of the invention.

XX SQ Sequence 16 AA;

Query Match 78.7%; Score 70; DB 9; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 0.00061;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 |||:||||:||||:  
 Db 1 YISFDGTNDYNPSLKN 16

RESULT 11

ADZ42098  
 ID ADZ42098 standard; peptide; 16 AA.

XX AC ADZ42098;

XX DT 30-JUN-2005 (first entry)

XX DE Mouse anti-s AR antibody heavy chain CDR 2 SEQ ID NO 41.

XX KW viral infection; neoplasm; immune disorder; bleeding; infection;  
 KW cardiovascular disease; Virucide; Hepatotropic; Antiinflammatory;  
 KW Neuroprotective; Hemostatic; Cytostatic; Immunotherapy; antibody.

XX OS Mus musculus.

XX PN WO2005035754-A1.

XX PD 21-APR-2005.

XX PF 14-OCT-2003; 2003WO-JP013123.

XX PR 14-OCT-2003; 2003WO-JP013123.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;  
 PI Kasutani K, Ishii S;

XX DR WPI; 2005-315561/32.

XX PT Novel bispecific antibody substituting for functional protein and having  
 PT ligand functional alternative activity to receptor containing  
 PT heteromolecule, useful for preventing/treating viral disease,  
 PT immunological disease or bleeding.

XX PS Claim 28; SEQ ID NO 41; 151pp; Japanese.

XX CC The invention relates to a bispecific antibody (I) substituting for: a  
 CC functional protein and having ligand functional alternative activity with  
 CC respect to receptor containing heteromolecule; or a functional cofactor  
 CC which enhances an enzyme reaction and recognizes both substrates of  
 CC enzyme. Also claimed are a composition (II) containing (I). (I) and (II)  
 CC are useful for preventing and/or treating viral disease, neoplasm, or  
 CC immunological disease, or bleeding or disease resulting from bleeding.  
 CC The viral disease is a hepatitis C virus or hepatitis B virus infection  
 CC such as an acute or chronic liver cirrhosis or hepatic carcinoma. The  
 CC neoplasms are chronic myeloid leukemia, malignant melanoma, multiple  
 CC myeloma, renal carcinoma, glioblastoma, medulloblastoma, astrocytoma,  
 CC hairy cell leukemia, AIDS-related Kaposi's sarcoma, skin T cell lymphoma  
 CC or non-Hodgkin's lymphoma. The immunological disease is multiple  
 CC sclerosis. The bleeding disease is the disease resulting from the active  
 CC reduction or a defect of blood coagulation factor VIII such as hemophilia  
 CC or von Willebrand disease. (II) is useful for manufacturing (I). (I) has  
 CC high stability and low antigenicity in blood. The present sequence  
 CC represents a mouse anti-s AR antibody CDR.

XX SQ Sequence 16 AA;

Query Match 78.7%; Score 70; DB 9; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 0.00061;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNYKPSLKD 16  
 |||:||||:||||:  
 Db 1 YISFDGTNDYNPSLKN 16





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RESULT 14
AAR24718
ID AAR24718 standard; protein; 16 AA.
AC AAR24718;
XX
DT 25-MAR-2003 (revised)
DT 28-DEC-1992 (first entry)
XX
DE Sequence of an anti-urokinase antibody heavy chain variable region chain
DE designated 'K'.
XX
KW Chimeric monoclonal antibody; anti-urokinase antibody;
KW antithrombotic agent; myocardial infarction therapy.
XX
OS Mus musculus.
XX
PN EP491351-A2.
XX
PD 24-JUN-1992.
XX
PF 17-DEC-1991; 91EP-00121591.
XX
PR 18-DEC-1990; 90JP-00413829.
PR 11-NOV-1991; 91JP-00294464.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Iwasa S, Tada H, Watanabe T;
XX
DR WPI; 1992-209528/26.
XX
XX Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.
XX
XX Claim 21; Page 50; 87pp; English.
XX
XX The inventors claim a chimeric monoclonal antibody which contains a
CC urokinase-recognising antibody heavy chain variable region contg. at least
CC one of the polypeptide chains G, H and I(AAR24717,R24718,AAR24719) and a
CC human antibody heavy chain constant region. The chimeric Abs can be used
CC both in vivo and in vitro and, since they have very low immunogenicity as
CC compared with mouse Abs, they can be administered to humans for
CC diagnostic and therapeutic purposes. They are also more stable and show a
CC longer half-life in the blood as compared with the original mouse Abs.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 16 AA;
Query Match 65.2%; Score 58; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.048;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
||:||||:|||||
Db 1 YINYSGTTSYNPSLK 15

RESULT 15
AEC20782
ID AEC20782 standard; peptide; 16 AA.
XX
AC AEC20782;
XX
DT 20-OCT-2005 (first entry)
XX
DE M-CSF specific murine antibody consensus heavy chain CDR2.
DE
DE endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;
KW antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer;
KW
```

```
KW cardiovascular-gen.; degeneration; eating-disorders-gen.;
KW endocrine disease; endocrine-gen.; endocrine-gen.; gastrointestinal-gen.;
KW genetic disorder; heavy chain; hepatotropic; hypercalcemia;
KW immune disorder; immunotherapy; inflammation; monoclonal antibody;
KW mouth disease; musculoskeletal disease; neoplasia; nephrotropic;
KW osteopathic; osteoporosis; osteoporosis; osteoporosis; osteoporosis;
KW periodontal disease; pharmaceutical; rheumatoid arthritis.
XX
XX Mus musculus.
OS
XX WO2005068503-A2.
PN
XX 28-JUL-2005.
PD
XX
XX 06-JAN-2005; 2005WO-US000546.
XX
XX 07-JAN-2004; 2004US-0535181P.
PR
XX 02-JUN-2004; 2004US-0576417P.
XX
XX (CHIR ) CHIRON CORP.
PA (XOMA ) XOMA TECHNOLOGY LTD.
XX
XX Liu C, Zimmerman DL, Harrowe GM, Koths K, Kavanaugh WM, Long L;
PI Calderon-Cacia M, Horwitz AH;
XX
XX WPI; 2005-597707/61.
DR
XX
XX Novel non-murine antibody that competes with monoclonal antibody RX1 for
PT binding to macrophage colony stimulating factor, useful for treating
PT hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,
PT osteoporosis.
XX
XX Claim 14; SEQ ID NO 21; 269pp; English.
XX
XX The invention describes a non-murine antibody (I) that competes with
CC monoclonal antibody RX1 for binding to macrophage colony stimulating
CC factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has
CC the heavy chain and light chain amino acid sequences having a fully
CC defined 447 amino acids (SEQ ID NO. 2) and 214 amino acids (SEQ ID NO. 4)
CC sequences given in the specification, respectively. (I) is useful for
CC preventing a subject afflicted with a disease that causes or contributes
CC to osteolysis, where the antibody effectively reduces the severity of
CC bone loss associated with the disease. The disease is chosen from
CC metabolic bone diseases associated with relatively increased osteoclast
CC activity, including endocrinopathies, hypercalcemia, deficiency states,
CC chronic diseases, and hereditary diseases, cancer, osteoporosis,
CC osteoporosis, inflammation of bone associated with arthritis and
CC rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or
CC Paget's disease. (I) is useful for preventing or treating metastatic
CC cancer. Antibodies of the invention are useful for preventing or reducing
CC bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is
CC useful for manufacturing a medicament for preventing or reducing bone
CC loss in a patient exhibiting osteolysis, manufacturing a medicament for
CC treating a patient afflicted with a disease that causes or contributes to
CC osteolysis, and metastatic cancer to bone in a patient suffering from
CC metastatic cancer, for manufacturing a medicament for treating a patient
CC having cancer. (I) in synergistic combination, is useful for preparing a
CC medicament for treating a patient exhibiting osteolysis. This is the
CC amino acid sequence of macrophage colony stimulating factor (M-CSF)
CC specific murine antibody consensus heavy chain CDR1.
XX
XX Sequence 16 AA;
Query Match 64.0%; Score 57; DB 9; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.07;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
|||:|:|:|
Db 1 YISYSGTTSYNPSLK 15
```

Search completed: December 30, 2005, 14:20:02

Job time : 134.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:07:14 ; Search time 22.5 Seconds  
(without alignments)  
68.421 Million cell updates/sec

Title: US-10-735-916a-10  
Perfect score: 89  
Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	33.7	16	2 PH1589	Ig H chain V-D-J r
2	28	31.5	16	2 PH0749	T-cell receptor be
3	27	30.3	16	2 A49255	T-cell receptor be
4	23	25.8	16	2 A42291	tail fiber protein
5	23	25.8	16	2 A31963	pyruvate dehydroge
6	22	24.7	16	2 PH1351	Ig heavy chain DJ
7	22	24.7	16	2 E28027	protein P8 - curle
8	20	22.5	16	2 C45133	casein kinase II (
9	20	22.5	16	2 S01669	rRNA N-glycosidase
10	20	22.5	16	2 S28213	glutathione transf
11	20	22.5	16	2 PH1778	T cell receptor al
12	20	22.5	16	2 F49039	T-cell receptor be
13	20	22.5	16	2 B60278	24K antigen - Myco
14	19	21.3	16	2 PH0137	protein kinase, 80
15	19	21.3	16	2 S23184	redoxendonuclease
16	19	21.3	16	2 C44896	heat shock protein
17	18	20.2	16	2 S51610	hypothetical prote
18	18	20.2	16	2 B45895	T-cell surface gly
19	18	20.2	16	2 PH1622	Ig H chain V-D-J r
20	17	19.1	16	2 S00123	dihydroliipoamide S
21	17	19.1	16	2 A44101	calmodulin, vasoac
22	17	19.1	16	2 G49039	T-cell receptor be
23	17	19.1	16	2 PH1474	T-cell receptor be
24	17	19.1	16	2 PH1472	T-cell receptor be
25	17	19.1	16	2 PH1477	T-cell receptor be
26	17	19.1	16	2 PH1473	T-cell receptor be
27	17	19.1	16	2 PH1480	T-cell receptor be
28	17	19.1	16	2 A41170	photosystem II 6.1
29	17	19.1	16	2 PA0048	protein QA100047 -

ALIGNMENTS

RESULT 1

PH1589  
Ig H chain V-D-J region (wild-type clone 140) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1589  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A/Reference number: PH1580; MUID:93301609; PMID:8315387  
A/Accession: PH1589  
A/Molecule type: DNA  
A/Residues: 1-16 <LEV>

A/Cross-references: UNIPARC:UPI000017C6B0  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 33.7%; Score 30; DB 2; Length 16;  
Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYDGTNNY 10  
|||:|:  
Db 5 SYDGSPHY 12

RESULT 2

PH0749  
T-cell receptor beta chain (B83) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C/Accession: PH0749  
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-allelic exclusion and antigen-specific repertoire.  
A/Reference number: PH0746; MUID:92078846; PMID:1836010  
A/Accession: PH0749  
A/Molecule type: mRNA  
A/Residues: 1-16 <CAS>

A/Cross-references: UNIPARC:UPI0000115FA8; EMBL:X60840; NID:G50116; PIDN:CAA43233.1; PID  
A/Experimental source: T lymphocyte  
C/Keywords: T-cell receptor

Query Match 31.5%; Score 28; DB 2; Length 16;  
Best Local Similarity 71.4%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTNNYKP 12  
|||:|:  
Db 7 GTNNQAP 13

```
RESULT 3
A49255
T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: A49255
R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A:Reference number: A49039; MUID:92164737; PMID:1311263
A:Accession: A49255
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-16 <ROS>
A:Cross-references: UNIPARC:UPI000017C3B9
A>Note: sequence extracted from NCBI backbone (NCBIP:90722)
C:Keywords: T-cell receptor

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYDGTNN 9
DB 4 SYPGTQN 10

RESULT 4
A42291
tail fiber protein I - phage P2 (fragment)
C:Species: phage P2
C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: A42291
R:Haggard-Ljungquist, E.; Halling, C.; Calendar, R.
J. Bacteriol. 174, 1462-1477, 1992
A:Title: DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizon
A:Reference number: A42291; MUID:92165720; PMID:1531648
A:Accession: A42291
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <HAG>
A:Cross-references: UNIPROT:P26701; UNIPARC:UPI000017A829; GB:M64677

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDG 6
DB 4 VAYDG 8

RESULT 5
A31963
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (frag
C:Species: Ascaris suum (pig roundworm)
C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C:Accession: A31963
R:Thiesen, J.; Komuniecki, R.
J. Biol. Chem. 263, 19092-19097, 1988
A:Title: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaerob
A:Reference number: A31963; MUID:89066711; PMID:3198613
A:Accession: A31963
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <THI>
A:Cross-references: UNIPROT:P26267; UNIPARC:UPI000017B69C
C:Keywords: mitochondrion; oxidoreductase; phosphoprotein

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 ISYDGTNNYK 11
DB 7 MSDPGTSSYR 16

RESULT 6
PH1351
Ig heavy chain DJ region (clone C100-109B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1351
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1351
A:Molecule type: DNA
A:Residues: 1-16 <WAS>
A:Cross-references: UNIPARC:UPI000017C21F
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.7%; Score 22; DB 2; Length 16;
Best Local Similarity 30.8%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 YDGTNNYKPSLMD 16
DB 3 YDGPIGSTPGARE 15

RESULT 7
E28027
protein P8 - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C:Accession: E28027
R:Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
A:Reference number: A94167
A:Accession: E28027
A:Molecule type: protein
A:Residues: 1-16 <BAU>
A:Cross-references: UNIPROT:Q7M1V7; UNIPARC:UPI000017B09F
A>Note: 10-Lys was also found

Query Match 24.7%; Score 22; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 2.9e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISYDGTNNY 10
DB 8 VANDGSKTY 16

RESULT 8
C45133
casein kinase II (EC 2.7.1.-) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C45133
R:Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.
J. Biol. Chem. 267, 23789-23796, 1992
A:Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the asso
A:Reference number: A45133; MUID:93054738; PMID:1331100
A:Accession: C45133
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <OU1>
A:Cross-references: UNIPROT:Q9TRK9; UNIPARC:UPI0000088890
A:Experimental source: endoplasmic reticulum, pancreas
A>Note: sequence extracted from NCBI backbone (NCBIP:118799)
```

C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; heterotetramer; phosphotransferase; serine/threonine-specific protein kinase

Query Match 22.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 6.1e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YDGTNNY 10  
:|:|:  
Db 9 PHGHDNY 15

## RESULT 9

S01669  
rRNA N-glycosidase (EC 3.2.2.22) trichokirin - Mongolian snake-gourd (fragment)  
N;Alternate names: ribosome-inactivating protein trichokirin  
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
C;Accession: S01669  
R;Casellas, P.; Dussossoy, D.; Falasca, A.I.; Barbieri, L.; Guillemot, J.C.; Ferrara, P.  
Eur. J. Biochem. 176, 581-588, 1988  
A;Title: Trichokirin, a ribosome-inactivating protein from the seeds of Trichosanthes kirilowii  
A;Reference number: S01669; MUID:89005108; PMID:3262509  
C;Accession: S01669  
A;Molecule type: protein  
A;Residues: 1-16 <CAS>  
A;Cross-references: UNIPROT:P16093; UNIPARC:UPI000002BB47  
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C;Keywords: glycoprotein; glycosidase; hydrolase

Query Match 22.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 6.1e+03;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISYDGTNNYK 11  
:|:|:|:  
Db 6 LSGGGTASYE 15

## RESULT 10

S28213  
glutathione transferase (EC 2.5.1.18) - European toad (fragments)  
C;Species: Bufo bufo (European toad)  
C;Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C;Accession: S28213  
R;Aceto, A.; Dragani, B.; Bucciarelli, T.; Sacchetta, P.; Martini, F.; Angelucci, S.; Amadio, J. 289, 417-422, 1993  
A;Title: Purification and characterization of the major glutathione transferase from adult European toad (Bufo bufo)  
A;Reference number: S28213; MUID:93143709; PMID:8424786  
C;Accession: S28213  
A;Molecule type: protein  
A;Residues: 1-16 <ACE>  
A;Cross-references: UNIPARC:UPI000017BFA9  
A;Experimental source: liver  
C;Keywords: transferase

Query Match 22.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 28.6%; Pred. No. 6.1e+03;  
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSL 14  
:|:|:|:  
Db 1 FIFWDNEANFLEEL 14

## RESULT 11

PHI778  
T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: PHI778  
R;Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes  
A;Reference number: PHI754; MUID:93301585; PMID:8391057  
A;Accession: PHI778  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-16 <POR>  
A;Cross-references: UNIPARC:UPI000017C36C

Query Match 22.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NNYKPS 13  
:|:|:  
Db 10 NDYKLS 15

## RESULT 12

F49039  
T-cell receptor beta chain V-D-J-C region (V beta 2, J beta 1.5) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C;Accession: F49039  
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.  
Eur. J. Immunol. 22, 541-549, 1992  
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using cDNA sequencing  
A;Reference number: A49039; MUID:92164737; PMID:1311263  
C;Accession: F49039  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-16 <ROS>  
A;Cross-references: UNIPARC:UPI000017C3B3  
A;Note: sequence extracted from NCBI backbone (NCBI:90718)  
C;Keywords: T-cell receptor

Query Match 22.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 57.1%; Pred. No. 6.1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYDGTNN 9  
:|:|:  
Db 2 SASGTDN 8

## RESULT 13

B60278  
24K antigen - Mycobacterium bovis (fragment)  
C;Species: Mycobacterium bovis  
C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 09-Jul-2004  
C;Accession: B60278  
R;Fifis, T.; Costopoulos, C.; Radford, A.J.; Basic, A.; Wood, P.R.  
Infect. Immun. 59, 800-807, 1991  
A;Title: Purification and characterization of major antigens from a Mycobacterium bovis strain  
A;Reference number: A60278; MUID:91147217; PMID:1900061  
C;Accession: B60278  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <FIF>  
A;Cross-references: UNIPROT:Q7M199; UNIPARC:UPI000017AD42

Query Match 22.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.1e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 YKPSLK 15  
:|:|:  
Db 5 YKPSLK 10

## RESULT 14

PL0137  
protein kinase, 80K - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 18-Jun-1993  
C;Accession: PLO137  
R;Deichert, U.; Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.  
J. Neurochem. 53, 1268-1275, 1989  
A;Title: Isolation and partial characterization of an 80,000-dalton protein kinase from  
A;Reference number: PLO137; MUID:89361455; PMID:2769266  
A;Accession: PLO137  
A;Molecule type: protein  
A;Residues: 1-16 <DEC>  
A;Cross-references: UNIPARC:UPI0000177D3E  
C;Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match 21.3%; Score 19; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 8.8e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGT 7  
: |||  
Db 4 VDVDT 9

RESULT 15  
S23184  
redoxynucleonuclease (EC 4.2.99.-) - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C;Accession: S23184  
R;Huq, I.; Haukanes, B.I.; Helland, D.E.  
Eur. J. Biochem. 206, 833-839, 1992  
A;Title: Purification to homogeneity and characterization of a redoxynucleonuclease from  
A;Reference number: S23184; MUID:92299012; PMID:1376689  
A;Accession: S23184  
A;Molecule type: protein  
A;Residues: 1-16 <HUQ>  
A;Cross-references: UNIPARC:UPI000017C559  
A;Experimental source: thymus  
C;Function:  
A;Description: recognizes and induces cleavage of DNA damaged by UV  
C;Keywords: carbon-oxygen lyase

Query Match 21.3%; Score 19; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 8.8e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYDGTN 8  
: |||  
Db 5 AYTGT 10

Search completed: December 30, 2005, 14:25:37  
Job time : 23.5 secs



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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:06:48 ; Search time 141.5 Seconds  
(without alignments)  
79.777 Million cell updates/sec

Title: US-10-735-916A-10  
Perfect score: 89  
Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1144

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	32.6	16	2	Q9UC75_HUMAN
2	26	29.2	16	2	Q50L92_DROBP
3	24	27.0	16	2	Q9KJ10_STAHA
4	23	25.8	16	2	Q7RJE1_PLAYO
5	23	25.8	16	2	Q9F1R9_STRSU
6	23	25.8	16	2	Q9F1S1_STRSU
7	23	25.8	16	2	Q9QVL2_9MURI
8	23	25.8	16	2	Q9YQ11_9CORO
9	22	24.7	16	2	Q7M1V7_NICPL
10	22	24.7	16	2	Q3PRR9_9AVES
11	21	23.6	16	2	Q35214_9ENBE
12	21	23.6	16	2	Q9G1A6_9PHAE
13	20	22.5	16	1	ARCDC_PSEFU
14	20	22.5	16	1	RIPK1_TRIKI
15	20	22.5	16	2	Q3TRK9_CANFA
16	20	22.5	16	2	Q21922_9CAUD
17	20	22.5	16	2	Q7Y0M3_MAIZE
18	20	22.5	16	2	Q79AT0_AGRRH
19	20	22.5	16	2	Q7M199_MYCBO
20	20	22.5	16	2	Q9R4J4_PSEPR
21	20	22.5	16	2	Q506K8_9CALI
22	19	21.3	16	2	Q4X7B4_PLACH
23	19	21.3	16	2	Q3PRV4_CHICK
24	18	20.2	16	2	Q96KQ2_HUMAN
25	18	20.2	16	2	Q9T2V8_HUMAN
26	18	20.2	16	2	Q3UCR2_HUMAN
27	18	20.2	16	2	Q50L70_9DIPT
28	18	20.2	16	2	Q50L82_9DIPT
29	18	20.2	16	2	Q6RY72_TRIMO
30	18	20.2	16	2	Q8LLT9_PINRA
31	18	20.2	16	2	Q5YE54_PHOGU

32	17.5	19.7	16	2	Q9F9S4_HELPY	Q9f9s4 helicobacte
33	17	19.1	16	1	FORM1_MYRGU	P81438 myrmecia gu
34	17	19.1	16	1	FORM2_MYRGU	P81437 myrmecia gu
35	17	19.1	16	1	MK2B_FALPR	P80410 palomena pr
36	17	19.1	16	1	MK3_FALPR	P80411 palomena pr
37	17	19.1	16	1	ODO2_BOVIN	P11179 bos taurus
38	17	19.1	16	1	SSIT_STRMB	P83544 streptomyce
39	17	19.1	16	2	Q9TNN9_HUMAN	Q9tnn9 homo sapien
40	17	19.1	16	2	Q9UCG5_HUMAN	Q9ucg5 homo sapien
41	17	19.1	16	2	Q9TRL9_BOVIN	Q9trl9 bos taurus
42	17	19.1	16	2	Q7MIW7_ARATH	Q7miw7 arabidopsis
43	17	19.1	16	2	Q9S8C0_LUPAL	Q9s8c0 lupinus alb
44	17	19.1	16	2	Q9S8G3_ORYSA	Q9s8g3 oryza sativ
45	17	19.1	16	2	Q9S8N2_TOBAC	Q9s8n2 nicotiana t

## ALIGNMENTS

### RESULT 1

Q9UC75_HUMAN	PRELIMINARY;	PRT;	16 AA.
ID	Q9UC75_HUMAN	PRELIMINARY;	PRT;
AC	Q9UC75;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	DIPEPTIDYLPEPTIDASE IV (EC 3.4.14.5) (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	PROTEIN SEQUENCE.		
RX	MDLINE=5294018; PubMed=7539799; DOI=10.1074/jbc.270.23.14107;		
RA	Duke-Cohan J.S., Morimoto C., Rocker J.A., Schlossman S.F.;		
RT	"A novel form of dipeptidylpeptidase IV found in human serum.		
RT	Isolation, characterization, and comparison with T lymphocyte membrane		
RT	dipeptidylpeptidase IV (CD26).";		
RL	J. Biol. Chem. 270:14107-14114 (1995).		
DR	GO; GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.		
SQ	SEQUENCE 16 AA; 1600 MW; DFB3DD95FEE0A1EB CRC64;		

Query Match	32.6%;	Score 29;	DB 2;	Length 16;
Best Local Similarity	71.4%;	Pred. No. 1.2e+03;		
Matches	5;	Conservative	0;	Mismatches 2;
				Indels 0;
				Gaps 0;

Qy	5	DGTNNYK 11
Db	10	DGPGNYK 16

### RESULT 2

Q50L92_DROBP	PRELIMINARY;	PRT;	16 AA.
ID	Q50L92_DROBP	PRELIMINARY;	PRT;
AC	Q50L92;		
DT	13-SEP-2005 (TrEMBLrel. 31, Created)		
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)		
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)		
DE	Nos protein (Fragment).		
GN	Name=nos;		
OS	Drosophila bipectinata (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=42026;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Nozawa M., Aotsuka T., Tamura K.;		
RT	"A novel chimeric gene, sirene, found in the Drosophila bipectinata		
RT	species complex: potential of retroposition with regulatory		
RT	sequence.";		
RL	Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.		

```
DR EMBL; AB194429; BAD98205.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1933 MW; BFCABI719C58E7D3 CRC64;

Query Match 29.2%; Score 26; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 YKPSLK 15
   |||
Db 10 YKPMK 15

RESULT 3
Q9KJ10 STAHA PRELIMINARY; PRT; 16 AA.
AC Q9KJ10;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DE Heparin-binding protein (Fragment).
OS Staphylococcus haemolyticus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1283;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SM131;
RX MEDLINE=21284478; PubMed=11393292;
RA Fallgren C., Utt M., Ljungh A.;
RT Isolation and characterisation of a 17-kDa staphylococcal heparin-
binding protein with broad specificity.";
RL J. Med. Microbiol. 50:547-557(2001).
DR EMBL; AF169242; AAF89664.1; -; Genomic_DNA.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1909 MW; 30C19B931B50FF11 CRC64;

Query Match 27.0%; Score 24; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSYDG 6
   |||
Db 9 YSYNG 14

RESULT 4
Q7RJ11 PLAYO PRELIMINARY; PRT; 16 AA.
AC Q7RJ11;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY03321;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguotli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedeghan M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
```

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RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000947; EAA22886.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 16 AA; 1824 MW; AEB5951B681C02A1 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DGTNNY 10
   |||
Db 9 DDLNNY 14

RESULT 5
Q9F1R9 STRSU PRELIMINARY; PRT; 16 AA.
AC Q9F1R9;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Phosphoribosyl carboxyamide aminoimidazole transformylase (EC 6.3.2.6)
DE (Fragment).
GN Name=purH;
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=212;
RX MEDLINE=20576151; PubMed=11133943; DOI=10.1128/JB.183.2.500-511.2001;
RA Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoji Y.;
RT "Evidence for horizontal transfer of the SUDATII restriction-
modification genes to the Streptococcus suis genome.";
J. Bacteriol. 183:500-511(2001).
DR EMBL; AB045616; BAB20846.1; -; Genomic_DNA.
DR GO; GO:0016874; P:ligase activity; IEA_
DR GO; GO:0004639; P:phosphoribosylaminoimidazolesuccinocarboxam. . ; IEA.
KW Ligase.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1980 MW; A73BD79FAE3C0946 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 30.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGTNNYK 11
   |||
Db 6 VVYTGVRHYR 15

RESULT 6
Q9F1S1 STRSU PRELIMINARY; PRT; 16 AA.
AC Q9F1S1;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Phosphoribosyl carboxyamide aminoimidazole transformylase (EC 6.3.2.6)
DE (Fragment).
GN Name=purH;
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=211;
RX MEDLINE=20576151; PubMed=11133943; DOI=10.1128/JB.183.2.500-511.2001;
```

RA Sekizaki T., Otani Y., Oeaki M., Takamatsu D., Shimoji Y.;  
 RT "Evidence for horizontal transfer of the SmaATRII restriction-  
 RL modification genes to the Streptococcus suis genome.";  
 RL J. Bacteriol. 183:500-511(2001).  
 DR EMBL; AB045614; BAB20842.1; -; Genomic DNA.  
 DR GO; GO:0016874; F:ligase activity; IEA-  
 DR GO; GO:0004639; F:phosphoribosylaminimidazole succinocarboxam. .; IEA.  
 KW Ligase.  
 FT NON TER  
 SQ SEQUENCE 16 AA; 1998 MW; BAFBD79FAE3C0943 CRC64;  
 Query Match 25.8%; Score 23; DB 2; Length 16;  
 Best Local Similarity 30.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 ISYDGTNNYK 11  
 Db :|:|:|:  
 6 VYTGVRHYR 15  
 RESULT 7  
 ID QSOVL2\_9MURI PRELIMINARY; PRT; 16 AA.  
 AC QSOVL2;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE MEPRIN=METALLOENDOPEPTIDASE (Fragment).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10095;  
 [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=91363409; PubMed=1888759; DOI=10.1016/0167-4838(91)90032-U;  
 RA Flannery A.V., Macadam G.C., Beynon R.J.;  
 RT "Immunological characterisation of different meprin species in mice.";  
 RL Biochim. Biophys. Acta 1079:119-122(1991).  
 FT NON TER 1  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1922 MW; B0379F6803B42FAD CRC64;  
 Query Match 25.8%; Score 23; DB 2; Length 16;  
 Best Local Similarity 42.9%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 YDGTNNY 10  
 Db :|:|:|:  
 6 YEGESSY 12  
 RESULT 8  
 ID QSOVL1\_9CORO PRELIMINARY; PRT; 16 AA.  
 AC QSOVL1;  
 DT 01-MAY-1999 (TRENBLrel. 10, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE Hypothetical fusion protein.  
 OS Transmissible gastroenteritis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus; Group 1 species.  
 OC NCBI\_TaxID=11149;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=88078100; PubMed=2825819; DOI=10.1016/0300-9084(87)90178-7;  
 RA Rassechaert D., Gelfi J., Laude H.;  
 RT "Enteric Coronavirus TGSV; partial sequence of the genomic RNA, its  
 RT organization and expression.";  
 RL Biochimie 69:591-600(1987).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=95159435; PubMed=7856095;  
 RA Eleonet J., Rassechaert D., Lambert P., Levy L., Vende P., Laude H.;  
 RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1  
 of transmissible gastroenteritis virus.";  
 RL Virology 206:817-822(1995).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99099045; PubMed=9802359;  
 RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,  
 RA Enjuanes L.;  
 RT "Replication and packaging of transmissible gastroenteritis  
 RT coronavirus-derived synthetic minigenomes.";  
 RL J. Virol. 73:1535-1545(1999).  
 DR EMBL; AJ011482; CAA09624.1; -; Genomic RNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 16 AA; 2015 MW; B37776CE7AF3B62D CRC64;  
 Query Match 25.8%; Score 23; DB 2; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 YISYDGTNNY 10  
 Db :|:|:|:  
 7 YYSFNLTNNW 16  
 RESULT 9  
 ID Q7M1V7\_NICPL PRELIMINARY; PRT; 16 AA.  
 AC Q7M1V7;  
 DT 01-MAR-2004 (TRENBLrel. 26, Created)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Protein P8 (fragment).  
 OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamids; Solanales; Solanaceae; Nicotiana.  
 OC NCBI\_TaxID=4092;  
 [1]  
 RP PROTEIN SEQUENCE.  
 RA Bauw G., De Loose M., Inze D., Van Montagu M., Vandekerckhove J.;  
 RT "Alterations in the phenotype of plant cells studied by NH2-terminal  
 RT amino acid-sequence analysis of proteins electrophoretically separated from two-  
 RT dimensional gel-separated total extracts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).  
 DR PIR; E28027; E28027.  
 FT NON TER 1  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1637 MW; CB85CCF71E3FFA30 CRC64;  
 Query Match 24.7%; Score 22; DB 2; Length 16;  
 Best Local Similarity 33.3%; Pred. No. 1.7e+04;  
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 ISYDGTNNY 10  
 Db :|:|:|:  
 8 VANDGSKTY 16  
 RESULT 10  
 ID Q9PRR9\_9AVES PRELIMINARY; PRT; 16 AA.  
 AC Q9PRR9;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
 DE NA/K adenosine triphosphatase alpha subunit (fragment).  
 OS Anas (ducks).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae.  
 OC NCBI\_TaxID=8835;  
 [1]

```
RP PROTEIN SEQUENCE.
RX MEDLINE=96074598; PubMed=7488178;
RA Boldyrev A.A., Lopina O.D., Kenney M., Johnson P.;
RT "Characterization of the subunit isoforms of duck salt gland Na/K
RL adenosine triphosphatase."
RL Biochem Biophys Res Commun. 216:1048-1053(1995).
SQ SEQUENCE 16 AA; 1784 MW; 1A338D2CEFF6B920 CRC64;

Query Match      24.7%; Score 22; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 1.7e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      6 GTNNYKPS 13
DB      | : | : |
      1 GRDKYEPT 8

RESULT 11
Q35214 OENBE
ID Q35214 OENBE PRELIMINARY; PRT; 16 AA.
AC Q35214;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ATPase alpha subunit (16 aa) (Fragment).
OS Oenothera lutea (Bertero's evening primrose).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=3950;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86312871; PubMed=2875433;
RA Schuster W., Hiesel R., Isaac P.G., Leaver C.J., Brennicke A.;
RT "Transcript termini of messenger RNAs in higher plant mitochondria."
RL Nucleic Acids Res. 14:5943-5954(1986).
DR EMBL; X04203; CAA27800.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1820 MW; 118AC961C9322C91 CRC64;

Query Match      23.6%; Score 21; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      9 NYKPSLK 15
DB      | | | : |
      9 NAKPYIK 15

RESULT 12
Q9GIA6 9PHAE
ID Q9GIA6 9PHAE PRELIMINARY; PRT; 16 AA.
AC Q9GIA6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (Fragment).
GN Name=rbcS;
OS Sargassum palmeri.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OX NCBI_TaxID=129344;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Phillips N.E., Smith C.M., Morden C.W.;
RT "Testing systematic concepts of Sargassum (Fucales, Phaeophyceae)
RT using portions of the rbcLs operon."
RL Phcol. Res. 53:1-10(2005).
```

```
RN [2] NUCLEOTIDE SEQUENCE.
RP Phillips N.E.;
RA "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
RT (Fucales, Phaeophyceae).";
RL Thesis (1998) University of Hawaii.
DR EMBL; AF244335; AAF98104.2; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .); IEA.
DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
DR InterPro; IPR000894; RuBisCO_small.
DR Pfam; PF00101; RuBisCO_small; 1.
DR ProDom; PD000290; RuBisCO_small; 1.
KW Chloroplast.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1830 MW; B2096FF5A23D1210 CRC64;

Query Match      23.6%; Score 21; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 2.5e+04;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      6 GTNNYKPSLK 16
DB      | : | : | |
      6 GCFSFLPDLSD 16

RESULT 13
ARCD PSEPU
ID ARCD PSEPU STANDARD; PRT; 16 AA.
AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Arginine/ornithine antiporter (Fragment).
GN Name=arcD;
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 4359;
RA Wilson S.D., Wang M., Filpula D.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes an electroneutral exchange between arginine
CC and ornithine to allow high-efficiency energy conversion in the
CC arginine deiminase pathway.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: Belongs to the amino acid-polyamine-organocation (APC)
CC superfamily.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR EMBL; U07185; AAA16963.1; -; Unassigned DNA.
KW Amino-acid transport; Antiport; Inner membrane; Membrane;
KW Transmembrane; Transport.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1644 MW; 90B48A7C8FAA9705 CRC64;

Query Match      22.5%; Score 20; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 3.6e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 YISYDG 6
DB      | | | |
      7 YGLYDG 12
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RESULT 14
RIPK TRIKI
ID RIPK TRIKI STANDARD; PRT; 16 AA.
AC P16093;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ribosome-inactivating protein trichokirin (EC 3.2.2.22) (rRNA N-
glycosidase) (Fragment).
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=9305108; PubMed=3262509;
RA Casellas P., Dussosoy D., Falasca A.I., Barbieri L., Guillemot J.C.,
RA Ferrara P., Bolognesi A., Cennini P., Stirpe F.;
RT "Trichokirin, a ribosome-inactivating protein from the seeds of
RT Trichosanthes kirilowii Maximowicz. Purification, partial
RT characterization and use for preparation of immunotoxins.";
RL Eur. J. Biochem. 176:581-588(1988).
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -|- PTM: Glycosylated.
CC -|- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC Type 1 RIP subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; S01669; S01669.
DR InterPro; IPR001574; RIP.
DR PROSITE; PS00275; SHIGA_RICIN; PARTIAL.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
KW protein synthesis inhibitor; Toxin.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1605 MW; 5E268A7F345935A2 CRC64;
Query Match 22.5%; Score 20; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.6e+04;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 ISYDGTNNYK 11
Db 6 LSGGGTASYE 15
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RESULT 15
Q9TRK9 CANFA
ID Q9TRK9 CANFA PRELIMINARY; PRT; 16 AA.
AC Q9TRK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Casein kinase II=24 kDa polypeptide (fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93054738; PubMed=13311100;
RA Ou W.J., Thomas D.Y., Bell A.W., Bergeron J.J.;
RT "Casein kinase II phosphorylation of signal sequence receptor alpha
RT and the associated membrane chaperone calnexin.";
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RL J. Biol. Chem. 267:23789-23796 (1992).
DR PIR; C45133; C45133.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004672; P:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR ProDom; PD000001; Prot_kinase; 1.
FT NON_TER 16
SQ SEQUENCE 16 AA; 2053 MW; F31011034124F59B CRC64;
Query Match 22.5%; Score 20; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 3.6e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 4 YDGTNNY 10
Db 9 FHGHNDY 15
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Job time : 143.5 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:15:20 ; Search time 31.5 Seconds  
(without alignments)  
41.994 Million cell updates/sec

Title: US-10-735-916A-10  
Perfect score: 89  
Sequence: 1 YISYDGTNNYKPSLK 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 7712

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	57	64.0	16	2	US-09-170-769A-14
2	56	62.9	16	2	US-09-424-840B-110
3	55	61.8	16	2	US-09-424-840B-112
4	54	60.7	16	1	US-08-137-117D-126
5	54	60.7	16	1	US-08-436-717-126
6	51	57.3	16	2	US-09-424-840B-35
7	49	55.1	16	1	US-08-672-345C-53
8	49	55.1	16	2	US-09-214-095D-53
9	49	55.1	16	2	US-09-940-727B-53
10	48	53.9	16	2	US-09-996-288-25
11	48	53.9	16	2	US-09-996-288-37
12	48	53.9	16	2	US-09-996-288-41
13	48	53.9	16	2	US-09-996-288-103
14	48	53.9	16	2	US-09-996-265-25
15	48	53.9	16	2	US-09-996-265-37
16	48	53.9	16	2	US-09-996-265-41
17	48	53.9	16	2	US-09-996-265-103
18	46	51.7	16	2	US-09-889-480A-2
19	42	47.2	16	2	US-09-996-288-100
20	42	47.2	16	2	US-09-996-288-106
21	42	47.2	16	2	US-09-996-288-114
22	42	47.2	16	2	US-09-996-265-100
23	42	47.2	16	2	US-09-996-265-106
24	42	47.2	16	2	US-09-996-265-114
25	41	46.1	16	2	US-09-996-288-19
26	41	46.1	16	2	US-09-996-288-45
27	41	46.1	16	2	US-09-996-288-86

28	41	46.1	16	2	US-09-996-265-19	Sequence 19, Appl
29	41	46.1	16	2	US-09-996-265-45	Sequence 45, Appl
30	41	46.1	16	2	US-09-996-265-86	Sequence 86, Appl
31	37	41.6	16	1	US-08-483-636-24	Sequence 24, Appl
32	37	41.6	16	1	US-08-483-632-24	Sequence 24, Appl
33	37	41.6	16	2	US-09-759-112A-15	Sequence 15, Appl
34	35	39.3	16	1	US-08-290-592E-44	Sequence 44, Appl
35	35	39.3	16	2	US-09-771-415-7	Sequence 7, Appl
36	35	39.3	16	2	US-09-996-288-2	Sequence 2, Appl
37	35	39.3	16	2	US-09-996-288-82	Sequence 82, Appl
38	35	39.3	16	2	US-09-996-288-91	Sequence 91, Appl
39	35	39.3	16	2	US-09-996-288-93	Sequence 93, Appl
40	35	39.3	16	2	US-09-996-288-109	Sequence 109, App
41	35	39.3	16	2	US-09-996-288-111	Sequence 111, App
42	35	39.3	16	2	US-09-996-265-2	Sequence 2, Appl
43	35	39.3	16	2	US-09-996-265-82	Sequence 82, Appl
44	35	39.3	16	2	US-09-996-265-91	Sequence 91, Appl
45	35	39.3	16	2	US-09-996-265-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1  
US-09-170-769A-14  
; Sequence 14, Application US/09170769A  
; Patent No. 6444206  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: LETURCO, Didier  
; APPLICANT: MORIATRY, Ann  
; APPLICANT: ULEVITCH, Richard  
; APPLICANT: TOBIAS, Peter  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA  
; FILE REFERENCE: SCRIP1140-3  
; CURRENT APPLICATION NUMBER: US/09/170,769A  
; CURRENT FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: US 08/070,160  
; PRIOR FILING DATE: 1993-05-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Murine  
US-09-170-769A-14

Query Match 64.0%; Score 57; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 0.0089;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15  
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Db 1 YISYSGSTSYNPSLK 15

RESULT 2  
US-09-424-840B-110  
; Sequence 110, Application US/09424840B  
; Patent No. 6790938  
; GENERAL INFORMATION:  
; APPLICANT: Berchtold, Peter  
; APPLICANT: Escher, Robert F. A.  
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
; FILE REFERENCE: 100564-09049  
; CURRENT APPLICATION NUMBER: US/09/424,840B  
; CURRENT FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: DE 19820663.1  
; PRIOR FILING DATE: 1998-05-08  
; PRIOR APPLICATION NUMBER: DE 19755227.7  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: DE 19723904.8  
; PRIOR FILING DATE: 1997-06-06

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; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-110

Query Match      62.9%; Score 56; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
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Db 1 YIYSGTNNYPSLK 15

RESULT 3
US-09-424-840B-112
; Sequence 112, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-112

Query Match      61.8%; Score 55; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
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Db 1 YIYSGTNNYPSLK 15

RESULT 4
US-08-137-117D-126
; Sequence 126, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
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APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-436-717-126

Query Match 60.7%; Score 54; DB 1; Length 16;  
Best Local Similarity 66.7%; Pred. No. 0.027; 5; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15  
Db 1 YISYSGITTYNPSLK 15

RESULT 6  
US-09-424-840B-35  
Sequence 35, Application US/09424840B  
Patent No. 6790338  
GENERAL INFORMATION:  
APPLICANT: Berchtold, Peter  
APPLICANT: Escher, Robert F. A.  
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
FILE REFERENCE: 100564-09049  
CURRENT APPLICATION NUMBER: US/09/424,840B  
CURRENT FILING DATE: 1999-12-03  
PRIOR APPLICATION NUMBER: DE 19820663.1  
PRIOR FILING DATE: 1998-05-08  
PRIOR APPLICATION NUMBER: DE 19755227.7  
PRIOR FILING DATE: 1997-12-12  
PRIOR APPLICATION NUMBER: DE 19723904.8  
PRIOR FILING DATE: 1997-06-06  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 35  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-424-840B-35

Query Match 57.3%; Score 51; DB 2; Length 16;  
Best Local Similarity 64.3%; Pred. No. 0.084; 3; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYKPSLK 15  
Db 2 ISYSGSTKYKPSLR 15

RESULT 7  
US-08-672-345C-53  
Sequence 53, Application US/08672345C  
Patent No. 5948658  
GENERAL INFORMATION:  
APPLICANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper and Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,345C  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-672-345C-53

Query Match 55.1%; Score 49; DB 1; Length 16;  
Best Local Similarity 60.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15  
Db 1 YIRYSGITRYNPSLK 15

RESULT 8  
US-09-214-095D-53  
Sequence 53, Application US/09214095D  
Patent No. 6280987  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 51400-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/214,095D  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 53  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Murinae gen. sp.  
US-09-214-095D-53

Query Match 55.1%; Score 49; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15  
Db 1 YIRYSGITRYNPSLK 15

RESULT 9  
US-09-940-727B-53  
Sequence 53, Application US/09940727B

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; Patent No. 6913917
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 53
; LENGTH: 16
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-53

Query Match      55.1%; Score 49; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
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Db 1 YIRSGITRYNPSLK 15

RESULT 10
US-09-996-288-25
; Sequence 25, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-25

Query Match      53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGTNNYKPSLK 16
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Db 2 IWWDGKKHYNPSLK 16

RESULT 11
US-09-996-288-37
; Sequence 37, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
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; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 37
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-37

Query Match      53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGTNNYKPSLK 16
   ||| :|||
Db 2 IWWDGKKDYNPSLK 16

RESULT 12
US-09-996-288-41
; Sequence 41, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 41
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-41

Query Match      53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGTNNYKPSLK 16
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Db 2 IWWDGKKSYNPSLK 16

RESULT 13
US-09-996-288-103
; Sequence 103, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 103
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-103

Query Match      53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGTNNYKPSLK 16
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Db 2 IWWDGKKSYNPSLK 16
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Db      2 IWDGKKDYNPSLKD 16
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RESULT 14
US-09-996-265-25
; Sequence 25, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-25
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Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 ISYDGTNNYKPSLKD 16
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Db      2 IWDGKKDYNPSLKD 16

RESULT 15
US-09-996-265-37
; Sequence 37, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-37
Query Match      53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 ISYDGTNNYKPSLKD 16
      |.:||.:|:|||||
Db      2 IWDGKKDYNPSLKD 16
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Job time : 32.5 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:25:05 ; Search time 110 Seconds  
(without alignments)  
60.775 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 11256

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA\_Main:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	89	100.0	16	5	US-10-735-916A-10
2	60	67.4	16	5	US-10-822-306A-26
3	58	65.2	16	5	US-10-822-306A-21
4	58	65.2	16	5	US-10-822-306A-23
5	56	62.9	16	4	US-10-312-316-8
6	56	62.9	16	4	US-10-844-424-110
7	55	61.8	16	4	US-10-844-424-112
8	55	61.8	16	5	US-10-893-576-107
9	54	60.7	16	3	US-09-791-551-89
10	52	58.4	16	3	US-09-791-551-84
11	51	57.3	16	4	US-10-393-701-5
12	51	57.3	16	4	US-10-844-424-35
13	50	56.2	16	4	US-10-173-551-26
14	50	56.2	16	5	US-10-822-306A-19
15	49	55.1	16	3	US-09-940-727B-53
16	49	55.1	16	5	US-10-822-306A-18
17	49	55.1	16	6	US-11-003-731-23
18	48	53.9	16	3	US-09-796-848A-27
19	48	53.9	16	3	US-09-796-848A-28
20	48	53.9	16	3	US-09-796-848A-30
21	48	53.9	16	3	US-09-796-848A-55
22	48	53.9	16	3	US-09-996-288-25
23	48	53.9	16	3	US-09-996-288-37
24	48	53.9	16	3	US-09-996-288-41
25	48	53.9	16	3	US-09-996-288-103
26	48	53.9	16	3	US-09-996-265-25
27	48	53.9	16	3	US-09-996-265-37

#### ALIGNMENTS

##### RESULT 1

US-10-735-916A-10

; Sequence 10, Application US/10735916A

; Publication No. US20050084906A1

; GENERAL INFORMATION:

; APPLICANT: GOETSCH, Liliane

; APPLICANT: CORVAIA, Nathalie

; APPLICANT: LAGER, Olivier

; APPLICANT: DUFLOS, Alain

; APPLICANT: BECK, Alain

; APPLICANT: HAEUW, Jean-Francois

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 017753-183

; CURRENT APPLICATION NUMBER: US/10735,916A

; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 03/08 538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 02/00 653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 02/00 654

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 02/05 753

; PRIOR FILING DATE: 2002-05-07

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-735-916A-10

Query Match 100.0%; Score 89; DB 5; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.7e-07; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0

Qy 1 YISYDGTNNYKPSLKD 16

Db 1 YISYDGTNNYKPSLKD 16

##### RESULT 2

US-10-822-306A-26

; Sequence 26, Application US/10822306A

; Publication No. US20050227289A1

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Reilly, Edward B.

; APPLICANT: Lacy, Susan E.

```
; APPLICANT: Fung, Emma
; APPLICANT: Belk, Jonathan P.
; APPLICANT: Roguska, Michael
; TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 7349USPI
; CURRENT APPLICATION NUMBER: US/10/822,306A
; CURRENT FILING DATE: 2004-04-12
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-306A-26

Query Match      67.4%; Score 60; DB 5; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.012;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|:|:|:|
Db 1 YIGYSGSTNNYPSLK 15

RESULT 3
US-10-822-306A-21
; Sequence 21, Application US/10822306A
; Publication No. US2005027289A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Reilly, Edward B.
; APPLICANT: Lacy, Susan E.
; APPLICANT: Fung, Emma
; APPLICANT: Belk, Jonathan P.
; APPLICANT: Roguska, Michael
; TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 7349USPI
; CURRENT APPLICATION NUMBER: US/10/822,306A
; CURRENT FILING DATE: 2004-04-12
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-306A-21

Query Match      65.2%; Score 58; DB 5; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.025;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|:|:|:|
Db 1 YIGYSGSTNNYPSLK 15

RESULT 4
US-10-822-306A-23
; Sequence 23, Application US/10822306A
; Publication No. US2005027289A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Reilly, Edward B.
; APPLICANT: Lacy, Susan E.
; APPLICANT: Fung, Emma
; APPLICANT: Belk, Jonathan P.
; APPLICANT: Roguska, Michael
```

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; TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 7349USPI
; CURRENT APPLICATION NUMBER: US/10/822,306A
; CURRENT FILING DATE: 2004-04-12
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-306A-23

Query Match      65.2%; Score 58; DB 5; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.025;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|:|:|:|
Db 1 YIYEGSTNNYPSLK 15

RESULT 5
US-10-312-316-8
; Sequence 8, Application US/10312316
; Publication No. US20040137513A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Hongo, Jo-Anne S.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shelton, David L.
; TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
; FILE REFERENCE: GENENT.04QPC
; CURRENT APPLICATION NUMBER: US/10/312,316
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/238,319
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-316-8

Query Match      62.9%; Score 56; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.053;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|:|:|:|
Db 1 YIYSGSTNNYPSLK 15

RESULT 6
US-10-844-424-110
; Sequence 110, Application US/10844424
; Publication No. US20040202859A1
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
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; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-844-424-110

Query Match      62.9%; Score 56; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.053;
Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

Qy      1 YISYDGTNNYKPSLK 15
      ||| | | | | | | |
Db      1 YIYSGSTNNYKPSLK 15

RESULT 7
US-10-844-424-112
; Sequence 112, Application US/10844424
; Publication No. US20040202659A1
; GENERAL INFORMATION:
; APPLICANT: BERTHOID, Peter
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-844-424-112

Query Match      61.8%; Score 55; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy      1 YISYDGTNNYKPSLK 15
      ||| | | | | | | |
Db      1 YIYSGSTNNYKPSLK 15

RESULT 8
US-10-893-576-107
; Sequence 107, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 107
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy chain
; OTHER INFORMATION: variable region CDR peptide
US-10-893-576-107

Query Match      61.8%; Score 55; DB 5; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.076;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 YISYDGTNNYKPSLK 15
      |.:|.:|.:|.:|.:|.:|
Db      1 YVYSGSTNNYKPSLK 15

RESULT 9
US-09-791-551-89
; Sequence 89, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-89

Query Match      60.7%; Score 54; DB 3; Length 16;
Best Local Similarity 50.0%; Pred. No. 0.11;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YISYDGTNNYKPSLK 16
      |.:|.:|.:|.:|.:|.:|
Db      1 YLSYDGSKSHNPRLN 16

RESULT 10
US-09-791-551-84
; Sequence 84, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-84
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Query Match      58.4%; Score 52; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.23;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YISFGSTGYNPSLK 15

RESULT 11
US-10-399-701-5
; Sequence 5, Application US/10399701
; Publication No. US20040022791A1
; GENERAL INFORMATION:
; APPLICANT: ASAT AG
; TITLE OF INVENTION: Rekombinant anti-GPIIB/IIIA-antibodies as agents for
; FILE OF INVENTION: inhibiting angiogenesis
; FILE REFERENCE: 23600PWO DRAS
; CURRENT APPLICATION NUMBER: US/10/399,701
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 100 57 443.2
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2-region of
; OTHER INFORMATION: an optimized antibody against GPIIB/IIIA
US-10-399-701-5

Query Match      57.3%; Score 51; DB 4; Length 16;
Best Local Similarity 64.3%; Pred. No. 0.34;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISYDGTNNYKPSLK 15
   |||:|||||
Db 2 ISYSGSTKYKPSLR 15

RESULT 12
US-10-844-424-35
; Sequence 35, Application US/10844424
; Publication No. US20040202659A1
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-844-424-35

Query Match      57.3%; Score 51; DB 4; Length 16;
Best Local Similarity 64.3%; Pred. No. 0.34;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YISFGSTGYNPSLK 15

RESULT 13
US-10-173-551-26
; Sequence 26, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855.2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-551-26

Query Match      56.2%; Score 50; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.49;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 HIYSGNTYNNPSLK 15

RESULT 14
US-10-822-306A-19
; Sequence 19, Application US/10822306A
; Publication No. US20050227289A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Reilly, Edward B.
; APPLICANT: Lacy, Susan E.
; APPLICANT: Fung, Emma
; APPLICANT: Belk, Jonathan P.
; APPLICANT: Roguska, Michael
; TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 7349USP1
; CURRENT APPLICATION NUMBER: US/10/822,306A
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 10/821,497
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-306A-19

Query Match      56.2%; Score 50; DB 5; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.49;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YIGGEGSTYNNPSLK 15

RESULT 15
US-09-940-727B-53
; Sequence 53, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
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; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-53

Query Match 55.1%; Score 49; DB 3; Length 16;  
Best Local Similarity 60.0%; Pred. No. 0.7;  
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Oy 1 YISYDGTNNYKPSLK 15  
Db 1 YIRYSGITRYNPSLK 15

Search completed: December 30, 2005, 14:43:48  
Job time : 110 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:25:45 ; Search time 8 Seconds  
(without alignments)  
14.978 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89  
Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	16	7 US-11-012-353-10	Sequence 10, Appl
2	45	50.6	16	7 US-11-009-939-24	Sequence 24, Appl
3	31	34.8	16	7 US-11-054-515-3140	Sequence 3140, Ap
4	29	32.6	16	6 US-10-502-145-33	Sequence 33, Appl
5	26	29.2	16	7 US-11-054-515-2799	Sequence 2799, Ap
6	25	28.1	16	6 US-10-507-662-5	Sequence 5, Appl
7	25	28.1	16	7 US-11-054-515-2263	Sequence 2263, Ap
8	25	28.1	16	7 US-11-128-440-61	Sequence 61, Appl
9	24	27.0	16	7 US-11-125-837-11	Sequence 11, Appl
10	24	27.0	16	7 US-11-105-708-15	Sequence 15, Appl
11	23	25.8	16	7 US-11-054-515-2261	Sequence 2261, Ap
12	23	25.8	16	7 US-11-054-515-2266	Sequence 2266, Ap
13	23	25.8	16	7 US-11-054-515-2323	Sequence 2323, Ap
14	22	24.7	16	7 US-11-055-163-20	Sequence 20, Appl
15	21	23.6	16	6 US-10-503-575-38	Sequence 38, Appl
16	21	23.6	16	6 US-10-999-866-59	Sequence 59, Appl
17	21	23.6	16	7 US-11-054-515-2745	Sequence 2745, Ap
18	21	23.6	16	7 US-11-054-515-2792	Sequence 2792, Ap
19	21	23.6	16	7 US-11-054-515-2891	Sequence 2891, Ap
20	21	23.6	16	7 US-11-093-274-6	Sequence 6, Appl
21	21	23.6	16	7 US-11-021-305-167	Sequence 167, App
22	20	22.5	16	7 US-11-054-515-2221	Sequence 2221, Ap
23	20	22.5	16	7 US-11-054-515-2274	Sequence 2274, Ap
24	20	22.5	16	7 US-11-054-515-2847	Sequence 2847, Ap
25	20	22.5	16	7 US-11-054-515-3004	Sequence 3004, Ap

#### ALIGNMENTS

##### RESULT 1

US-11-012-353-10  
; Sequence 10, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFIOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 01763-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 10  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-10

Query Match 100.0%; Score 89; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16  
Db 1 YISYDGTNNYKPSLKD 16  
|||||

RESULT 2  
US-11-009-939-24  
; Sequence 24, Application US/11009939

Sequence 2307, Ap  
Sequence 2153, Ap  
Sequence 2157, Ap  
Sequence 2780, Ap  
Sequence 2783, Ap  
Sequence 3090, Ap  
Sequence 183, Appl  
Sequence 6, Appl  
Sequence 453, Appl  
Sequence 33, Appl  
Sequence 2137, Ap  
Sequence 2143, Ap  
Sequence 2145, Ap  
Sequence 2214, Ap  
Sequence 2215, Ap  
Sequence 2216, Ap  
Sequence 2217, Ap  
Sequence 2218, Ap  
Sequence 2219, Ap  
Sequence 2220, Ap

16 7 US-11-054-515-2307  
16 7 US-11-054-515-2153  
16 7 US-11-054-515-2157  
16 7 US-11-054-515-2780  
16 7 US-11-054-515-2783  
16 7 US-11-054-515-3090  
16 7 US-11-116-144-183  
16 6 US-10-507-662-6  
16 6 US-10-623-155-453  
16 7 US-11-089-764-33  
16 7 US-11-054-515-2137  
16 7 US-11-054-515-2143  
16 7 US-11-054-515-2145  
16 7 US-11-054-515-2214  
16 7 US-11-054-515-2215  
16 7 US-11-054-515-2216  
16 7 US-11-054-515-2217  
16 7 US-11-054-515-2218  
16 7 US-11-054-515-2219  
16 7 US-11-054-515-2220

```

; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-24

Query Match      50.6%; Score 45; DB 7; Length 16;
Best Local Similarity 53.3%; Pred. No. 0.053;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||||:|
Db 1 YIHSGVTDNFPSLK 15

RESULT 3
US-11-054-515-3140
; Sequence 3140, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3140
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3140

Query Match      34.8%; Score 31; DB 7; Length 16;
Best Local Similarity 44.4%; Pred. No. 12;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISYDGTNNY 10
```

```

Db 4 LNYDGDY 12
   ::|||:|

RESULT 4
US-10-502-145-33
; Sequence 33, Application US/10502145
; Publication No. US20050244406A1
; GENERAL INFORMATION:
; APPLICANT: MACKAY, CHARLES REAY
; TITLE OF INVENTION: Anti-C5aR antibodies and uses thereof
; FILE REFERENCE: RICE-032
; CURRENT APPLICATION NUMBER: US/10/502,145
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: USSN 60/350,961
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-502-145-33

Query Match      32.6%; Score 29; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GTNNYKPSLK 15
   |::|||
Db 6 GSTNTNSALK 15

RESULT 5
US-11-054-515-2799
; Sequence 2799, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2799
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2799

Query Match      29.2%; Score 26; DB 7; Length 16;
Best Local Similarity 41.7%; Pred. No. 80;
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Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYKPS 13  
: || ||  
Db 1 LDYDILGYTYS 12

## RESULT 6

US-10-507-662-5  
; Sequence 5, Application US/10507662  
; Publication No. US20050255102A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN INC.  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES  
; FILE REFERENCE: A136PCT  
; CURRENT APPLICATION NUMBER: US/10/507,662  
; CURRENT FILING DATE: 2004-09-13  
; PRIOR APPLICATION NUMBER: 60/364,991  
; PRIOR FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: 60/426,286  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-507-662-5

Query Match 28.1%; Score 25; DB 6; Length 16;  
Best Local Similarity 42.9%; Pred. No. 1.2e+02;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYKPSLK 15  
: || || || ||  
Db 2 ISSGGSTYYPDSVK 15

## RESULT 7

US-11-054-515-2263  
; Sequence 2263, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2263  
; LENGTH: 16

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-2263

Query Match 28.1%; Score 25; DB 7; Length 16;  
Best Local Similarity 45.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 YDGTNNYKPSL 14  
: || || || ||  
Db 3 YDTLTSYVPLL 13

## RESULT 8

US-11-128-440-61  
; Sequence 61, Application US/11128440  
; Publication No. US20050261478A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden-Ledbetter, Martha  
; APPLICANT: Brady, William A.  
; APPLICANT: Grosmaire, Laura S.  
; APPLICANT: Law, Che-Leung  
; APPLICANT: Dua, Raj  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING  
; TITLE OF INVENTION: LYMPHOCYTE ACTIVATION  
; FILE REFERENCE: 980034.408D1  
; CURRENT APPLICATION NUMBER: US/11/128,440  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/646,381  
; PRIOR FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 09/252,150  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/108,683  
; PRIOR FILING DATE: 1998-11-16  
; PRIOR APPLICATION NUMBER: 60/075,274  
; PRIOR FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 61  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-128-440-61

Query Match 28.1%; Score 25; DB 7; Length 16;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISYDG 6  
: || || ||  
Db 6 YYDYDG 11

## RESULT 9

US-11-125-837-11  
; Sequence 11, Application US/11125837  
; Publication No. US20050266003A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Rong-Hwa  
; APPLICANT: Chang, Chung Nan  
; APPLICANT: Chen, Pei-Jiun  
; APPLICANT: Huang, Chiu-Chen  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: 13062-011001  
; CURRENT APPLICATION NUMBER: US/11/125,837  
; CURRENT FILING DATE: 2005-05-10  
; PRIOR APPLICATION NUMBER: US 60/569,892  
; PRIOR FILING DATE: 2004-05-10  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 16

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; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-11

Query Match      27.0%; Score 24; DB 7; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 GTNNKPSLK 15
   | : | | |
Db  6 GGTSYNPKF 15

RESULT 10
US-11-105-708-15
; Sequence 15, Application US/11105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
; APPLICANT: Pernaesetti, Flavia
; APPLICANT: Freimark, Bruce
; APPLICANT: Van Epps, Dennis
; APPLICANT: Brooks, Peter C
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
; FILE REFERENCE: 30797-704.501
; CURRENT APPLICATION NUMBER: US/11/105,708
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 09/478,977
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: 60/152,496
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/143,534
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/114,878
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/114,877
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 15
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-105-708-15

Query Match      27.0%; Score 24; DB 7; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 ISYDGTNNKPSLK 15
   | : | | |
Db  2 IWDDNKYTNPSLK 15

RESULT 11
US-11-054-515-2261
; Sequence 2261, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2266

Query Match      25.8%; Score 23; DB 7; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 YDGTNNYKP 12
   | | | : |
Db  3 YDTLTSYVP 11

RESULT 12
US-11-054-515-2266
; Sequence 2266, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2266
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2266

Query Match      25.8%; Score 23; DB 7; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 YDGTNNYKP 12
   | | | : |
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Db 3 YDTILTSYVP 11

## RESULT 13

US-11-054-515-2323  
; Sequence 2323, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 03/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2323  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-2323

Query Match 25.8%; Score 23; DB 7; Length 16;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 YDGTNNY 10  
| | | |  
Db 3 YDTILTY 9

## RESULT 14

US-11-055-163-20  
; Sequence 20, Application US/11055163  
; Publication No. US20050271655A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, DANIEL H. S.  
; APPLICANT: PEPINSKY, R. BLAKE  
; APPLICANT: LI, WEIWEI  
; APPLICANT: RABACCHI, SYLVIA A.  
; APPLICANT: RELTON, JANE K.  
; APPLICANT: WORLEY, DANE S.  
; APPLICANT: STRITTMATTER, STEPHEN M.  
; APPLICANT: SAH, DINAH Y.W.  
; TITLE OF INVENTION: NOGO RECEPTOR ANTAGONISTS  
; FILE REFERENCE: A170 CON (00455.271)  
; CURRENT APPLICATION NUMBER: US/11/055,163  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: PCT/US03/25004  
; PRIOR FILING DATE: 2003-08-07  
; PRIOR APPLICATION NUMBER: 60/402,866  
; PRIOR FILING DATE: 2002-08-10  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 20  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: heavy chain peptide sequence  
US-11-055-163-20

Query Match 24.7%; Score 22; DB 7; Length 16;  
Best Local Similarity 55.8%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TNNYKPSLK 15  
| | | |  
Db 7 TKYYSLSLK 15

## RESULT 15

US-10-503-575-38  
; Sequence 38, Application US/10503575  
; Publication No. US20050244823A1  
; GENERAL INFORMATION:  
; APPLICANT: Drijfhout, Jan Wouter  
; APPLICANT: van Veelen, Petrus Antonius  
; APPLICANT: Koning, Frits  
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHODS  
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS  
; FILE REFERENCE: 2799/72843-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/503,575  
; CURRENT FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: PCT/NL03/00077  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: EP 02075456.0  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-503-575-38

Query Match 23.6%; Score 21; DB 6; Length 16;  
Best Local Similarity 37.5%; Pred. No. 5.5e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTNNYKPS 13  
| | | |  
Db 3 GQGSFQPS 10

Search completed: December 30, 2005, 14:44:10  
Job time : 8 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 71.0968 Seconds  
(without alignments)  
49.440 Million cell updates/sec

Title: US-10-735-916A-12  
Perfect score: 47  
Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	7 ADJ76846	Adj76846 CDR seque
2	47	100.0	8	9 ADZ67016	Adz67016 Murine in
3	47	100.0	117	7 ADJ76903	Adj76903 Anti-IGF-
4	47	100.0	117	7 ADJ76909	Adj76909 Anti-IGF-
5	47	100.0	117	7 ADJ76917	Adj76917 Anti-IGF-
6	47	100.0	117	7 ADJ76913	Adj76913 Anti-IGF-
7	47	100.0	117	9 ADZ67083	Adz67083 Human ant
8	47	100.0	117	9 ADZ67087	Adz67087 Human ant
9	47	100.0	117	9 ADZ67073	Adz67073 Murine im
10	47	100.0	117	9 ADZ67079	Adz67079 Human ant
11	47	100.0	127	7 ADJ76886	Adj76886 Anti-IGF-
12	47	100.0	127	9 ADZ67056	Adz67056 Murine im
13	47	100.0	135	7 ADJ76911	Adj76911 Anti-IGF-
14	47	100.0	135	7 ADJ76919	Adj76919 Anti-IGF-
15	47	100.0	135	7 ADJ76915	Adj76915 Anti-IGF-
16	47	100.0	135	9 ADZ67089	Adz67089 Human ant
17	47	100.0	135	9 ADZ67081	Adz67081 Human ant
18	47	100.0	135	9 ADZ67085	Adz67085 Human ant
19	38	80.9	138	7 AB071408	Ab071408 Pseudomon
20	37	78.7	221	6 ABM70706	Abm70706 Photorhab
21	37	78.7	2920	8 ADG65227	Adg65227 Mcf1 sequ
22	36	76.6	410	3 AAY68969	Aay68969 Cps2T whi
23	35	74.5	233	7 ADH86117	Adh86117 Enterococ
24	35	74.5	390	7 AB084316	Ab084316 Pseudomon

25	35	74.5	395	5	ABB54242	Abb54242 Lactococc
26	35	74.5	1425	4	ABB71908	Abb71908 Drosophil
27	34	72.3	12	2	AAW62012	AAw62012 Heavy cha
28	34	72.3	12	3	AAy82339	AAy82339 Humanise
29	34	72.3	12	8	ADG39000	Adg39000 Humanise
30	34	72.3	17	2	AAr73928	AAr73928 B.catarrh
31	34	72.3	26	2	AAr73925	AAr73925 B.catarrh
32	34	72.3	71	2	AAr73923	AAr73923 B.catarrh
33	34	72.3	116	2	AAy29452	AAy29452 Human IGG
34	34	72.3	116	3	AAy77755	AAy77755 Human IGG
35	34	72.3	116	3	AAE30312	AAE30312 Human IGG
36	34	72.3	116	6	ABU13789	ABu13789 Human IGG
37	34	72.3	116	6	ABU59502	ABu59502 Human IGG
38	34	72.3	116	7	AAE39085	AAe39085 Heavy cha
39	34	72.3	121	2	AAW62013	AAw62013 Heavy cha
40	34	72.3	121	2	AAW62019	AAw62019 Rhesusise
41	34	72.3	121	2	AAW63542	AAw63542 Murine MH
42	34	72.3	121	2	AAW63531	AAw63531 Murine MH
43	34	72.3	121	2	AAW63532	AAw63532 Humanise
44	34	72.3	121	3	AAy82348	AAy82348 Rhesusise
45	34	72.3	121	3	AAy82336	AAy82336 Humanise

ALIGNMENTS

RESULT 1  
ADJ76846  
ID ADJ76846 standard; peptide; 8 AA.  
XX  
AC ADJ76846;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE CDR sequence for anti-IGF-1R antibody.  
XX  
KW cytostatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX  
OS Mus musculus.  
XX  
EN WO2003059951-A2.  
XX  
PD 24-JUL-2003.  
XX  
PF 20-JAN-2003; 2003WO-FR000178.  
XX  
PR 18-JAN-2002; 2002FR-00000653.  
PR 18-JAN-2002; 2002FR-00000854.  
PR 07-MAY-2002; 2002FR-00005753.  
XX  
PA (PABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
FI Goetsch L, Corvaia N, Leger O;  
XX WPI; 2003-569653/53.  
DR N-PSDB; ADJ76845.  
XX  
PT New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.  
PS Claim 1; SEQ ID NO 12; 164pp; French.  
XX  
CC The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC IR) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 7; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;

QY 1 YGRVFFDY 8  
 |||||  
 Db 1 YGRVFFDY 8

RESULT 2  
 ID ADZ67016  
 AC ADZ67016 standard; peptide; 8 AA.  
 AC ADZ67016;

XX  
 DT 30-JUN-2005 (first entry)  
 XX Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:12.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasms; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.  
 XX  
 OS Mus musculus.  
 XX US2005084906-A1.  
 XX 21-APR-2005.  
 XX 16-DEC-2003; 2003US-00735916.  
 XX 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 PR 20-JAN-2003; 2003WO-FR000178.  
 PR 11-JUL-2003; 2003FR-00008538.  
 XX (GOET/) GOETSCH L.  
 PA (CORV/) CORVAIA N.  
 PA (LEGE/) LEGER O.  
 PA (DUFEL/) DUFLOS A.  
 PA (HAEU/) HAEUW J.  
 PA (BECK/) BECK A.  
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 XX WPI; 2005-321968/33.  
 DR N-PSDB; ADZ67015.  
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.  
 XX Claim 1; SEQ ID NO 12; 125pp; English.  
 PS The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;

QY 1 YGRVFFDY 8  
 |||||  
 Db 1 YGRVFFDY 8

RESULT 3  
 ADJ76903  
 ID ADJ76903 standard; protein; 117 AA.  
 XX  
 AC ADJ76903;  
 XX 06-MAY-2004 (first entry)  
 DT Anti-IGF-1R related protein #16.  
 XX  
 DE Cytostatic; antipsoriatic; antibody;  
 XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW insulin-like growth factor receptor; EGFR; signal transduction pathway;  
 KW or epidermal growth factor receptor; cancer; osteosarcoma; complementarity determining region;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX Homo sapiens.  
 OS  
 XX WO2003059951-A2.  
 XX 24-JUL-2003.  
 PD  
 XX 20-JAN-2003; 2003WO-FR000178.  
 PF  
 XX 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;  
 XX DR WPI; 2003-569653/53.  
 XX PT New antibodies that bind to human insulin-like growth factor receptor,  
 XX PT useful for treatment, prevention and diagnosis of cancers.  
 XX PS Disclosure; SEQ ID NO 69; 164pp; French.  
 XX CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX SQ Sequence 117 AA;  
 Query Match 100.0%; Score 47; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YGRVFFDY 8  
 | | | | | | | |  
 Db 99 YGRVFFDY 106  
 RESULT 4  
 ADJ76909  
 ID ADJ76909 standard; protein; 117 AA.  
 XX AC ADJ76909;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Anti-IGF-1R related protein #22.  
 XX KW cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX OS Homo sapiens.  
 XX PN WO2003059951-A2.  
 XX PD 24-JUL-2003.  
 XX PF 20-JAN-2003; 2003WO-FR000178.  
 XX PR 18-JAN-2002; 2002FR-00000653.  
 XX PR 18-JAN-2002; 2002FR-00000654.  
 XX PR 07-MAY-2002; 2002FR-00005753.  
 XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
 XX PI Goetsch L, Corvaia N, Leger O;  
 XX DR WPI; 2003-569653/53.  
 XX PT New antibodies that bind to human insulin-like growth factor receptor,  
 XX PT useful for treatment, prevention and diagnosis of cancers.  
 XX PS Disclosure; SEQ ID NO 83; 164pp; French.  
 XX CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX SQ Sequence 117 AA;  
 Query Match 100.0%; Score 47; DB 7; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YGRVFFDY 8  
 | | | | | | | |  
 Db 99 YGRVFFDY 106  
 RESULT 5  
 ADJ76917  
 ID ADJ76917 standard; protein; 117 AA.  
 XX AC ADJ76917;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Anti-IGF-1R related protein #26.  
 XX KW cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX OS Homo sapiens.  
 XX PN WO2003059951-A2.  
 XX PD 24-JUL-2003.  
 XX PF 20-JAN-2003; 2003WO-FR000178.  
 XX PR 18-JAN-2002; 2002FR-00000653.  
 XX PR 18-JAN-2002; 2002FR-00000654.  
 XX PR 07-MAY-2002; 2002FR-00005753.  
 XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
 XX PI Goetsch L, Corvaia N, Leger O;  
 XX DR WPI; 2003-569653/53.  
 XX PT New antibodies that bind to human insulin-like growth factor receptor,  
 XX PT useful for treatment, prevention and diagnosis of cancers.  
 XX PS Disclosure; SEQ ID NO 83; 164pp; French.  
 XX CC The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
CC hyperactivity of signal transduction pathways mediated by interaction of  
CC these receptors with their ligands. Especially they inhibit  
CC transformation of normal cells to tumor cells, inhibit growth and/or  
CC proliferation of tumor cells, so are useful against cancers of the  
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
CC protein sequence used to generate the Ab of the invention.  
XX  
SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
Db |||||||  
99 YGRVFFDY 106

RESULT 6  
ADJ76913  
ID ADJ76913 standard; protein; 117 AA.

XX AC ADJ76913;  
XX DT 06-MAY-2004 (first entry)  
XX DE Anti-IGF-1R related protein #24.  
XX KW cytostatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX OS Homo sapiens.  
XX PN WO2003059951-A2.  
XX PD 24-JUL-2003.  
XX PF 20-JAN-2003; 2003WO-FR000178.  
XX PR 18-JAN-2002; 2002FR-0000653.  
XX PR 18-JAN-2002; 2002FR-0000654.  
XX PR 07-MAY-2002; 2002FR-00005753.  
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX PI Goetsch L, Corvaia N, Leger O;  
XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.  
XX

PS Disclosure; SEQ ID NO 79; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC 1R) and optionally; (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
CC hyperactivity of signal transduction pathways mediated by interaction of  
CC these receptors with their ligands. Especially they inhibit  
CC transformation of normal cells to tumor cells, inhibit growth and/or  
CC proliferation of tumor cells, so are useful against cancers of the

CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
CC protein sequence used to generate the Ab of the invention.  
XX  
SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
Db |||||||  
99 YGRVFFDY 106

RESULT 7  
ADZ67083  
ID ADZ67083 standard; protein; 117 AA.

XX AC ADZ67083;  
XX DT 30-JUN-2005 (first entry)  
XX DE Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.  
XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
KW musculoskeletal disease; respiratory disease; lung tumor;  
KW endocrine disease; gynecology and obstetrics; breast tumor;  
KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
KW heavy chain variable region.

XX OS Homo sapiens.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-0000653.

XX PR 18-JAN-2002; 2002FR-0000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOET/) GOETSCH L.

XX PA (CORV/) CORVAIA N.

XX PA (LEGE/) LEGER O.

XX PA (DUFJ/) DUFLOS A.

XX PA (HAUJ/) HAEUW J.

XX PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
PT antibody or its functional fragment, being capable of binding human IGF-  
PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
PT useful for treating cancer.

PS Example 13; SEQ ID NO 79; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor  
CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
CC capable of binding to human IGF-IR and, if necessary, capable of  
CC specifically inhibiting tyrosine kinase activity of the receptor,  
CC comprising a light or heavy chain having at least one complementary  
CC determining region (CDR) consisting of one of two fully defined 16 amino  
CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in

CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 9; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
 DB 99 YGRVFFDY 106

RESULT 8

ID ADZ67087 standard; protein; 117 AA.

XX AC ADZ67087;

DT 30-JUN-2005 (first entry)

DE Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;  
 KW antiproliferative; psoriasis; dermatological disease; immune disorder;  
 KW heavy chain variable region.

XX OS Homo sapiens.

XX FN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOETZ) GOETSCH L.

(CORV/) CORVAIA N.  
 (LEGE/) LEGER O.  
 (DUFEL/) DUFLOS A.  
 (HAEU/) HAEUW J.  
 (BECK/) BECK A.

Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
 WPI, 2005-321968/33.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
 PT antibody or its functional fragment, being capable of binding human IGF-  
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
 PT useful for treating cancer.

PS Example 13; SEQ ID NO 83; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor  
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
 CC capable of binding to human IGF-IR and, if necessary, capable of  
 CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 9; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
 DB 99 YGRVFFDY 106

RESULT 9

ID ADZ67073

XX AC ADZ67073 standard; protein; 117 AA.

XX AC ADZ67073;

XX DT 30-JUN-2005 (first entry)

XX DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.



CC of an illness connected with an overexpression and/or an abnormal  
CC activation of the IGF-IR and/or EGFR, and/or connected with a  
CC hyperactivation of the transduction pathway of the signal mediated by the  
CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
CC the administration of the medicament does not induce or only elicits  
CC induces secondary effects connected with inhibition of the insulin  
CC receptor. The antibody is useful for preparation of a medicament intended  
CC to inhibit the transformation of normal cells into cells with tumoral  
CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
CC useful for preparation of a medicament intended to inhibit the growth  
CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
CC medicament intended for prevention or for the treatment of cancer, where  
CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
CC preparation of a medicament intended for the prevention or for the  
CC treatment of psoriasis. (I) is useful in preparation of a medicament  
CC intended for the specific targeting of a biologically active compound to  
CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
CC is useful for in vitro diagnosis of illnesses induced by an  
CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
CC starting from a biological sample in which the abnormal presence, of IGF-  
CC IR and/or EGFR receptor is suspected, which involves contacting the  
CC biological sample with (I), which is optionally labeled. The present  
CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 9; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8  
| | | | |  
Db 99 YGRVFFDY 106

RESULT 11  
ADJ76886  
ID ADJ76886 standard; protein; 127 AA.

AC ADJ76886;

DT 06-MAY-2004 (first entry)

XX Anti-IGF-IR related protein #4.

XX cytostatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.

OS Mus musculus.

XX WO2003059951-A2.

PN 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

PT New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 52; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC IR) and optionally; (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
CC hyperactivity of signal transduction pathways mediated by interaction of  
CC these receptors with their ligands. Especially they inhibit  
CC transformation of normal cells to tumor cells, inhibit growth and/or  
CC proliferation of tumor cells, so are useful against cancers of the  
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 127 AA;

Query Match 100.0%; Score 47; DB 7; Length 127;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8  
| | | | |  
Db 109 YGRVFFDY 116

RESULT 12  
ADZ67056

ID ADZ67056 standard; protein; 127 AA.

AC ADZ67056;

XX 30-JUN-2005 (first entry)

XX Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
KW musculoskeletal disease; respiratory disease; lung tumor;  
KW endocrine disease; gynecology and obstetrics; breast tumor;  
KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
KW immunoglobulin; heavy chain variable region.

XX OS Mus musculus.

XX Key Location/Qualifiers  
FH Peptide 1..10  
FT Region /note= "leader peptide"

FT Region 41..46  
FT /note= "CDR1"

FT Region 61..76  
FT /note= "CDR2"

FT Region 109..116  
FT /note= "CDR3"

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 20-JAN-2002; 2002FR-00005753.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.  
PA (CORV/) CORVAIA N.  
PA (LEGE/) LEGER O.  
PA (DUFL/) DUFLOS A.  
PA (HAUJ/) HAEUW J.  
PA (BECK/) BECK A.  
XX  
XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;  
PI WPI: 2005-321968/33.  
XX N-PSDB; AD267055.  
DR  
DR  
XX  
XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)  
PT antibody or its functional fragment, being capable of binding human IGF-  
PT IR and specifically inhibiting tyrosine kinase activity of receptor,  
PT useful for treating cancer.  
XX  
XX  
PS Example 8; SEQ ID NO 52; 125pp; English.  
XX  
XX The invention relates to a novel isolated anti-insulin-like growth factor  
CC I receptor (IGF-IR) antibody (I) or its functional fragment, being  
CC capable of binding to human IGF-IR and, if necessary, capable of  
CC specifically inhibiting tyrosine kinase activity of the receptor,  
CC comprising a light or heavy chain having at least one complementary  
CC determining region (CDR) consisting of one of two fully defined 16 amino  
CC acids (AD267006 and AD267014). An antibody of the invention is useful in  
CC the preparation of a medicament intended for the prevention or treatment  
CC of an illness connected with an overexpression and/or an abnormal  
CC activation of the IGF-IR and/or EGFR, and/or connected with a  
CC hyperactivation of the transduction pathway of the signal mediated by the  
CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
CC the administration of the medicament does not induce or only slightly  
CC induces secondary effects connected with inhibition of the insulin  
CC receptor. The antibody is useful for preparation of a medicament intended  
CC to inhibit the transformation of normal cells into cells with tumoral  
CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
CC useful for preparation of a medicament intended to inhibit the growth  
CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
CC medicament intended for prevention or for the treatment of cancer, where  
CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
CC preparation of a medicament intended for the prevention or for the  
CC treatment of psoriasis. (I) is useful in preparation of a medicament  
CC intended for the specific targeting of a biologically active compound to  
CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
CC is useful for in vitro diagnosis of illnesses induced by an  
CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
CC starting from a biological sample in which the abnormal presence, of IGF-  
CC IR and/or EGFR receptor is suspected, which involves contacting the  
CC biological sample with (I), which is optionally labeled. The present  
CC sequence is used in the exemplification of the invention.  
XX  
XX  
SQ Sequence 127 AA;  
Query Match 100.0%; Score 47; DB 9; Length 127;  
Best Local Similarity 100.0%; Pred. No. 0.97; Mismatches 0; Gaps 0;  
Matches 8; Conservative 0; Indels 0; Indels 0; Gaps 0;  
QY 1 YGRVFFDY 8  
DB 109 YGRVFFDY 116  
RESULT 13  
ADJ76911  
ID ADJ76911 standard; protein; 135 AA.  
XX  
XX  
AC ADJ76911,  
XX

DT 06-MAY-2004 (first entry)  
XX Anti-IGF-IR related protein #23.  
DE  
XX  
XX cytostatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX  
OS Homo sapiens.  
XX  
XX WO2003059951-A2.  
XX  
XX 24-JUL-2003.  
PD  
XX  
XX 20-JAN-2003; 2003WO-FR000178.  
PF  
XX  
XX 18-JAN-2002; 2002FR-00000653.  
PR  
XX 18-JAN-2002; 2002FR-00000654.  
PR  
XX 07-MAY-2002; 2002FR-00005753.  
PR  
XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
PA  
XX Goetsch L, Corvaia N, Leger O;  
PI WPI: 2003-569653/53.  
XX  
XX New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.  
XX  
XX Disclosure; SEQ ID NO 77; 164pp; French.  
XX  
XX The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC IR) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-IR. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with  
CC hyperactivity of signal transduction pathways mediated by interaction of  
CC these receptors with their ligands. Especially they inhibit  
CC transformation of normal cells to tumor cells, inhibit growth and/or  
CC proliferation of tumor cells, so are useful against cancers of the  
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents a  
CC protein sequence used to generate the Ab of the invention.  
XX  
XX Sequence 135 AA;  
Query Match 100.0%; Score 47; DB 7; Length 135;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YGRVFFDY 8  
DB 117 YGRVFFDY 124  
RESULT 14  
ADJ76919  
ID ADJ76919 standard; protein; 135 AA.  
XX  
XX ADJ76919;  
AC  
XX  
XX 06-MAY-2004 (first entry)  
DT  
XX  
XX Anti-IGF-IR related protein #27.  
DE  
XX  
XX cytostatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW



KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003059951-A2.  
 XX  
 XX  
 PD 24-JUL-2003.  
 XX  
 XX 20-JAN-2003; 2003WO-FR000178.  
 XX  
 XX 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA  
 XX Goetsch L, Corvaia N, Leger O;  
 PI WPI; 2003-569653/53.  
 XX  
 XX New antibodies that bind to human insulin-like growth factor receptor,  
 PR useful for treatment, prevention and diagnosis of cancers.  
 PT  
 XX Disclosure; SEQ ID NO 85; 164pp; French.  
 PS  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 135 AA;  
 Query Match 100.0%; Score 47; DB 7; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YGRVFFDY 8  
 |||||  
 Db 117 YGRVFFDY 124  
 RESULT 15  
 ADJ76915  
 ID ADJ76915 standard; protein; 135 AA.  
 XX  
 XX AC ADJ76915;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-IGF-1R related protein #25.  
 XX  
 KW cytostatic; antipsoriatic; antibody;  
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
 KW CDR.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003059951-A2.  
 XX

PD 24-JUL-2003.  
 XX  
 XX 20-JAN-2003; 2003WO-FR000178.  
 XX  
 XX 18-JAN-2002; 2002FR-00000653.  
 PR 18-JAN-2002; 2002FR-00000654.  
 PR 07-MAY-2002; 2002FR-00005753.  
 XX  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA  
 XX Goetsch L, Corvaia N, Leger O;  
 PI WPI; 2003-569653/53.  
 XX  
 XX New antibodies that bind to human insulin-like growth factor receptor,  
 PR useful for treatment, prevention and diagnosis of cancers.  
 PT  
 XX Disclosure; SEQ ID NO 81; 164pp; French.  
 PS  
 XX The invention relates to an isolated antibody (Ab), and its functional  
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
 CC treat diseases associated with overexpression and/or abnormal activity of  
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
 CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
 CC protein sequence used to generate the Ab of the invention.  
 XX  
 SQ Sequence 135 AA;  
 Query Match 100.0%; Score 47; DB 7; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YGRVFFDY 8  
 |||||  
 Db 117 YGRVFFDY 124  
 Search completed: December 30, 2005, 13:24:02  
 Job time : 72.0968 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 11.3548 Seconds  
(without alignments)  
67.789 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: Pirl.\*

2: Pirl2.\*

3: Pirl3.\*

4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	74.5	90	2 AC1030	hypothetical prote
2	35	74.5	293	2 D90456	oxydoreductase, pr
3	35	74.5	384	2 A11566	B. subtilis TagF p
4	35	74.5	395	2 F86740	teichoic acid bios
5	35	74.5	682	2 C84295	UDP-sugar hydrolas
6	34	72.3	87	2 E81191	hypothetical prote
7	34	72.3	117	2 S01822	Ig heavy chain V-D
8	34	72.3	125	2 G69523	hypothetical prote
9	34	72.3	142	2 D69515	hypothetical prote
10	34	72.3	297	2 C84509	hypothetical prote
11	34	72.3	453	2 S39865	outer membrane pro
12	34	72.3	477	2 T33531	hypothetical prote
13	34	72.3	483	2 A38560	nitrate transport
14	34	72.3	731	2 S16595	gene CARS12 prote
15	34	72.3	739	2 A81430	outer membrane pr
16	33	70.2	119	2 S03077	Ig heavy chain V r
17	33	70.2	174	2 C69037	hypothetical prote
18	33	70.2	220	2 D71946	hypothetical prote
19	33	70.2	222	2 F64563	hypothetical prote
20	33	70.2	255	2 AB2109	hypothetical prote
21	33	70.2	285	2 F95289	conserved hypotet
22	33	70.2	317	2 T20302	hypothetical prote
23	33	70.2	341	1 CTNHP2	site-specific DNA-
24	33	70.2	363	2 S42379	hypothetical prote
25	33	70.2	373	2 JC6053	glycerol-3-phospha
26	33	70.2	427	2 AB3025	methionine gamma-1
27	33	70.2	427	2 G98259	methionine gamma-1
28	33	70.2	450	2 D97885	conserved hypotet
29	33	70.2	603	2 T28278	ORF MSV117 probabl

## ALIGNMENTS

### RESULT 1

AC1030

hypothetical protein STY4564 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AC1030  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium  
A;Reference number: AB0502; UID:21534947; PMID:11677608  
A;Accession: AC1030  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-90 <PAR>  
A;Cross-references: UNIPARC:UPI000005A8A2; GB:AL513382; PIDN:CAD09340.1; PTD:gl6505340; C;Genetics:  
A;Gene: STY4564

Query Match 74.5%; Score 35; DB 2; Length 90;

Best Local Similarity 85.7%; Pred. No. 6.3;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GRVFFDY 8

Db 44 GRVFFDY 50

### RESULT 2

D90456

oxydoreductase, probable [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C;Accession: D90456

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan, J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: D90456

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-293 <KUR>

A;Cross-references: UNIPROT:Q97V38; UNIPARC:UPI0000064866; GB:AE006641; NID:gl3816140; P

C;Genetics:

A;Gene: SS02794

Query Match 74.5%; Score 35; DB 2; Length 293;

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Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 159 YGNRFFDY 166

RESULT 3
A: subtilis TagF protein (probable CDPGlycerol glycerophosphotransferase) homolog lin107
A:Accession: A11566
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: A11566
R: Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11566
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-384 <GLA>
A:Cross-references: UNIPROT:Q92CU7; UNIPARC:UPI000000CC457; GB:AL592022; PIDN:CAC96305.1;
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin1074

Query Match 74.5%; Score 35; DB 2; Length 384;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 292 YSSVFFDY 299

RESULT 4
R86740
telchoic acid biosynthesis protein F [imported] - Lactococcus lactis subsp. lactis (stra
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: R86740
R: Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: R86740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <STO>
A:Cross-references: UNIPROT:Q9CH15; UNIPARC:UPI000000C6947; GB:AE005176; PID:g12723861; F
A:Experimental source: strain ILI403
C:Genetics:
A:Gene: tagF

Query Match 74.5%; Score 35; DB 2; Length 395;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 304 YSSVFFDY 311

RESULT 5
R84295
UDP-sugar hydrolase [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

```

```

C:Accession: C84295
R: Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: C84295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-682 <STO>
A:Cross-references: UNIPROT:Q9HPZ0; UNIPARC:UPI00000638A1; GB:AE004437; NID:g10580911; P
C:Genetics:
A:Gene: ush

Query Match 74.5%; Score 35; DB 2; Length 682;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 494 YGTVLFDY 501

RESULT 6
E81191
hypothetical protein NMB0510 [imported] - Neisseria meningitidis (strain MCS8 serogroup I
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: E81191
R: Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: E81191
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <TET>
A:Cross-references: UNIPROT:Q9JR23; UNIPARC:UPI000000C4E2B; GB:AE002407; GB:AE002098; NID:
A:Experimental source: serogroup B, strain MCS8
C:Genetics:
A:Gene: NMB0510

Query Match 72.3%; Score 34; DB 2; Length 87;
Best Local Similarity 62.5%; Pred. No. 9.6;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 49 YGKDFDY 56

RESULT 7
S01822
Ig heavy chain V-D-J region (hybridoma 10B10S) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: S01822
R: Foerster, I.; Gu, H.; Rajewsky, K.
EMBO J. 7, 3693-3703, 1988
A:Title: Germ-line antibody V regions as determinants of clonal persistence and malignant
A:Reference number: S01822; MUID:89091115; PMID:3264787
A:Accession: S01822
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <FOE>
A:Cross-references: UNIPARC:UPI0000176B35; EMBL:X12388; NID:g51924; PIDN:CAA30945.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

```

F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 34; DB 2; Length 117;  
Best Local Similarity 62.5%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 YGRVFFDY 8  
|||  
Db 99 YGNYYFDY 106  
  
RESULT 8  
G69523  
hypothetical protein AF2191 - Archaeoglobus fulgidus  
C/Species: Archaeoglobus fulgidus  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: G69523  
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A/Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A/Reference number: A69250; MUID:98049343; PMID:9389475  
A/Accession: G69523  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-125 <KLE>  
A/Cross-references: UNIPROT:O28092; UNIPARC:UPI0000056A38; GB:AE000954; GB:AE000782; NID

Query Match 72.3%; Score 34; DB 2; Length 125;  
Best Local Similarity 71.4%; Pred. No. 14;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YGRVFFD 7  
|||  
Db 3 YGRIFPN 9

RESULT 9  
D69515  
hypothetical protein AF2124 - Archaeoglobus fulgidus  
C/Species: Archaeoglobus fulgidus  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: D69515  
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A/Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A/Reference number: A69250; MUID:98049343; PMID:9389475  
A/Accession: D69515  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-142 <KLE>  
A/Cross-references: UNIPROT:O28156; UNIPARC:UPI0000056A66; GB:AE000957; GB:AE000782; NID

Query Match 72.3%; Score 34; DB 2; Length 142;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YGRVFF 6  
|||  
Db 72 YGRVFF 77

RESULT 10  
C64509  
hypothetical protein At2g13630 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 31-Dec-2004  
C/Accession: C84509  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 403, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: C84509  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-297 <STO>  
A/Cross-references: UNIPROT:Q9SIT4; UNIPARC:UPI000000A248E; GB:AE002093; NID:94558667; PI

C/Genetics:  
A/Map position: 2  
C/Superfamily: hypothetical protein containing F-box domain

Query Match 72.3%; Score 34; DB 2; Length 297;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8  
|||  
Db 281 RVFFDY 286

#### RESULT 11

S39866  
outer membrane protein CD precursor - Moraxella catarrhalis  
C/Species: Moraxella catarrhalis  
C/Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
C/Accession: S39866  
R/Murphy, T.F.; Kirkham, C.; Lesse, A.J.  
Mol. Microbiol. 10, 87-97, 1993  
A/Title: The major heat-modifiable outer membrane protein CD is highly conserved among s  
A/Reference number: S39866; MUID:95058186; PMID:7968522  
A/Accession: S39866  
A/Molecule type: DNA  
A/Residues: 1-453 <MUR>  
A/Cross-references: UNIPROT:Q08657; UNIPARC:UPI000000B88DE; EMBL:L10755; NID:9149756; PID

C/Keywords: membrane protein  
P;1-26/Domain: signal sequence #status predicted <SIG>  
P;27-453/Product: outer membrane protein CD #status predicted <MAT>

Query Match 72.3%; Score 34; DB 2; Length 453;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8  
|||  
Db 329 RVFFDY 334

#### RESULT 12

T33531  
hypothetical protein F58E1.4 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T33531  
R/Wamsley, P.; Twyman, B.  
submitted to the EMBL Data Library, October 1998  
A/Description: The sequence of C. elegans cosmid F58E1.  
A/Reference number: Z21365  
A/Accession: T33531  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-477 <WAM>  
A/Cross-references: UNIPROT:Q9TZG7; UNIPARC:UPI0000007C654; EMBL:AF098995; PIDN:AAC67482.

A/Experimental source: strain Bristol N2; clone F58E1  
C/Genetics:  
A/Gene: CESP:F58E1.4  
A/Map position: 2

A;Introns: 32/1; 104/1; 269/3; 424/3

C;Superfamily: Caenorhabditis elegans hypothetical protein T05A6.4

Query Match 72.3%; Score 34; DB 2; Length 477;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFF 6

Db 472 YGRVFF 477

RESULT 13

A38560

nitrate transport protein crnA - Emericella nidulans

C;Species: Emericella nidulans, Aspergillus nidulans

C;Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 09-Jul-2004

C;Accession: A38560

R;Unkies, S.B.; Hawker, K.L.; Grieve, C.; Campbell, E.I.; Montague, P.; Kinghorn, J.R.  
Proc. Natl. Acad. Sci. U.S.A. 88, 204-208, 1991

A;Title: crnA encodes a nitrate transporter in Aspergillus nidulans.

A;Reference number: A38560; MUID:91095428; PMID:1986367

A;Accession: A38560

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-483 <UNK>

A;Cross-references: UNIPROT:P22152; UNIPARC:UPI0000178CA8; GB:M57647

C;Superfamily: nitrate transporter component

C;Keywords: transmembrane protein

Query Match 72.3%; Score 34; DB 2; Length 483;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFF 6

Db 32 YGRVFF 37

RESULT 14

S16595

gene CARSR12 protein - clove pink

C;Species: Dianthus caryophyllus (clove pink)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C;Accession: S16595

R;Raghothama, K.G.; Lawton, K.A.; Goldsbrough, P.B.; Woodson, W.R.

Plant Mol. Biol. 17, 61-71, 1991

A;Title: Characterization of an ethylene-regulated flower senescence-related gene from C

A;Reference number: S16595; MUID:91329738; PMID:1868223

A;Accession: S16595

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-731 <RAG>

A;Cross-references: UNIPROT:Q00662; UNIPARC:UPI00001268DC; EMBL:X57171; NID:g18327; PIDN

C;Genetics:

A;Introns: 60/3; 92/3; 130/2; 152/3; 183/3; 232/3; 262/2; 297/3; 326/1; 365/3; 423/3; 48

C;Superfamily: beta-galactosidase bga

Query Match 72.3%; Score 34; DB 2; Length 731;  
Best Local Similarity 62.5%; Pred. No. 82;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8

Db 28 YGNVWIDY 35

RESULT 15

A81430

outer membrane protein Cj0129c [imported] - Campylobacter jejuni (strain NCTC 11168)

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C;Accession: A81430

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barril  
Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: A81430

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-739 <PAR>

A;Cross-references: UNIPROT:O9PIZ8; UNIPARC:UPI00000C2051; GB:AL139074; GB:AL1111168; NID:

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj0129c

Query Match 72.3%; Score 34; DB 2; Length 739;  
Best Local Similarity 85.7%; Pred. No. 82;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVFFDY 8

Db 677 GSVFFDY 683

Search completed: December 30, 2005, 13:34:58

Job time : 13.3548 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 72 Seconds  
(without alignments)

78.392 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	85.1	345	2	Q7M880 WOLSU
2	39	83.0	149	2	Q4IUN5 AZOVI
3	37	78.7	213	2	Q7N273 FHOHL
4	37	78.7	331	2	Q93HL7 STRAW
5	37	78.7	366	2	Q5VLJ6 HEVBR
6	37	78.7	366	2	Q6T4P0 HEVBR
7	37	78.7	552	2	Q9LJB0 ARATH
8	37	78.7	1838	2	Q8IDZ6 PLAF7
9	36	76.6	298	2	Q8RAL0 THETN
10	35	74.5	90	2	Q82IK0 SALT1
11	35	74.5	113	2	Q6GUD4 EDWIC
12	35	74.5	270	2	Q96ZJ6 SULFO
13	35	74.5	289	1	END4 MYCPE
14	35	74.5	293	2	Q97V38 SULSO
15	35	74.5	298	2	Q5L810 BACFN
16	35	74.5	298	2	Q64N90 BACFR
17	35	74.5	300	2	Q8A9T6 BACTN
18	35	74.5	305	2	Q8A7X8 BACTN
19	35	74.5	382	2	Q6LNN6 PHOPR
20	35	74.5	384	2	Q720Y4 LISTER
21	35	74.5	395	2	Q92CU7 LISTIN
22	35	74.5	395	2	Q92CU7 LISTIN
23	35	74.5	398	2	Q4MJH6 BACCE
24	35	74.5	401	2	Q5WDC3 BACSK
25	35	74.5	443	2	Q5TVP9 ANOGA
26	35	74.5	455	2	Q9HJZ7 THEAC
27	35	74.5	493	2	Q7QGY9 ANOGA
28	35	74.5	514	2	Q5TVQ3 ANOGA
29	35	74.5	560	2	Q82YY7 ENTFA
30	35	74.5	568	2	Q7PSH8 ANOGA
31	35	74.5	682	2	Q9HPZ0 HALSA

32	35	74.5	710	2	Q4MJH5 BACCE	Q4mjh5 bacillus ce
33	35	74.5	722	2	Q5WDC6 BACSK	Q5wdc6 bacillus cl
34	35	74.5	775	2	Q8CQJ9 STAPR	Q8cqj9 staphylococ
35	35	74.5	839	2	Q8D518 VIBVU	Q8d518 vibrio vuln
36	35	74.5	858	2	Q7MBV1 VIBVU	Q7mbv1 vibrio vuln
37	35	74.5	1496	2	Q9VIT9 DROME	Q9vit9 drosophila
38	35	74.5	1496	2	Q9NFV5 DROME	Q9nfv5 drosophila
39	34	72.3	77	2	Q4ZSS0 PLABE	Q4zss0 plasmodium
40	34	72.3	87	2	Q9JR23 NEIME	Q9jrr23 neisseria m
41	34	72.3	87	2	Q7DDN6 NEIMB	Q7ddn6 neisseria m
42	34	72.3	125	1	Y2191_ARCFU	Y2191 archaeoglob
43	34	72.3	142	1	Y2124_ARCFU	Y2124 archaeoglob
44	34	72.3	159	2	Q5GTD1 WOLTR	Q5gttd1 wolbachia s
45	34	72.3	199	2	Q856Z7_9CAUD	Q856z7 mycobacteri

#### ALIGNMENTS

RESULT 1

Q7M880 WOLSU  
ID Q7M880\_WOLSU PRELIMINARY; PRT; 345 AA.

AC Q7M880;  
DT 01-MAR-2004 (Tremblrel. 26, Created)  
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE MEMBRANE PROTEIN-Predicted permease.  
GN Name=AMAA; OrderedLocusNames=WS1824;  
OS Wolinella succinogenes.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Wolinella.  
OX NCBI\_TaxID=844;  
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=DSMZ 1740;

RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;

RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,

RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,

RA Meyer P., Lederer H., Schuster S.C.;

RT "Complete genome sequence and analysis of Wolinella succinogenes.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).

DR EMBL; BX571661; CAB10839.1; -; Genomic\_DNA.

DR InterPro; IPR002549; UPF0118.

DR Pfam; PF01594; UPF0118; 1.

DR Complete proteome.

SK SEQUENCE 345 AA; 38928 MW; 595AF3430F1C444E CRC64;

Query Match 85.1%; Score 40; DB 2; Length 345;

Best Local Similarity 75.0%; Pred. No. 16;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8

Db 163 YGRAFYDY 170

RESULT 2

Q4IUN5 AZOVI

ID Q4IUN5\_AZOVI PRELIMINARY; PRT; 149 AA.

AC Q4IUN5;

DT 13-SEP-2005 (Tremblrel. 31, Created)

DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)

DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=AvinDRAFT\_1630;

OS Azotobacter vinelandii AvOp.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Azotobacter.

OX NCBI\_TaxID=322710;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AvOp;

RG US DOE Joint Genome Institute (JGI-PGF);

Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
 Hammon N., Israni S., Pitluck S., Richardson P.;  
 "Sequencing of the draft genome assembly of *Azotobacter vinelandii*  
 AVOP";  
 Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 [2]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AVOP;  
 RG US DOE Joint Genome Institute (JGI-ORNL);  
 RA Larimer F., Land M.;  
 RT "Annotation of the draft genome assembly of *Azotobacter vinelandii*  
 AVOP";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AVOP;  
 RG US DOE Joint Genome Institute;  
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RL [4]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AVOP;  
 RG US DOE Joint Genome Institute (JGI-PGP);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
 Hammon N., Israni S., Pitluck S., Richardson P.;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AAU03000012; EAM04553.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 DR  
 SQ SEQUENCE 149 AA; 16436 MW; B03FD0348C9CFDE CRC64;  
 Query Match 83.0%; Score 39; DB 2; Length 149;  
 Best Local Similarity 87.5%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps  
 QY 1 YGRVFDDY 8  
 || |||||  
 Db 119 YGFVFDDY 126  
 RESULT 3  
 ID Q7N273 PHOLL PRELIMINARY; PRT; 213 AA.  
 AC Q7N273;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DT Complete genome; segment 11/17.  
 OS OrderedLocutusNames=plu3218;  
 GN Photobacterium luminescens (subsp. laumondii).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Photobacterium.  
 OX NCBI\_TaxID=141679;  
 RP [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=TT01;  
 RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;  
 RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,  
 RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,  
 RA Dassa E., Deroose R., Derzelle S., Freysinet G., Gaudriault S.,  
 RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,  
 RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;  
 RT "The genome sequence of the entomopathogenic bacterium *Photobacterium*  
 RT *luminescens*.";  
 RL Nat. Biotechnol. 21:1307-1313 (2003).  
 DR EMBL; BX571869; CAB15592.1; -; Genomic\_DNA.  
 DR Photolist; plu3218; -;  
 KW Complete proteome.  
 SQ SEQUENCE 213 AA; 24684 MW; FB69E290F8C4116C CRC64;  
 Query Match 78.7%; Score 37; DB 2; Length 213;  
 Best Local Similarity 85.7%; Pred. No. 40;

Matches	6;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	GRVFFDY 8	:	:	:	:	:	:	:
Dd	121	GVKFFDY 127	:	:	:	:	:	:	:
 RESULT 4									
ID	Q93HL7	STRAW PRELIMINARY;	PRT;	331 AA.					
AC	Q93HL7								
DT	01-DEC-2001	(T-EMBLrel. 19, Created)							
DT	01-DEC-2001	(T-EMBLrel. 19, Last sequence update)							
DT	13-SEP-2005	(T-EMBLrel. 31, Last annotation update)							
DE	O-methyltransferase.								
GN	OrderedLocusNames=SAV2843;								
OS	Streptomyces avermitilis.								
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;								
OC	Streptomycineae; Streptomycetaceae; Streptomyces.								
OX	NCBI_TaxID=33903;								
RN	[1]								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;								
RX	MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;								
RA	Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,								
RA	Shinoe M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,								
RA	Kikuchi H., Shiba T., Sakaki Y., Hattori M.,								
RT	"Genome sequence of an industrial microorganism Streptomyces								
RT	avermitilis; deducing the ability of producing secondary								
RT	metabolites.";								
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).								
RN	[2]								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;								
RX	MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;								
RA	Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,								
RA	Sakaki Y., Hattori M., Omura S.,								
RT	"Complete genome sequence and comparative analysis of the industrial								
RT	microorganism Streptomyces avermitilis.";								
RL	Nat. Biotechnol. 21:526-531(2003).								
DR	EMBL; AB070937; BAB69170.1; -; Genomic DNA.								
DR	EMBL; BA000300; BAC70354.1; -; Genomic DNA.								
DR	GO; GO:0008171; F:O-methyltransferase activity; IEA.								
DR	GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . ; IEA.								
DR	GO; GO:0016740; F:transferase activity; IEA.								
DR	InterPro; IPR001601; Methyltransf.								
DR	InterPro; IPR001077; O_Mectransf.								
DR	InterPro; IPR000051; SAM_bind.								
DR	InterPro; IPR011991; Wing_hlx DNA_bd.								
DR	pfam; PF00891; Methyltransf 2; 1.								
KW	Complete proteome; Methyltransferase; Transferase.								
SQ	SEQUENCE 331 AA; 36302 MW; AL3E700B7F81AB5B CRC64;								
 Query Match 78.7%; Score 37; DB 2; Length 331; Best Local Similarity 75.0%; Pred. No. 63; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;									
Qy	1	YGRVFDDY 8	:	:	:	:	:	:	:
Dd	121	YGRGFDDY 128	:	:	:	:	:	:	:
 RESULT 5									
QSVLJ6_HEVR									
ID	QSVLJ6	HEVR PRELIMINARY;	PRT;	366 AA.					
AC	QSVLJ6;								
DT	01-FEB-2005	(T-EMBLrel. 29, Created)							
DT	01-FEB-2005	(T-EMBLrel. 29, Last sequence update)							
DT	01-FEB-2005	(T-EMBLrel. 29, Last annotation update)							
DE	50 kDa protein.								
OS	Hveva brasiliensis (Para rubber tree).								
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;								

Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
 Hammon N., Israni S., Pitluck S., Richardson P.;  
 "Sequencing of the draft genome assembly of *Azotobacter vinelandii*  
 AVOP";  
 Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 [2]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AVOP;  
 RG US DOE Joint Genome Institute (JGI-ORNL);  
 RA Larimer F., Land M.;  
 RT "Annotation of the draft genome assembly of *Azotobacter vinelandii*  
 AVOP";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 [3]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AVOP;  
 RG US DOE Joint Genome Institute;  
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 [4]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AVOP;  
 RG US DOE Joint Genome Institute (JGI-PGP);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
 Hammon N., Israni S., Pitluck S., Richardson P.;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AAU03000012; EAM04553.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 DR  
 SQ SEQUENCE 149 AA; 16436 MW; B03FD0348C9CFDE CRC64;  
 Query Match 83.0%; Score 39; DB 2; Length 149;  
 Best Local Similarity 87.5%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps  
 QY 1 YGRVFDFY 8  
 || |||||  
 Db 119 YGVVFDFY 126  
 RESULT 3  
 Q7N273 PHOLL  
 ID Q7N273 PHOLL PRELIMINARY; PRT; 213 AA.  
 AC Q7N273;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DT Complete genome; segment 11/17.  
 OS OrderedLocutusNames=plu3218;  
 QS Photobacterium luminescens (subsp. laumondii).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Photobacterium.  
 OX NCBI\_TaxID=141679;  
 [1]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=TT01;  
 RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;  
 RA Duchaud E., Rusniok K., Frangeul L., Buchrieser C., Givaudan A.,  
 TAouit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,  
 RA Dassa E., Deroose R., Derzelle S., Freysinet G., Gaudriault S.,  
 RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,  
 RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;  
 RT "The genome sequence of the entomopathogenic bacterium *Photobacterium*  
 luminescens.";  
 RL Nat. Biotechnol. 21:1307-1313 (2003).  
 DR EMBL; BX571869; CAB15592.1; -; Genomic\_DNA.  
 DR Photolist; plu3218; -;  
 KW Complete proteome.  
 SQ SEQUENCE 213 AA; 24684 MW; FB69E290F8C4116C CRC64;  
 Query Match 78.7%; Score 37; DB 2; Length 213;  
 Best Local Similarity 85.7%; Pred. No. 40;



OC	euroside I; Malpighiales; Euphorbiaceae; Crotonoideae; Micrandreae;
OC	Hevea.
OX	NCBI_TaxID=3981;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Kongswadworakul P., Chrestin H.;
RT	"Cloning and characterization of a cDNA encoding 50 kDa protein
RL	involved in latex coagulation.";
DR	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY207386; AAP41849.1; -; mRNA.
DR	GO; GO:0003824; F:catalytic activity; IEA.
DR	InterPro; IPR001087; Lipase_GDSL.
DR	Pfam; PF00657; Lipase_GDSL; 1.
SQ	SEQUENCE 366 AA; 41163 MW; 006F1389E29DCBAD CRC64;
Query Match	78.7%; Score 37; DB 2; Length 366;
Best Local Similarity	75.0%; Pred. No. 70;
Matches	6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1 YGRVFFDY 8
Db	59 YGTTFFDY 66
RESULT 6	
Q6T4P0	HEVBR
ID	Q6T4P0 HEVBR PRELIMINARY; PRT; 366 AA.
AC	Q6T4P0
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Major latex allergen Hev b 4 precursor.
OS	Hevea brasiliensis (para rubber tree).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC	rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
OC	Micrandreae; Hevea.
OX	NCBI_TaxID=3981;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Sunderasan E.; Yeang H.Y.;
RT	"Hevea brasiliensis latex lecithinase homolog.";
RL	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY437086; AAR98518.1; -; mRNA.
DR	GO; GO:0003824; F:catalytic activity; IEA.
DR	InterPro; IPR001087; Lipase_GDSL.
DR	Pfam; PF00657; Lipase_GDSL; 1.
KW	Signal.
FT	SIGNAL
SQ	SEQUENCE 366 AA; 41177 MW; 5PD2BCC136D7F8EE CRC64;
Query Match	78.7%; Score 37; DB 2; Length 366;
Best Local Similarity	75.0%; Pred. No. 70;
Matches	6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1 YGRVFFDY 8
Db	59 YGTTFFDY 66
RESULT 7	
Q9LJB0	ARATH
ID	Q9LJB0 ARATH PRELIMINARY; PRT; 552 AA.
AC	Q9LJB0
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE	Emb CAB77936.1.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;

RN	NUCLEOTIDE SEQUENCE.
RP	MEDLINE=20363099; PubMed=10907853;
RA	Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT	"Structural analysis of Arabidopsis thaliana chromosome 3. II.
RL	Sequence features of the 4,251,695 bp regions covered by 90 PL, TAC
RT	and BAC clones.";
RL	DNA Res. 7:217-221(2000).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RA	Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AP000606; BAB01195.1; -; Genomic DNA.
SQ	SEQUENCE 552 AA; 63036 MW; 740EA16CDEBB2447 CRC64;
Query Match	78.7%; Score 37; DB 2; Length 552;
Best Local Similarity	75.0%; Pred. No. 1.1e+02;
Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy	1 YGRVFFDY 8
Db	283 WGRYFFDY 290
RESULT 8	
Q8IDZ6	PLAF7
ID	Q8IDZ6 PLAF7 PRELIMINARY; PRT; 1838 AA.
AC	Q8IDZ6
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothetical protein FF13_0182.
GN	Names=PF13_0182;
OS	Plasmodium falciparum (isolate 3D7).
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX	NCBI_TaxID=36329;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=3D7;
RA	Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA	Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA	Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrett B.;
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AL844509; CAD52471.1; -; Genomic DNA.
DR	GO; GO:0003824; F:catalytic activity; IEA.
DR	GO; GO:0004839; F:ubiquitin activating enzyme activity; IEA.
DR	GO; GO:0006512; P:ubiquitin cycle; IEA.
DR	InterPro; IPR000594; ThiF domain.
DR	InterPro; IPR000127; UBact_repeat.
DR	InterPro; IPR000011; UBQ_activ_enz_E1.
DR	Pfam; PF00899; ThiF; 2.
DR	Pfam; PF02134; UBACT; 1.
DR	PRINTS; PR01849; UBQUITINACT.
KW	Hypothetical protein.
SQ	SEQUENCE 1838 AA; 218523 MW; 460029B7943F3143 CRC64;
Query Match	78.7%; Score 37; DB 2; Length 1838;
Best Local Similarity	75.0%; Pred. No. 3.8e+02;
Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy	1 YGRVFFDY 8
Db	309 FGRVFDY 316
RESULT 9	
Q8RAL0	THETN
ID	Q8RAL0 THETN PRELIMINARY; PRT; 298 AA.
AC	Q8RAL0
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Chey-like receiver domains.

```
GN Name=ChetV6; OrderedLocusNames=FTE1203;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=2192816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700 (2002).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AEO13083; AAM24433.1; -; Genomic_DNA.
DR HSSP; Q56312; 1TWY.
DR GO; GO:0003577; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg.1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS01110; RESPONSE REGULATORY; 1.
DR Complete proteome; DNA-binding; Sensory transduction; Transcription;
KW Transcription regulation; Two-component regulatory system.
SQ SEQUENCE 298 AA; 34210 MW; ABB5DE49DDC3C539 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 298;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
DB 253 YGVLFDY 260

RESULT 10
O821K0_SALTI
ID Q821K0_SALTI PRELIMINARY; PRT; 90 AA.
AC Q821K0; Q7C5G8;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
DE Hypothetical protein STY4564
GN OrderedLocusNames=STY4564, t4262;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar P.,
RA Feltwell T., Hamilton N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18."
RL Nature 413:848-852 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
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RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337 (2003).
DR EMBL; AL627282; CAD09340.1; -; Genomic_DNA.
DR EMBL; AE016848; AAO71720.1; -; Genomic_DNA.
DR InterPro; IPR010040; Plasmid_RAQPRD.
DR TIGRFAMs; TIGR01690; plasmid_RAQPRD; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 90 AA; 10309 MW; 133893BFF86FEDF0 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 90;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVFFDY 8
DB 44 GRVFFDY 50

RESULT 11
Q6GUD4_EDWIC
ID Q6GUD4_EDWIC PRELIMINARY; PRT; 113 AA.
AC Q6GUD4;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Edwardsiella ictaluri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Edwardsiella.
OX NCBI_TaxID=67780;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Thune R.L., Fernandez D.H., Benoit J.L., Kelly-Smith M., Rogge M.L.,
RA Booth N.J., Bologna R.A.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641981; AAT47192.1; -; Genomic_DNA.
DR InterPro; IPR010040; Plasmid_RAQPRD.
DR TIGRFAMs; TIGR01690; plasmid_RAQPRD; 1.
KW Hypothetical protein.
SQ SEQUENCE 113 AA; 12533 MW; 4F556CE8590CC469 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVFFDY 8
DB 68 GRVFFDY 74

RESULT 12
Q96ZJ6_SULTO
ID Q96ZJ6_SULTO PRELIMINARY; PRT; 270 AA.
AC Q96ZJ6;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (T-EMBLrel. 26, Last annotation update)
DE 270aa long hypothetical thiosulfate reductase electron transport
protein phsB.
GN OrderedLocusNames=ST1839;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
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RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
RA Ohnima T., Kikuchi H.;  
RT "Complete genome sequence of an aerobic thermoacidophilic  
RL Crenarchaeon, Sulfolobus tokodaii strain7.";  
RL DNA Res. 8:123-140(2001).  
DR EMBL: BA000023; BAB66929.1; -; Genomic\_DNA.  
DR HSP: P11349; 1R27.  
DR GO: GO:0005489; F:electron transporter activity; IEA.  
DR GO: GO:0005506; F:iron ion binding; IEA.  
DR GO: GO:0046872; F:metal ion binding; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR InterPro: IPR001450; 4Fe4S\_Fe\_S\_bd.  
DR Pfam: PF00037; Fer4; 1.  
DR PRINTS: PR00353; 4FE4SPDOXIN.  
DR 4Fe-4S; Complete proteome; Electron transport; Hypothetical protein;  
KW Iron; Iron-sulfur; Metal-binding; Transport.  
SQ SEQUENCE 270 AA; 30000 MW; 4600F746D8BF1685 CRC64;  
  
Query Match 74.5%; Score 35; DB 2; Length 270;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 YGRVFFDY 8  
DB 138 YGNRFFDY 145  
  
RESULT 13  
END4 MYCPE  
ID END4\_MYCPE STANDARD; PRT; 289 AA.  
AC QSEW2; 2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Probable endonuclease IV (EC 3.1.21.2) (Endodeoxyribonuclease IV).  
GN Name=info; OrderedLocusNames=MYPE1190;  
OS Mycoplasma penetrans.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=28227;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=HF-2;  
RX MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;  
RA Sasaki Y., Ishikawa J., Yamashita A., Ohnima K., Kenri T., Furuya K.,  
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;  
RT "The complete genomic sequence of Mycoplasma penetrans, an  
RT intracellular bacterial pathogen in humans.";  
RL Nucleic Acids Res. 30:5293-5300(2002).  
CC -1- FUNCTION: Endonuclease IV plays a role in DNA repair. It cleaves  
CC phosphodiester bonds at apurinic or apyrimidinic sites (AP sites)  
CC to produce new 5' ends that are base-free deoxyribose 5-phosphate  
CC residues. It preferentially attacks modified AP sites created by  
CC bleomycin and neocarzinostatin (By similarity).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-  
CC phosphooligonucleotide end-products.  
CC -1- COFACTOR: Binds 3 zinc ions (By similarity).  
CC -1- SIMILARITY: Belongs to the AP endonuclease 2 family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL: BA000026; BAC43911.1; ALT\_INIT; Genomic\_DNA.  
DR HSP: P12638; 1QW.  
DR HAMAP: MF\_00152; -; 1.  
DR InterPro: IPR001719; AP endonuclease2.  
DR InterPro: IPR012307; Xylisom TIMbar1.  
DR Pfam: PF01261; AP endonuc 2; 1.  
DR TIGRFAMs: TIGR00587; nfo; 1.  
DR PROSITE: PS00729; AP\_NUCLEASE\_F2\_1; 1.

DR PROSITE: PS00730; AP\_NUCLEASE\_F2\_2; 1.  
DR PROSITE: PS00731; AP\_NUCLEASE\_F2\_3; 1.  
KW Complete proteome; DNA damage; DNA repair; Endonuclease; Hydrolase;  
KW Metal-binding; Nuclease; Zinc  
FT METAL 76 Zinc 1 (By similarity).  
FT METAL 116 Zinc 1 (By similarity).  
FT METAL 152 Zinc 1 and 2 (By similarity).  
FT METAL 186 Zinc 2 (By similarity).  
FT METAL 189 Zinc 2 (By similarity).  
FT METAL 220 Zinc 2 (By similarity).  
FT METAL 220 Zinc 2 (By similarity).  
FT METAL 233 Zinc 3 (By similarity).  
FT METAL 235 Zinc 3 (By similarity).  
FT METAL 265 Zinc 2 (By similarity).  
SQ SEQUENCE 289 AA; 32583 MW; 985835176E016EB9 CRC64;  
  
Query Match 74.5%; Score 35; DB 1; Length 289;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YGRVFFDY 8  
DB 240 YGKVGFDY 247

RESULT 14  
Q97V38 SULSO  
ID Q97V38\_SULSO PRELIMINARY; PRT; 293 AA.  
AC Q97V38; 2001 (TRENBLrel. 18, Created)  
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)  
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Oxydoreductase, putative.  
GN OrderedLocusNames=SSO2794;  
OS Sulfolobus solfataricus.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=2287;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;  
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
RA Aways M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,  
RA De Moers A., Ekaus G., Fletcher C., Gordon P.M.K.,  
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland I.,  
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;  
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
DR EMBL: AE006873; AAK42907.1; -; Genomic\_DNA.  
DR PIR: D90456; D90456.  
DR HSP: P00214; 2PD2.  
DR GO: GO:0005489; F:electron transporter activity; IEA.  
DR GO: GO:0005506; F:iron ion binding; IEA.  
DR GO: GO:0046872; F:metal ion binding; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR InterPro: IPR001450; 4Fe4S\_Fe\_S\_bd.  
DR Pfam: PF00037; Fer4; 1.  
DR PRINTS: PR00353; 4FE4SPDOXIN.  
KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;  
KW Metal-binding; Transport.  
SQ SEQUENCE 293 AA; 32382 MW; C13A04963619EDAD CRC64;  
  
Query Match 74.5%; Score 35; DB 2; Length 293;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 YGRVFFDY 8  
DB 159 YGNRFFDY 166

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ID Q5L810 BACFN PRELIMINARY; PRT; 298 AA.
AC Q5L810;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative AraC-family transcriptional regulator.
GN OrderedLocusNames=BF4113;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression.";
RL Science 307:1463-1465(2005).
DR EMBL; CR626927; CAH09787.1; -; Genomic_DNA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR000005; HTHARAC.
DR Pfam; PF00165; HTH_AraC; 1.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Activator; Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 298 AA; 34641 MW; A08394D705F34AD1 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 298;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db ||| :||
61 YGRKYDY 68
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Search completed: December 30, 2005, 13:33:33  
Job time : 75 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 17.9355 Seconds  
(without alignments)  
36.877 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgm2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
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6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	80.9	138	2	US-09-252-991A-20154
2	35	74.5	72	2	US-09-248-796A-21727
3	35	74.5	233	2	US-09-134-000C-4002
4	35	74.5	390	2	US-09-252-991A-33062
5	34	72.3	12	2	US-08-974-899-12
6	34	72.3	12	2	US-09-795-798-12
7	34	72.3	17	1	US-08-306-871-41
8	34	72.3	17	1	US-08-569-959-41
9	34	72.3	26	1	US-08-306-871-33
10	34	72.3	26	1	US-08-569-959-33
11	34	72.3	71	1	US-08-306-871-28
12	34	72.3	71	1	US-08-569-959-28
13	34	72.3	92	2	US-09-270-767-61481
14	34	72.3	116	2	US-09-027-449-50
15	34	72.3	116	2	US-08-804-444A-50
16	34	72.3	116	2	US-09-026-985-50
17	34	72.3	116	2	US-09-121-952A-50
18	34	72.3	116	2	US-09-234-340A-50
19	34	72.3	116	2	US-09-355-014-50
20	34	72.3	121	2	US-08-974-899-4
21	34	72.3	121	2	US-08-974-899-5
22	34	72.3	121	2	US-08-974-899-24
23	34	72.3	121	2	US-09-795-798-4
24	34	72.3	121	2	US-09-795-798-5
25	34	72.3	121	2	US-09-795-798-24
26	34	72.3	133	2	US-09-540-236-3221
27	34	72.3	142	1	US-08-860-174A-7

28 34 72.3 274 1 US-08-860-174A-12 Sequence 12, Appl  
29 34 72.3 282 1 US-08-860-174A-10 Sequence 10, Appl  
30 34 72.3 306 2 US-09-270-767-45943 Sequence 45943, A  
31 34 72.3 514 2 US-09-502-540-12330 Sequence 12330, A  
32 34 72.3 731 1 US-08-696-944-20 Sequence 20, Appl  
33 33 70.2 375 2 US-09-248-796A-15005 Sequence 15005, A  
34 33 70.2 878 2 US-09-937-908-1 Sequence 1, Appl  
35 32 68.1 10 2 US-09-406-535-7 Sequence 7, Appl  
36 32 68.1 119 2 US-09-406-535-2 Sequence 2, Appl  
37 32 68.1 120 1 US-08-497-312-26 Sequence 26, Appl  
38 32 68.1 120 1 US-08-497-312-28 Sequence 28, Appl  
39 32 68.1 122 2 US-10-092-246-10 Sequence 10, Appl  
40 32 68.1 122 2 US-10-092-246-11 Sequence 11, Appl  
41 32 68.1 122 2 US-10-096-246A-10 Sequence 10, Appl  
42 32 68.1 122 2 US-10-096-246A-11 Sequence 11, Appl  
43 32 68.1 123 2 US-09-840-459-91 Sequence 91, Appl  
44 32 68.1 123 2 US-09-497-625A-91 Sequence 91, Appl  
45 32 68.1 139 2 US-08-454-899G-15 Sequence 15, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-252-991A-20154  
; Sequence 20154, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20154  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20154

Query Match 80.9%; Score 38; DB 2; Length 138;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8  
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Db 98 YGRIFRY 105

##### RESULT 2

US-09-248-796A-21727  
; Sequence 21727, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 21727  
; LENGTH: 72  
; TYPE: PRT

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; ORGANISM: Candida albicans
US-09-248-796A-21727

Query Match      74.5%; Score 35; DB 2; Length 72;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFD 7
Db 11 YGRIFFE 17

RESULT 3
US-09-134-000C-4002
; Sequence 4002, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4002
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4002

Query Match      74.5%; Score 35; DB 2; Length 233;
Best Local Similarity 62.5%; Pred. No. 64;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 131 YGKISFDY 138

RESULT 4
US-09-252-991A-33062
; Sequence 33062, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33062
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33062

Query Match      74.5%; Score 35; DB 2; Length 390;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 350 YGRIFFY 357
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RESULT 5
US-08-974-899-12
; Sequence 12, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-974-899-12

Query Match      72.3%; Score 34; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 5.1;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 5 YGTYTFDY 12

RESULT 6
US-09-795-798-12
; Sequence 12, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/795,798  
FILING DATE: 28-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/974,899  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P1014R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-795-798-12

Query Match 72.3%; Score 34; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 5.1;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
DB 5 YGTYFDY 12

RESULT 7  
US-08-306-871-41  
Sequence 41, Application US/08306871  
Patent No. 5712118  
GENERAL INFORMATION:  
APPLICANT: Timothy F. Murphy  
TITLE OF INVENTION: Vaccine For Branhamella catarrhalis  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1  
SOFTWARE: Wordperfect for Windows 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,871  
FILING DATE: 20-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/129,719  
FILING DATE: September 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 11520.0053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 residues  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Branhamella catarrhalis  
STRAIN: 25240  
FEATURE:  
LOCATION: CD amino acid positions 295-311

US-08-306-871-41

Query Match 72.3%; Score 34; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8  
DB 9 RVFFDY 14

RESULT 8  
US-08-569-959-41  
Sequence 41, Application US/08569959  
Patent No. 5725862  
GENERAL INFORMATION:  
APPLICANT: Timothy F. Murphy  
TITLE OF INVENTION: Vaccine For Branhamella catarrhalis  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1  
SOFTWARE: Wordperfect for Windows 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,959  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/129,719  
FILING DATE: September 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 11520.0053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 residues  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Branhamella catarrhalis  
STRAIN: 25240  
FEATURE:  
LOCATION: CD amino acid positions 295-311

US-08-569-959-41

Query Match 72.3%; Score 34; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8  
DB 9 RVFFDY 14

RESULT 9  
US-08-306-871-33  
Sequence 33, Application US/08306871  
Patent No. 5712118  
GENERAL INFORMATION:  
APPLICANT: Timothy F. Murphy  
TITLE OF INVENTION: Vaccine For Branhamella catarrhalis

```
/
/
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
/ STREET: 1800 One M&T Plaza
/ CITY: Buffalo
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 14203-2391
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
/ SOFTWARE: Wordperfect for Windows 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,871
/ FILING DATE: 20-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/129,719
/ FILING DATE: September 29, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nelson, M. Bud
/ REGISTRATION NUMBER: 35,300
/ REFERENCE/DOCKET NUMBER: 11520.0053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (716) 856-4000
/ TELEFAX: (716) 849-0349
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 residues
/ TYPE: amino acid
/ TOPOLOGY: linear
/ ORGANISM: Branhamella catarrhalis
/ STRAIN: 25240
/ FEATURE:
/ LOCATION: CD amino acid positions 286-311
/ US-08-306-871-33

Query Match 72.3%; Score 34; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8
Db 18 RVFFDY 23

RESULT 10
US-08-569-959-33
/ Sequence 33, Application US/08569959
/ Patent No. 5725862
/ GENERAL INFORMATION:
/ APPLICANT: Timothy F. Murphy
/ TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
/ STREET: 1800 One M&T Plaza
/ CITY: Buffalo
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 14203-2391
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
/ SOFTWARE: Wordperfect for Windows 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/569,959
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: U.S. 08/129,719
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/
/
/ FILING DATE: September 29, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nelson, M. Bud
/ REGISTRATION NUMBER: 35,300
/ REFERENCE/DOCKET NUMBER: 11520.0053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (716) 856-4000
/ TELEFAX: (716) 849-0349
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 residues
/ TYPE: amino acid
/ TOPOLOGY: linear
/ ORGANISM: Branhamella catarrhalis
/ STRAIN: 25240
/ FEATURE:
/ LOCATION: CD amino acid positions 286-311
/ US-08-569-959-33

Query Match 72.3%; Score 34; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8
Db 18 RVFFDY 23

RESULT 11
US-08-306-871-28
/ Sequence 28, Application US/08306871
/ Patent No. 5712118
/ GENERAL INFORMATION:
/ APPLICANT: Timothy F. Murphy
/ TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
/ STREET: 1800 One M&T Plaza
/ CITY: Buffalo
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 14203-2391
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
/ SOFTWARE: Wordperfect for Windows 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,871
/ FILING DATE: 20-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/129,719
/ FILING DATE: September 29, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nelson, M. Bud
/ REGISTRATION NUMBER: 35,300
/ REFERENCE/DOCKET NUMBER: 11520.0053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (716) 856-4000
/ TELEFAX: (716) 849-0349
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 71 residues
/ TYPE: amino acid
/ TOPOLOGY: linear
/ ORGANISM: Branhamella catarrhalis
/ STRAIN: 25240
/ FEATURE:
/ LOCATION: CD amino acid positions 261-331
/ US-08-306-871-28
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Query Match 72.3%; Score 34; DB 1; Length 71;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 RVFFDY 8  
DB 43 RVFFDY 48

RESULT 12  
US-08-569-959-28  
; Sequence 28, Application US/08569959  
; Patent No. 5725862  
; GENERAL INFORMATION:  
; APPLICANT: Timothy F. Murphy  
; TITLE OF INVENTION: Vaccine For Branhamella catarrhalis  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
; STREET: 1800 One M&T Plaza  
; CITY: Buffalo  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 14203-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Dikette, 3.5 inch, 1.4 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1  
; SOFTWARE: Wordperfect for Windows 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/569,959  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/129,719  
; FILING DATE: September 29, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nelson, M. Bud  
; REGISTRATION NUMBER: 35,300  
; REFERENCE/DOCKET NUMBER: 11520.0053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 856-4000  
; TELEFAX: (716) 849-0349  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 71 residues  
; TYPE: amino acid  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Branhamella catarrhalis  
; STRAIN: 25240  
; FEATURE:  
; LOCATION: CD amino acid positions 261-331  
US-08-569-959-28

Query Match 72.3%; Score 34; DB 1; Length 71;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 RVFFDY 8  
DB 43 RVFFDY 48

RESULT 13  
US-09-270-767-61481  
; Sequence 61481, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 61481  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-61481

Query Match 72.3%; Score 34; DB 2; Length 92;  
Best Local Similarity 62.5%; Pred. No. 38;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YGRVFFDY 8  
DB 84 FGKVFYDY 91

RESULT 14  
US-09-027-449-50  
; Sequence 50, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,664  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-027-449-50

Query Match 72.3%; Score 34; DB 2; Length 116;  
Best Local Similarity 62.5%; Pred. No. 48;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YGRVFFDY 8  
DB 104 YGTTVFYDY 111

RESULT 15  
US-08-804-444A-50  
; Sequence 50, Application US/0880444A  
; Patent No: 6117980  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania N  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,444A  
; FILING DATE: 21-Feb-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-804-444A-50

Query Match 72.3%; Score 34; DB 2; Length 116;  
Best Local Similarity 62.5%; Pred. NO. 48;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||:|  
Db 104 YGTYFDY 111

Search completed: December 30, 2005, 13:37:19  
Job time : 17.9355 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 59.4839 Seconds  
(without alignments)  
56.194 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA\_Main.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	5	US-10-735-916A-12
2	47	100.0	117	5	US-10-735-916A-69
3	47	100.0	117	5	US-10-735-916A-75
4	47	100.0	117	5	US-10-735-916A-79
5	47	100.0	117	5	US-10-735-916A-83
6	47	100.0	127	5	US-10-735-916A-52
7	47	100.0	135	5	US-10-735-916A-77
8	47	100.0	135	5	US-10-735-916A-81
9	47	100.0	135	5	US-10-735-916A-85
10	37	78.7	101	4	US-10-424-599-232867
11	37	78.7	264	4	US-10-437-963-122750
12	37	78.7	331	4	US-10-156-761-10380
13	37	78.7	366	6	US-11-083-779-2
14	36	76.6	410	3	US-09-767-041-28
15	35	74.5	1425	6	US-11-097-143-42516
16	34	72.3	12	3	US-09-795-798-12
17	34	72.3	76	4	US-10-424-599-248530
18	34	72.3	116	3	US-09-726-258-50
19	34	72.3	121	3	US-09-795-798-4
20	34	72.3	121	3	US-09-795-798-5
21	34	72.3	121	3	US-09-795-798-24
22	34	72.3	121	4	US-10-727-737-4
23	34	72.3	121	4	US-10-727-737-5
24	34	72.3	121	4	US-10-727-737-17
25	34	72.3	121	5	US-10-877-532-6
26	34	72.3	126	4	US-10-041-860-25
27	34	72.3	126	4	US-10-041-860-210

28 34 72.3 126 4 US-10-041-860-246 Sequence 246, App  
29 34 72.3 126 4 US-10-041-860-306 Sequence 306, App  
30 34 72.3 126 4 US-10-665-383-30 Sequence 30, Appl  
31 34 72.3 201 4 US-10-425-115-190681 Sequence 190681, A  
32 34 72.3 218 4 US-10-282-122A-51409 Sequence 51409, A  
33 34 72.3 303 4 US-10-425-114-61737 Sequence 61737, A  
34 34 72.3 348 5 US-10-739-930-7547 Sequence 7547, Ap  
35 34 72.3 352 4 US-10-425-115-331492 Sequence 331492, A  
36 34 72.3 451 4 US-10-423-299-4 Sequence 4, Appl  
37 34 72.3 453 4 US-10-467-421-39 Sequence 39, Appl  
38 34 72.3 464 5 US-10-938-353-22 Sequence 22, Appl  
39 33 70.2 11 5 US-10-996-316-196 Sequence 196, App  
40 33 70.2 47 4 US-10-724-972A-7151 Sequence 7151, Ap  
41 33 70.2 56 4 US-10-424-599-234979 Sequence 234979, A  
42 33 70.2 68 4 US-10-424-599-191549 Sequence 191549, A  
43 33 70.2 118 5 US-10-938-992-15 Sequence 15, Appl  
44 33 70.2 220 4 US-10-335-977-6258 Sequence 6258, Ap  
45 33 70.2 220 4 US-10-335-977-6259 Sequence 6259, Ap

#### ALIGNMENTS

RESULT 1  
US-10-735-916A-12  
; Sequence 12, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-12

Query Match 100.0%; Score 47; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGRVFFDY 8  
Db 1 YGRVFFDY 8

RESULT 2  
US-10-735-916A-69  
; Sequence 69, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier

; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 69  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-69

Query Match 100.0%; Score 47; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||  
Db 99 YGRVFFDY 106

RESULT 3  
US-10-735-916A-75  
; Sequence 75, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 75  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-735-916A-75

Query Match 100.0%; Score 47; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||  
Db 99 YGRVFFDY 106

Db 99 YGRVFFDY 106  
RESULT 4  
US-10-735-916A-79  
; Sequence 79, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 79  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-735-916A-79

Query Match 100.0%; Score 47; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||  
Db 99 YGRVFFDY 106

RESULT 5  
US-10-735-916A-83  
; Sequence 83, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 83

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; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83

Query Match      100.0%; Score 47; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
      |||||
Db      99 YGRVFFDY 106

RESULT 6
US-10-735-916A-52
; Sequence 52, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52

Query Match      100.0%; Score 47; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
      |||||
Db      109 YGRVFFDY 116

RESULT 7
US-10-735-916A-77
; Sequence 77, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-81

Query Match      100.0%; Score 47; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
      |||||
Db      117 YGRVFFDY 124

RESULT 8
US-10-735-916A-81
; Sequence 81, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-81

Query Match      100.0%; Score 47; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
      |||||
Db      117 YGRVFFDY 124

RESULT 9
US-10-735-916A-85
; Sequence 85, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
```

; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGP-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 01753-183  
; CURRENT APPLICATION NUMBER: US/10/735,916A  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 85  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-735-916A-85

Query Match 100.0%; Score 47; DB 5; Length 135;  
Best Local Similarity 100.0%; Pred. No. 0.89; Length 135;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||  
Db 117 YGRVFFDY 124

RESULT 10  
US-10-424-599-232867  
; Sequence 232867, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 232867  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(101)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_52303C.1.pep  
US-10-424-599-232867

Query Match 78.7%; Score 37; DB 4; Length 101;  
Best Local Similarity 75.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||  
Db 77 YGRTLFY 84

RESULT 11

US-10-437-963-122750  
; Sequence 122750, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 122750  
; LENGTH: 264  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_2564C.1.pep  
US-10-437-963-122750

Query Match 78.7%; Score 37; DB 4; Length 264;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||  
Db 111 YGRIFFIY 118

RESULT 12  
US-10-156-761-10380  
; Sequence 10380, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 10380  
; LENGTH: 331  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-10380

Query Match 78.7%; Score 37; DB 4; Length 331;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||  
Db 121 YGKGFFDY 128

RESULT 13  
US-11-083-779-2

; Sequence 2, Application US/11083779  
; Publication No. US20050227292A1  
; GENERAL INFORMATION:  
; APPLICANT: Malaysian Rubber Board  
; APPLICANT: Sunderasan, Elumalai  
; APPLICANT: Arif, Siti Ajuma Mad  
; APPLICANT: Yeang, Hoong Vest  
; TITLE OF INVENTION: AN ALLERGENIC PROTEIN COMPLEX OF NATURAL RUBBER LATEX  
; FILE REFERENCE: SHP-PT086  
; CURRENT APPLICATION NUMBER: US/11/083,779  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: P120040947  
; PRIOR FILING DATE: 2004-03-18  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Hevea brasiliensis  
US-11-083-779-2

Query Match 78.7%; Score 37; DB 6; Length 366;  
Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 YGRVFFDY 8  
Db 59 YGTTFFDY 66

## RESULT 14

US-09-767-041-28  
; Sequence 28, Application US/09767041  
; Patent No. US20020055168A1  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Hilda  
; TITLE OF INVENTION: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS  
; FILE REFERENCE: 2183-4726  
; CURRENT APPLICATION NUMBER: US/09/767,041  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: PCT/NL99/00460  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: EP98202465.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: EP98202467.1  
; PRIOR FILING DATE: 1998-07-22  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Streptococcus suis  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: CPS2T  
US-09-767-041-28

Query Match 76.6%; Score 36; DB 3; Length 410;  
Best Local Similarity 71.4%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GRVFFDY 8  
Db 219 GRVFFDY 225

## RESULT 15

US-11-097-143-42516  
; Sequence 42516, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42516  
; LENGTH: 1425  
; TYPE: PRT  
; ORGANISM: DROSOPHILA  
US-11-097-143-42516

Query Match 74.5%; Score 35; DB 6; Length 1425;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YGRVFFDY 8  
Db 514 YGRVFFDY 521

Search completed: December 30, 2005, 14:15:03  
Job time : 64.4839 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 2.96774 Seconds  
(without alignments)  
20.187 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*

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- 2: /cgm2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgm2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgm2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgm2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
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- 7: /cgm2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgm2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	7	US-11-012-353-12
2	47	100.0	117	7	US-11-012-353-69
3	47	100.0	117	7	US-11-012-353-75
4	47	100.0	117	7	US-11-012-353-79
5	47	100.0	117	7	US-11-012-353-83
6	47	100.0	117	7	US-11-012-353-162
7	47	100.0	127	7	US-11-012-353-52
8	47	100.0	135	7	US-11-012-353-77
9	47	100.0	135	7	US-11-012-353-81
10	47	100.0	135	7	US-11-012-353-85
11	34	72.3	121	6	US-10-665-658-12
12	34	72.3	121	6	US-10-665-658-4
13	34	72.3	121	6	US-10-665-658-5
14	34	72.3	121	6	US-10-665-658-24
15	34	72.3	121	7	US-11-107-028-50
16	34	72.3	121	7	US-11-107-028-52
17	33	70.2	341	6	US-10-467-657-154
18	33	70.2	341	6	US-10-467-657-5822
19	33	70.2	341	6	US-10-467-657-7476
20	32	68.1	120	6	US-10-932-334-71
21	32	68.1	120	6	US-10-932-334-72
22	32	68.1	216	6	US-10-467-657-8102
23	31	66.0	161	6	US-10-467-657-8822
24	31	66.0	167	6	US-10-967-457-79
25	31	66.0	312	7	US-11-129-143-94

Sequence 1606, Ap  
Sequence 54, Appl  
Sequence 1097, Ap  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 51, Appl  
Sequence 10, Appl  
Sequence 8, Appl  
Sequence 2207, Ap  
Sequence 2374, Ap  
Sequence 3148, Ap  
Sequence 1899, Ap  
Sequence 199, App  
Sequence 983, App  
Sequence 950, App  
Sequence 2608, Ap  
Sequence 476, App  
Sequence 1770, Ap  
Sequence 208, App  
Sequence 227, App

#### ALIGNMENTS

##### RESULT 1

US-11-012-353-12

; Sequence 12, Application US/11012353

; Publication No. US20050249730A1

; GENERAL INFORMATION:

; APPLICANT: GOETSCH, LILIANE

; APPLICANT: CORVAIA, NATHALIE

; APPLICANT: DUFLLOS, ALAIN

; APPLICANT: HAEUW, JEAN-FRANCOIS

; APPLICANT: LEGER, OLIVIER

; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 017753-198

; CURRENT APPLICATION NUMBER: US/11/012,353

; CURRENT FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 10/735,916

; PRIOR FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 0308538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR03/00178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 0205753

; PRIOR FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: FR 0200653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 0200654

; PRIOR FILING DATE: 2002-01-18

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: Patent in Ver. 3.3

; SEQ ID NO 12

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Mus musculus

; US-11-012-353-12

Query Match 100.0%; Score 47; DB 7; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGRVFFDY 8

Db 1 YGRVFFDY 8

##### RESULT 2

US-11-012-353-69

; Sequence 69, Application US/11012353

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; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-69

Query Match      100.0%; Score 47; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
DB      99 YGRVFFDY 106

RESULT 3
US-11-012-353-75
; Sequence 75, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 75
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-79

Query Match      100.0%; Score 47; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
DB      99 YGRVFFDY 106

RESULT 4
US-11-012-353-79
; Sequence 79, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-79

Query Match      100.0%; Score 47; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
DB      99 YGRVFFDY 106

RESULT 5
US-11-012-353-83
; Sequence 83, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
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; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 83  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-83

Query Match 100.0%; Score 47; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8  
| | | | | | | |  
Db 99 YGRVFFDY 106

RESULT 6  
US-11-012-353-162  
; Sequence 162, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 162  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-162

Query Match 100.0%; Score 47; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8  
| | | | | | | |

Db 99 YGRVFFDY 106

RESULT 7  
US-11-012-353-52  
; Sequence 52, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 52  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-012-353-52

Query Match 100.0%; Score 47; DB 7; Length 127;  
Best Local Similarity 100.0%; Pred. No. 0.026;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8  
| | | | | | | |  
Db 109 YGRVFFDY 116

RESULT 8  
US-11-012-353-77  
; Sequence 77, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 162  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-162

Query Match 100.0%; Score 47; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8  
| | | | | | | |

; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 77  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-77

Query Match 100.0%; Score 47; DB 7; Length 135;  
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||||  
Db 117 YGRVFFDY 124

## RESULT 9

US-11-012-353-81  
; Sequence 81, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN  
; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 10/735,916  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 81  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-11-012-353-81

Query Match 100.0%; Score 47; DB 7; Length 135;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||||  
Db 117 YGRVFFDY 124

## RESULT 10

US-11-012-353-85  
; Sequence 85, Application US/11012353  
; Publication No. US20050249730A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, LILIANE  
; APPLICANT: CORVAIA, NATHALIE  
; APPLICANT: DUFLOS, ALAIN

; APPLICANT: HAEUW, JEAN-FRANCOIS  
; APPLICANT: LEGER, OLIVIER  
; APPLICANT: BECK, ALAIN  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID  
; FILE REFERENCE: 017753-198  
; CURRENT APPLICATION NUMBER: US/11/012,353  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 0308538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR03/00178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 0205753  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: FR 0200653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 0200654  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 85  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-012-353-85

Query Match 100.0%; Score 47; DB 7; Length 135;  
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
|||||  
Db 117 YGRVFFDY 124

## RESULT 11

US-10-665-658-12  
; Sequence 12, Application US/10665658  
; Publication No. US20050276801A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/665,658  
FILING DATE: 19-Sep-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/031971  
FILING DATE: 27-NOV-1996  
APPLICATION NUMBER: 08/974899  
FILING DATE: 20-NOV-1997  
APPLICATION NUMBER: 09/420745  
FILING DATE: 20-OCT-1999  
APPLICATION NUMBER: 09/975798  
FILING DATE: 28-FEB-2001  
ATTORNEY/AGENT INFORMATION:  
NAME: Tan, Lee K.

```

; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-665-658-12
Query Match 72.3%; Score 34; DB 6; Length 12;
Best Local Similarity 62.5%; Pred. No. 0.74; 2; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
Db 5 YGTYFFDY 12

RESULT 12
US-10-665-658-4
; Sequence 4, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-665-658-4
Query Match 72.3%; Score 34; DB 6; Length 12;
Best Local Similarity 62.5%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
Db 103 YGTYFFDY 110

RESULT 13
US-10-665-658-5
; Sequence 5, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-665-658-5
Query Match 72.3%; Score 34; DB 6; Length 121;
Best Local Similarity 62.5%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
Db 103 YGTYFFDY 110

RESULT 14
US-10-665-658-24
; Sequence 24, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

```

NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/665,658  
FILING DATE: 19-Sep-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/031971  
FILING DATE: 27-NOV-1996  
APPLICATION NUMBER: 08/974899  
FILING DATE: 20-NOV-1997  
APPLICATION NUMBER: 09/420745  
FILING DATE: 20-OCT-1999  
APPLICATION NUMBER: 09/975798  
FILING DATE: 28-FEB-2001  
ATTORNEY/AGENT INFORMATION:  
NAME: Tan, Lee K.  
REGISTRATION NUMBER: 39,447  
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-4462  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-10-665-658-24

Query Match 72.3%; Score 34; DB 6; Length 121;  
Best Local Similarity 62.5%; Pred. No. 5.7;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
||| :|||  
Db 103 YGTTYFDY 110

RESULT 15  
US-11-107-028-50  
; Sequence 50, Application US/11107028  
; Publication No. US20050276803A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAN, ANDREW C.  
; APPLICANT: GONG, QIAN  
; APPLICANT: MARTIN, FLAVIUS  
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion  
; FILE REFERENCE: P2112R1  
; CURRENT APPLICATION NUMBER: US/11/107,028  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/563,263  
; PRIOR FILING DATE: 2004-04-16  
; NUMBER OF SEQ ID NOS: 52  
; SEQ ID NO 50  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
US-11-107-028-50

Query Match 72.3%; Score 34; DB 7; Length 121;  
Best Local Similarity 62.5%; Pred. No. 5.7;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
||| :|||  
Db 103 YGTTYFDY 110

Search completed: December 30, 2005, 14:15:22  
Job time : 2.96774 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 15:35:45 ; Search time 182 Seconds

(without alignments)  
19.313 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 49824

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	7	ADJ76846 CDR seque
2	47	100.0	8	9	ADZ67016 Murine in
3	28	59.6	8	2	AAR80018 Cytotoxic
4	28	59.6	8	2	AAR84899 Epstein-B
5	28	59.6	8	2	AAW40865 Cytotoxic
6	28	59.6	8	2	AAV10595 HLA Class
7	28	59.6	8	2	AAV10107 T cell ep
8	28	59.6	8	5	ABG80278 MHC class
9	28	59.6	8	5	ABG79790 MHC class
10	28	59.6	8	8	ADK68717 Epitope 1
11	28	59.6	8	8	ADK69224 Epitope 1
12	28	59.6	8	8	ADJ84659 CTL epit
13	28	59.6	8	8	ADQ11023 Cercopith
14	28	59.6	8	8	ADQ10515 Cercopith
15	28	59.6	8	8	ADJ80395 Tumour-as
16	28	59.6	8	8	ADJ81503 Tumour-as
17	26	55.3	8	5	ABP47168 Human Bly
18	26	55.3	8	7	ADG97995 scFV VHCD
19	25	53.2	8	3	AAV77587 Anti-huma
20	25	53.2	8	4	ABJ78856 Anti-huma
21	25	53.2	8	5	ABG98099 Anti-neov
22	25	53.2	8	5	AAE28157 Murine 9F
23	25	53.2	8	6	ABP74517 Human PSM
24	25	53.2	8	7	ABR61876 Mouse Mab

25	25	53.2	8	7	ADC09376	Adc09376 Epitope w
26	25	53.2	8	8	ADL11879	Adl11879 CDR-1 hea
27	25	53.2	8	8	ADP84864	Adp84864 Complemen
28	25	53.2	8	8	ADQ31265	Adq31265 CDR3 pept
29	25	53.2	8	9	ADZ58521	Adz58521 VEGF rece
30	25	53.2	8	9	AEA40143	Aea40143 TNF resis
31	25	53.2	8	9	AEA38763	Aea38763 Humanized
32	25	53.2	8	9	AEA38795	Aea38795 Humanized
33	25	53.2	8	9	AEA53829	Aea53829 Novel hum
34	25	53.2	8	9	AEA53800	Aea53800 Novel hum
35	25	53.2	8	9	AEA53496	Aea53496 Novel hum
36	25	53.2	8	9	AEA45972	Aea45972 Apolipop
37	24	51.1	8	5	AAU99851	Aau99851 Mouse AC1
38	24	51.1	8	7	AAO29925	Aao29925 Mouse ant
39	24	51.1	8	8	ADJ87910	Adj87910 Mouse AC1
40	23	48.9	8	2	AAW29379	Aaw29379 Somatosta
41	23	48.9	8	2	AAV28181	Aay28181 Factor Xa
42	23	48.9	8	4	AAW98001	Aam98001 Human pep
43	23	48.9	8	5	ABB76371	Abb76371 Haemophil
44	23	48.9	8	8	ADO05137	Ado05137 Epsilon c
45	23	48.9	8	8	ADR04717	Adr04717 Factor XA

## ALIGNMENTS

RESULT 1  
ADJ76846  
ID ADJ76846 standard; peptide; 8 AA.  
XX  
AC ADJ76846;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DB CDR sequence for anti-IGF-1R antibody.  
XX  
KW cytostatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX  
OS Mus musculus.  
XX  
FN WO2003059951-A2.  
XX  
PD 24-JUL-2003.  
XX  
PF 20-JAN-2003; 2003WO-FR000178.  
XX  
PR 18-JAN-2002; 2002FR-00000653.  
PR 18-JAN-2002; 2002FR-00000654.  
PR 07-MAY-2002; 2002FR-00005753.  
XX  
FA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
PI Goetsch L, Corvaia N, Leger O;  
XX  
DR WPI; 2003-569653/53.  
DR N-PSDB; ADJ76845.  
XX  
PT New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.  
XX  
PS Claim 1; SEQ ID NO 12; 164pp; French.  
XX  
CC The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of  
 CC these receptors with their ligands. Especially they inhibit  
 CC transformation of normal cells to tumor cells, inhibit growth and/or  
 CC proliferation of tumor cells, so are useful against cancers of the  
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an  
 CC CDR sequence used to generate the Ab of the invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 7; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8

Db 1 YGRVFFDY 8

RESULT 2

ID ADZ67016

AC ADZ67016 standard; peptide; 8 AA.

XX ADZ67016;

XX 30-JUN-2005 (first entry)

XX Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:12.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
 KW musculoskeletal disease; respiratory disease; lung tumor;  
 KW endocrine disease; gynecology and obstetrics; breast tumor;  
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

OS US2005084906-A1.

PN 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFLO/) DUFLOS A.

PA (HAEU/) HAEUW J.

PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

PI WPI; 2005-321968/33.

XX N-PSDB; ADZ67015.

DR Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

XX antibody or its functional fragment, being capable of binding human IGF-

PT IR and specifically inhibiting tyrosine kinase activity of receptor,

XX useful for treating cancer.

PT Claim 1; SEQ ID NO 12; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor

XX I receptor (IGF-IR) antibody (I) or its functional fragment, being

XX capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,  
 CC comprising a light or heavy chain having at least one complementary  
 CC determining region (CDR) consisting of one of two fully defined 16 amino  
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in  
 CC the preparation of a medicament intended for the prevention or treatment  
 CC of an illness connected with an overexpression and/or an abnormal  
 CC activation of the IGF-IR and/or EGFR, and/or connected with a  
 CC hyperactivation of the transduction pathway of the signal mediated by the  
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where  
 CC the administration of the medicament does not induce or only slightly  
 CC induces secondary effects connected with inhibition of the insulin  
 CC receptor. The antibody is useful for preparation of a medicament intended  
 CC to inhibit the transformation of normal cells into cells with tumoral  
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-  
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is  
 CC useful for preparation of a medicament intended to inhibit the growth  
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,  
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or  
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a  
 CC medicament intended for prevention or for the treatment of cancer, where  
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,  
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the  
 CC preparation of a medicament intended for the prevention or for the  
 CC treatment of psoriasis. (I) is useful in preparation of a medicament  
 CC intended for the specific targeting of a biologically active compound to  
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)  
 CC is useful for in vitro diagnosis of illnesses induced by an  
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor  
 CC starting from a biological sample in which the abnormal presence, of IGF-  
 CC IR and/or EGFR receptor is suspected, which involves contacting the  
 CC biological sample with (I), which is optionally labeled. The present  
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 9; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8

Db 1 YGRVFFDY 8

RESULT 3

AAR80018

ID AAR80018 standard; peptide; 8 AA.

XX AAR80018;

XX 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 24-APR-1996 (first entry)

XX Cytotoxic Epstein-Barr virus T-cell epitope.

DE Epitope; EBV; cytotoxic T cell; lymphocyte; vaccine; immunisation; CD8+.

XX Human herpesvirus 4.

OS WO9524925-A1.

XX 21-SEP-1995.

PD 16-MAR-1995; 95WO-AU000140.

XX 16-MAR-1994; 94AU-00004465.

XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX (UYME) UNIV MELBOURNE.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX (BIOT-) BIOTECH AUSTRALIA PTY LTD.



PA (CSLC-) CSL LTD.  
 XX Moss DJ, Burrows SR, Khanna R, Kerr BM, Burrows JM, Suhribier A;  
 XX WPI; 1995-336817/43.  
 XX New cytotoxic T-cell epitope(s) of Epstein Barr virus - useful in sub-  
 XX unit vaccines to induce cytotoxic T cells.  
 XX Claim 1; Page 15; 23pp; English.  
 XX PS  
 XX New cytotoxic T-cell epitopes of Epstein-Barr virus have been isolated  
 XX and purified (AAR80017-R80028). Variants of these epitopes have also been  
 XX identified (AAR80029-R80033). The epitopes are small, stable peptides  
 XX whose manufacture does not involve use of any infectious material. The  
 XX epitopes may be used as components of subunit vaccines to induce  
 XX cytotoxic T lymphocytes in a subject. The vaccines are partic. useful  
 XX against viral infections where CD8+ cytotoxic T lymphocytes are  
 XX protective. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 16-  
 XX OCT-2003 to standardise OS field)  
 XX SQ Sequence 8 AA;  
 Query Match 59.6%; Score 28; DB 2; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VFDDY 8  
 Db :||||  
 4 IFDDY 8  
 RESULT 4  
 ID AAR84899 standard; peptide; 8 AA.  
 XX AAR84899;  
 AC  
 XX 27-AUG-2003 (revised)  
 DT 25-APR-1996 (first entry)  
 XX Epstein-Barr virus derived cytotoxic T cell epitope.  
 DE  
 XX Cytotoxic T cell; epitope; vaccine; antigen; tetanus; toxoid; helper;  
 KW poliovirus; diphtheria.  
 XX Human herpesvirus 4.  
 OS  
 XX WO9524926-A1.  
 PN  
 XX 21-SEP-1995.  
 PD  
 XX 16-MAR-1995; 95WO-AU000141.  
 PF  
 XX 16-MAR-1994; 94AU-00004465.  
 PR  
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
 PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA (UYME ) UNIV MELBOURNE.  
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.  
 PA (CSLC-) CSL LTD.  
 XX Cox JC, Suhribier A, Elliott SL;  
 PI  
 XX WPI; 1995-336818/43.  
 DR  
 XX Compsn. for induction of cytotoxic T cells - comprising CTL epitope and  
 PT at least one antigen, in a water in oil formulation.  
 XX  
 XX Claim 6; Page 23; 35pp; English.  
 XX A water in oil compsn. comprising at least 1 antigen to which an

CC individual will mount an anamnestic response, and at least one cytotoxic  
 CC T cell (CTL) epitope can be used to induce CD8+ CTL cells in a vaccine,  
 CC where the CTL epitope is known. The antigen is a diphtheria toxoid, a  
 CC pertussis or poliovirus antigen, a helper epitope or esp. a tetanus  
 CC toxoid, and the CTL epitope is 1 of the Epstein-Barr virus derived  
 CC peptides AAR84898-910. (Updated on 27-AUG-2003 to correct OS field.)  
 XX SQ Sequence 8 AA;  
 Query Match 59.6%; Score 28; DB 2; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VFDDY 8  
 Db :||||  
 4 IFDDY 8  
 RESULT 5  
 ID AAW40865 standard; peptide; 8 AA.  
 XX AAW40865;  
 AC  
 XX 09-JUN-1998 (first entry)  
 DT  
 XX Cytotoxic Epstein-Barr T-cell epitope 38.  
 DE  
 XX Herpes simplex virus type 4; Epstein-Barr virus; EBV; cytotoxic;  
 KW T-cell epitope; nuclear antigen; human leukocyte antigen; HLA; vaccine;  
 KW tetanus toxoid; diphtheria toxoid; Bordetella pertussis;  
 KW poliovirus antigen.  
 XX Herpes simplex virus 4.  
 OS  
 XX WO9745444-A1.  
 PN  
 XX 04-DEC-1997.  
 PD  
 XX 23-MAY-1997; 97WO-AU000328.  
 PF  
 XX 24-MAY-1996; 96AU-00000073.  
 PR  
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
 PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA (UYME ) UNIV MELBOURNE.  
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.  
 PA (CSLC-) CSL LTD.  
 XX Khanna R, Kerr BM, Misko IS, Moss DJ, Burrows SR;  
 FI  
 XX WPI; 1998-032576/03.  
 DR  
 XX Cytotoxic Epstein-Barr virus T cell epitope - useful to prepare vaccine  
 XX to prevent and treat infection.  
 PT  
 XX Claim 3; Page 32; 41pp; English.  
 PS  
 XX This amino acid sequence is a cytotoxic Epstein-Barr virus (EBV) T-cell  
 XX epitope of the EBV nuclear antigen 3A (EBNA3A), which binds the human  
 XX leukocyte antigen acceptor 24 (HLA 24). It is used to prepare a vaccine  
 XX which may include the cytotoxic EBV T-cell epitope (AAW40828- AAW40846),  
 XX or a nucleic acid sequence encoding it. The vaccine produced comprises or  
 XX encode at least one antigen (AAW40847-W40876) to which the individual  
 XX will mount an anamnestic response, e.g. a tetanus toxoid, diphtheria  
 XX toxoid, Bordetella pertussis antigen, poliovirus antigen, purified  
 XX protein derivative, glycoprotein 350 protein, and/or helper epitope  
 XX SQ Sequence 8 AA;  
 Query Match 59.6%; Score 28; DB 2; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 2e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFPDY 8  
:||||  
4 IFFDY 8

Db

RESULT 6  
AAV10595  
ID AAV10595 standard; peptide; 8 AA.

XX  
AC AAV10595;  
XX  
DT 12-MAY-1999 (first entry)  
XX  
DE HLA Class I motif peptide SEQ ID NO:525.  
XX  
KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
immunisation; tumour; infectious disease; immunotherapy; cancer;  
KW malignant melanoma; viral disease; hepatitis; AIDS.  
XX  
OS Synthetic.  
OS Human herpesvirus 4.  
XX  
PN WO9902183-A2.  
XX  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014289.  
XX  
PR 10-JUL-1997; 97CA-02209815.  
PR 10-DEC-1997; 97US-00988320.  
XX  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
XX  
PI Kuendig TM, Simard JUL;  
XX  
DR WPI; 1999-120514/10.  
XX  
PT Inducing a cytotoxic T lymphocyte response - by maintaining a level of  
PT antigen in the lymphatic system of a mammal so as to provide a sustained  
PT CTL response, used to treat, e.g. AIDS.  
XX  
PS Disclosure; Page 49; 199pp; English.  
XX  
CC The present invention describes a method of inducing and/or sustaining an  
CC immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
CC method comprises: (a) delivering an antigen to the mammal at a level to  
CC induce an immunological CTL response in the mammal; and (b) maintaining  
CC the level of the antigen in the mammal's lymphatic system to maintain the  
CC immunologic CTL response. The method can be used for the delivery of e.g.  
CC a differentiation antigen, a tumour-specific multilineage antigen, an  
CC embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene  
CC antigen, or a viral antigen. They can be used for the treatment of  
CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
CC to the lymphatic system provides for potent CTL stimulation that takes  
CC place in the milieu of the lymphoid organ, and it sustains stimulation  
CC that is necessary to keep CTL active, cytotoxic and recirculating through  
CC the body. AAV10071 to AAV10639 represent examples of peptide antigens  
CC given in the present invention  
XX  
SQ Sequence 8 AA;

Query Match 59.6%; Score 28; DB 2; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFPDY 8  
:||||  
4 IFFDY 8

Db

RESULT 8  
ABG80278  
ID ABG80278 standard; peptide; 8 AA.

XX  
AC ABG80278;  
XX  
DT 29-AUG-2003 (revised)

RESULT 7  
AAV10107  
ID AAV10107 standard; peptide; 8 AA.

XX  
AC AAV10107;  
XX  
DT 12-MAY-1999 (first entry)  
XX  
DE T cell epitope/MHC ligand SEQ ID NO:37.  
XX  
KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
immunisation; tumour; infectious disease; immunotherapy; cancer;  
KW malignant melanoma; viral disease; hepatitis; AIDS.  
XX  
OS Synthetic.  
OS Human herpesvirus 4.  
XX  
PN WO9902183-A2.  
XX  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014289.  
XX  
PR 10-JUL-1997; 97CA-02209815.  
PR 10-DEC-1997; 97US-00988320.  
XX  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
XX  
PI Kuendig TM, Simard JUL;  
XX  
DR WPI; 1999-120514/10.  
XX  
PT Inducing a cytotoxic T lymphocyte response - by maintaining a level of  
PT antigen in the lymphatic system of a mammal so as to provide a sustained  
PT CTL response, used to treat, e.g. AIDS.  
XX  
PS Disclosure; Page 24; 199pp; English.  
XX  
CC The present invention describes a method of inducing and/or sustaining an  
CC immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
CC method comprises: (a) delivering an antigen to the mammal at a level to  
CC induce an immunological CTL response in the mammal; and (b) maintaining  
CC the level of the antigen in the mammal's lymphatic system to maintain the  
CC immunologic CTL response. The method can be used for the delivery of e.g.  
CC a differentiation antigen, a tumour-specific multilineage antigen, an  
CC embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene  
CC antigen, or a viral antigen. They can be used for the treatment of  
CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
CC to the lymphatic system provides for potent CTL stimulation that takes  
CC place in the milieu of the lymphoid organ, and it sustains stimulation  
CC that is necessary to keep CTL active, cytotoxic and recirculating through  
CC the body. AAV10071 to AAV10639 represent examples of peptide antigens  
CC given in the present invention  
XX  
SQ Sequence 8 AA;

Query Match 59.6%; Score 28; DB 2; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFPDY 8  
:||||  
4 IFFDY 8

Db

RESULT 8  
ABG80278  
ID ABG80278 standard; peptide; 8 AA.

XX  
AC ABG80278;  
XX  
DT 29-AUG-2003 (revised)

DT 15-NOV-2002 (first entry)  
 XX MHC class I molecule, viral epitope #526.  
 DE  
 XX Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 KW acquired immune deficiency syndrome; AIDS.  
 XX  
 OS Viruses.  
 XX WO200262368-A2.  
 XX 15-AUG-2002.  
 XX 22-JAN-2002; 2002WO-US002033.  
 XX 02-FEB-2001; 2001US-00776232.  
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.  
 XX Kundig TM, Simard JJJ;  
 XX WPI; 2002-657506/70.  
 XX Inducing or sustaining immunological cytotoxic T lymphocyte response in a  
 PT mammal, useful for treating a mammal with malignant tumor or infectious  
 PT disease, by directly administering an antigen to the lymphatic system of  
 PT the mammal.  
 XX  
 PS Disclosure; Page 42; 73pp; English.  
 XX The invention relates to a method of inducing and/or sustaining an  
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal  
 CC comprising administering directly to the lymphatic system of the mammal:  
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a  
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
 CC method is useful for inducing and/or sustaining CTL response in a mammal.  
 CC This is particularly useful for treating a mammal having a malignant  
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
 CC malaria, measles or tuberculosis), or in an animal having a  
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,  
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-  
 CC ABG80319 represent viral epitopes on major histocompatibility complex  
 CC (MHC) class I molecules, used in the method of the invention. (Updated on  
 CC 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 8 AA;  
 Query Match 59.6%; Score 28; DB 5; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VFFDY 8  
 Db :|||  
 4 IFFDY 8  
 RESULT 9  
 ABG79790  
 ID ABG79790 standard; peptide; 8 AA.  
 XX  
 AC ABG79790;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE MHC class I molecule, viral epitope #38.  
 KW Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;

KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 XX acquired immune deficiency syndrome; AIDS.  
 OS Cercopithecine herpesvirus 15.  
 XX WO200262368-A2.  
 XX 15-AUG-2002.  
 XX 22-JAN-2002; 2002WO-US002033.  
 XX 02-FEB-2001; 2001US-00776232.  
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.  
 XX Kundig TM, Simard JJJ;  
 XX WPI; 2002-657506/70.  
 XX Inducing or sustaining immunological cytotoxic T lymphocyte response in a  
 PT mammal, useful for treating a mammal with malignant tumor or infectious  
 PT disease, by directly administering an antigen to the lymphatic system of  
 PT the mammal.  
 XX  
 PS Disclosure; Page 18; 73pp; English.  
 XX The invention relates to a method of inducing and/or sustaining an  
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal  
 CC comprising administering directly to the lymphatic system of the mammal:  
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a  
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
 CC method is useful for inducing and/or sustaining CTL response in a mammal.  
 CC This is particularly useful for treating a mammal having a malignant  
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
 CC malaria, measles or tuberculosis), or in an animal having a  
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,  
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-  
 CC ABG80319 represent viral epitopes on major histocompatibility complex  
 CC (MHC) class I molecules, used in the method of the invention. (Updated on  
 CC 06-AUG-2003 to correct OS field)  
 XX  
 SQ Sequence 8 AA;  
 Query Match 59.6%; Score 28; DB 5; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VFFDY 8  
 Db :|||  
 4 IFFDY 8  
 RESULT 10  
 ADK68717  
 ID ADK68717 standard; peptide; 8 AA.  
 XX  
 AC ADK68717;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Epitope liberation-related peptide SeqID80.  
 KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;  
 KW prozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;  
 KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;  
 KW virus; bacterium; protozoan; fungus; housekeeping proteasome system.  
 XX  
 OS Human herpesvirus 4.  
 XX  
 PN US2003228634-A1.  
 XX



OS Human herpesvirus 4.  
OS Synthetic.  
XX WO2004014957-A1.  
XX 19-FEB-2004.  
XX 12-AUG-2003; 2003WO-AU001019.  
XX 12-AUG-2002; 2002US-0403328P.  
XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
XX Jackson D, Zeng W;  
XX WPI; 2004-238736/22.  
XX New lipopeptide comprising a polypeptide comprising an amino acid  
XX sequence of a T helper cell and cytotoxic T cell epitope, useful for  
XX preparing a composition for treating or preventing cancer, or hepatitis C  
XX virus or influenza virus.  
XX Disclosure; SEQ ID NO 117; 166pp; English.  
XX The present invention describes a lipopeptide comprising a polypeptide  
XX conjugated to one or more lipid moieties, where the polypeptide comprises  
XX an amino acid sequence that comprises: (a) the amino acid sequence of a T  
XX helper cell (Th) epitope and the amino acid sequence of a cytotoxic T  
XX cell (CTL) epitope, where the amino acid sequences are different; and (b)  
XX one or more internal lysine residues or internal lysine analogue residues  
XX for covalent attachment of each of the lipid moieties via the epsilon-  
XX amino group or terminal side-chain group of the lysine or lysine  
XX analogue. Each of the one or more lipid moieties is covalently attached  
XX to an epsilon-amino group of the one or more internal lysine residues or  
XX to a terminal side-chain group of the one or more internal lysine  
XX analogue residues. Also described: (1) producing a lipopeptide; (2) a  
XX composition comprising the lipopeptide and an excipient or diluent; (3)  
XX eliciting an immune response in a subject; (4) immunising a subject  
XX against influenza or hepatitis C virus or Listeria monocytogenes; (5) a  
XX vaccine against an influenza virus or hepatitis C virus or Listeria  
XX monocytogenes comprising the lipopeptides, where the CTL epitope is from  
XX an influenza virus or hepatitis C virus or Listeria monocytogenes protein  
XX; (6) treating or preventing cancer; and (7) a vaccine against cancer  
XX comprising the lipopeptide, where the CTL epitope is a tumour-specific  
XX CTL epitope. The lipopeptide has cytostatic and virucide activities, and  
XX can be used in vaccine. The lipopeptide is useful for preparing a  
XX composition for treating or preventing cancer, or hepatitis C virus or  
XX influenza virus. The present invention is used in the exemplification of  
XX the present invention.

Sequence 8 AA;  
Query Match 59.6%; Score 28; DB 8; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VFFDY 8  
Db :|||  
4 IFFDY 8

RESULT 13  
ADQ11023  
ID ADQ11023 standard; peptide; 8 AA.  
XX  
XX ADQ11023;  
XX  
XX 23-SEP-2004 (first entry)  
XX Cercopithecine herpesvirus 15 T-cell epitope seqid 589.  
XX immunostimulant; cytostatic; vaccine; tumour-associated antigen SSX-2;  
XX SSX-2 antigen; epitope cluster; MHC receptor peptide binding cleft;  
XX immunogenic composition; immune response; cancer; vaccine vector;  
XX epitope liberation; human leukocyte antigen; HLA A2-specific CTL;  
XX cytotoxic T lymphocyte; T-cell epitope.

KW immunogenic composition; immune response; cancer; vaccine vector;  
KW epitope liberation; human leukocyte antigen; HLA A2-specific CTL;  
KW cytotoxic T lymphocyte; T-cell epitope.  
XX Cercopithecine herpesvirus 15.  
XX US20041132088-A1.  
XX 08-JUL-2004.  
XX 10-FEB-2004; 2004US-00777053.  
XX 07-NOV-2001; 2001US-0336968P.  
XX 07-NOV-2002; 2002US-00292413.  
XX (SIMA/) SIMARD J J L.  
XX (DIAM/) DIAMOND D C.  
XX (QIUZ/) QIU Z.  
XX (LEIX/) LEI X.  
XX Simard J J L, Diamond DC, Qiu Z, Lei X;  
XX WPI; 2004-517003/49.  
XX Novel nucleic acid encoding tumor-associated antigen SSX-2, useful in  
XX inducing an immune response and in treating cancer.  
XX Disclosure; SEQ ID NO 588; 260pp; English.  
XX The invention describes an isolated nucleic acid (I) comprising a reading  
XX frame comprising a first sequence, where the first sequence encodes one  
XX or more segments of tumour-associated antigen SSX-2, which comprises a  
XX sequence of 188 amino acids (SEQ ID NO: 40), where the first segment  
XX does not encode the complete SSX-2 antigen, and where each segment  
XX comprises an epitope cluster, the cluster comprising or encoding at least  
XX two amino acid sequences having a known or predicted affinity for a same  
XX MHC receptor peptide binding cleft. Also described are: an isolated  
XX polypeptide comprising the amino acid sequence encoded in the reading  
XX frame; and an immunogenic composition comprising (I) or the polypeptide  
XX of (I). (I) is a nucleic acid encoding a tumour-associated antigen SSX-2  
XX comprising a fully defined sequence of 188 amino acids (SEQ ID NO: 40).  
XX The nucleic acid, the encoded antigen, and composition are useful in  
XX inducing an immune response and in treating cancer. Expression cassettes  
XX are used in vaccine vectors. This is the amino acid sequence of a T-cell  
XX epitope MHC ligand associated with methods, therapies and compositions  
XX described in the invention.

Sequence 8 AA;  
Query Match 59.6%; Score 28; DB 8; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VFFDY 8  
Db :|||  
4 IFFDY 8

RESULT 14  
ADQ10515  
ID ADQ10515 standard; peptide; 8 AA.  
XX  
XX ADQ10515;  
XX  
XX 23-SEP-2004 (first entry)  
XX Cercopithecine herpesvirus 15 T-cell epitope seqid 80.  
XX immunostimulant; cytostatic; vaccine; tumour-associated antigen SSX-2;  
XX SSX-2 antigen; epitope cluster; MHC receptor peptide binding cleft;  
XX immunogenic composition; immune response; cancer; vaccine vector;  
XX epitope liberation; human leukocyte antigen; HLA A2-specific CTL;  
XX cytotoxic T lymphocyte; T-cell epitope.

```

XX OS Cercopithecine herpesvirus 15.
XX PN US2004132088-A1.
XX PD 08-JUL-2004.
XX PF 10-FEB-2004; 2004US-00777053.
XX PR 07-NOV-2001; 2001US-0336968P.
XX PR 07-NOV-2002; 2002US-00292413.
XX PA (SIMA/) SIMARD J J L.
XX PA (DIAM/) DIAMOND D C.
XX PA (QIUZ/) QIU Z.
XX PA (LEIX/) LEI X.
XX PI Simard J J L, Diamond DC, Qiu Z, Lei X;
XX WPI; 2004-517003/49.
XX DR Novel nucleic acid encoding tumor-associated antigen SSX-2, useful in
XX PT inducing an immune response and in treating cancer.
XX PT Disclosure; SEQ ID NO 80; 260pp; English.
XX PS
XX CC The invention describes an isolated nucleic acid (I) comprising a reading
XX CC frame comprising a first sequence, where the first sequence encodes one
XX CC or more segments of tumor-associated antigen SSX-2, which comprises a
XX CC sequence of 188 amino acids (SEQ ID NO: 40), where the first sequence
XX CC does not encode the complete SSX-2 antigen, and where each segment
XX CC comprises an epitope cluster, the cluster comprising or encoding at least
XX CC two amino acid sequences having a known or predicted affinity for a same
XX CC MHC receptor peptide binding cleft. Also described are: an isolated
XX CC polypeptide comprising the amino acid sequence encoded in the reading
XX CC frame; and an immunogenic composition comprising (I) or the polypeptide
XX CC of (I). (I) is a nucleic acid encoding a tumour-associated antigen SSX-2
XX CC comprising a fully defined sequence of 188 amino acids (SEQ ID NO: 40).
XX CC The nucleic acid, the encoded antigen, and composition are useful in
XX CC inducing an immune response and in treating cancer. Expression cassettes
XX CC are used in vaccine vectors. This is the amino acid sequence of a T-cell
XX CC epitope MHC ligand associated with methods, therapies and compositions
XX CC described in the invention.
XX SQ Sequence 8 AA;
XX CC
Query Match 59.6%; Score 28; DB 8; Length 8;
Best Local Similarity 80.0%; Pred. No. 2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 VFFDY 8
Db 4 IFFDY 8
RESULT 15
ADS80995
ID ADS80995 standard; peptide; 8 AA.
XX ADS80995;
AC ADS80995;
XX
DT 30-DEC-2004 (first entry)
XX
DE Tumour-associated antigen epitope seqid 80.
XX
KW tumour-associated antigen; NY-ESO; epitope cluster;
KW major histocompatibility complex; MHC receptor peptide binding cleft;
KW immunogenic composition; vaccine; sarcoma; fibro sarcoma;
KW osteogenic sarcoma; breast cancer; ovarian cancer; prostate cancer;
KW chronic leukaemia; Hodgkin's disease; non-Hodgkin's disease;
KW multiple myeloma; Waldenstrom's macroglobulinaemia; epitope.
XX OS Cercopithecine herpesvirus 15.
XX PN US2004203051-A1.
XX PD 14-OCT-2004.
XX PF 30-APR-2004; 2004US-00837217.
XX PR 07-NOV-2001; 2001US-0336968P.
XX PR 07-NOV-2002; 2002US-00292413.
XX PA (SIMA/) SIMARD J J L.
XX PA (DIAM/) DIAMOND D C.
XX PA (QIUZ/) QIU Z.
XX PA (LEIX/) LEI X.
XX PI Simard J J L, Diamond DC, Qiu Z, Lei X;
XX WPI; 2004-746974/73.
XX DR Novel isolated nucleic acid comprising reading frame having first
XX PT sequence that encodes segments of tumor-associated antigen NY-ESO, useful
XX PT in designing recombinant vaccines against tumors such as fibro sarcoma,
XX PT or breast cancer.
XX PS Disclosure; SEQ ID NO 80; 259pp; English.
XX CC The invention describes an isolated nucleic acid (I) comprising a reading
XX CC frame comprising a first sequence, where the first sequence encodes one
XX CC or more segments of tumour-associated antigen NY-ESO having a fully
XX CC defined sequence of 180 amino acids (S1) as given in the specification,
XX CC where the first sequence does not encode the complete NY-ESO antigen, and
XX CC where each segment comprises an epitope cluster, the cluster comprising
XX CC or encoding at least two amino acid sequences having a known or predicted
XX CC affinity for a same major histocompatibility complex (MHC) receptor
XX CC peptide binding cleft. Also described are: an isolated polypeptide (II)
XX CC comprising the amino acid sequence encoded in the reading frame of (S1);
XX CC and an immunogenic composition comprising (I) or (II). The following are
XX CC disclosed: epitope clusters identified in the tumour-associated antigen
XX CC NY-ESO; expression cassettes for use in vaccine vectors; vectors
XX CC including house-keeping epitope; and activating T-cell using the vector.
XX CC (I) is useful in designing recombinant vaccines against tumours such as
XX CC human sarcoma, fibro sarcoma, osteogenic sarcoma, breast cancer, ovarian
XX CC cancer, prostate cancer, chronic leukaemia, Hodgkin's disease, non-
XX CC Hodgkin's disease, multiple myeloma, Waldenstrom's macroglobulinaemia, or
XX CC against cells infected with virus, bacteria, protozoa or fungi. (II)
XX CC enables to manufacture a recombinant vaccine economically and rapidly, by
XX CC a simple process. The vaccine is highly safe as it consists of only a
XX CC fragment of the antigen rather than the whole protein. This is the amino
XX CC acid sequence of a tumour-associated antigen epitope useful in the
XX CC methods, therapies and composition discussed in the invention.
XX SQ Sequence 8 AA;
XX CC
Query Match 59.6%; Score 28; DB 8; Length 8;
Best Local Similarity 80.0%; Pred. No. 2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 VFFDY 8
Db 4 IFFDY 8
Search completed: December 30, 2005, 15:51:30
Job time : 185 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:45:25 ; Search time 36 Seconds  
(without alignments)  
21.382 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 149

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.\*

1: Pirl.\*

2: Pirl.\*

3: Pirl.\*

4: Pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	31.9	8	2 PC4373	telomeric and tetra
2	14	29.8	8	2 PT0311	Ig heavy chain CRD
3	14	29.8	8	2 PT0030	inulinase (EC 3.2.
4	14	29.8	8	2 T13818	cytochrome oxidase
5	13	27.7	8	2 PQ0012	cholecystokinin -
6	13	27.7	8	2 A43001	cholecystokinin -
7	13	27.7	8	2 PH1618	Ig H chain V-D-J r
8	13	27.7	8	2 PQ0701	unidentified 6.5/3
9	13	27.7	8	2 JS0318	leucokinin VIII -
10	13	27.7	8	2 S68325	blood cell protein
11	12	25.5	8	2 B33099	158K exoantigen -
12	12	25.5	8	2 B47393	neuropeptide calla
13	11	23.4	8	2 PT0279	Ig heavy chain CRD
14	11	23.4	8	2 B27867	homeotic protein U
15	11	23.4	8	2 A61467	penalbumin - Adeli
16	11	23.4	8	2 A25836	L-serine ammonia-1
17	11	23.4	8	2 T48890	hypothetical prote
18	10	21.3	8	2 S66646	cardioacceleratory
19	9	19.1	8	2 PH1407	Ig heavy chain V r
20	9	19.1	8	2 S16324	hypothetical prote
21	9	19.1	8	2 PT0298	Ig heavy chain CRD
22	9	19.1	8	2 B45800	serum albumin - do
23	9	19.1	8	2 PH0803	T-cell receptor al
24	9	19.1	8	2 S66296	Na+-transporting A
25	9	19.1	8	2 S11078	glucose-6-phosphat
26	9	19.1	8	2 H41978	calliFMRamide 8 -
27	9	19.1	8	2 D47393	neuropeptide calla
28	9	19.1	8	2 S65381	cytochrome-c oxida
29	9	19.1	8	2 A59028	MHC class I histoc

#### ALIGNMENTS

##### RESULT 1

PC4373

telomeric and tetraplex DNA binding protein qTBP42 III - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 09-Jul-2004

C;Accession: PC4373

R;Sarig, G.; Weisman-Shomer, P.; Fry, M.

Biochem. Biophys. Res. Commun. 237, 617-623, 1997

A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CAI

A;Reference number: PC4371; MUID:97445086; PMID:9299414

A;Accession: PC4373

A;Molecule type: protein

A;Residues: 1-8 <SAR>

A;Cross-references: UNIPROT:Q7M032; UNIPARC:UPI000017CA04

C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

F;1-4/Domain: RNPI #status predicted <RNP>

Query Match 31.9%; Score 15; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFF 6

DB 2 FGFIIF 7

##### RESULT 2

PT0311

Ig heavy chain CRD3 region (clone 6-100) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0311

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0311

A;Molecule type: DNA

A;Residues: 1-8 <YAM>

A;Cross-references: UNIPARC:UPI000017C20F

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 29.8%; Score 14; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 YGRVFFDY 8

DB 4 YG----DY 7

30 8 17.0 8 2 A44960 neuropeptide Led-C  
31 8 17.0 8 2 A58620 adipokinetic hormo  
32 8 17.0 8 2 S11545 adipokinetic hormo  
33 8 17.0 8 2 S53110 adipokinetic hormo  
34 8 17.0 8 2 S10596 hypotrehalosemic  
35 8 17.0 8 2 S08995 adipokinetic hormo  
36 8 17.0 8 2 A49823 adipokinetic hormo  
37 8 17.0 8 2 A28004 adipokinetic hormo  
38 8 17.0 8 2 S15422 adipokinetic hormo  
39 8 17.0 8 2 A58641 ipgf protein - Shi  
40 8 17.0 8 2 S70727 dissimilatory sulf  
41 8 17.0 8 2 S63493 phosphatidylethano  
42 8 17.0 8 2 PN0043 T-cell receptor be  
43 8 17.0 8 2 PT0724 acylase - Kluyvera  
44 8 17.0 8 2 S19288 variant surface gl  
45 8 17.0 8 2 A21440

## RESULT 3

PT0030  
inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)  
N:Alternate names: inulase  
C:Species: Aspergillus ficuum  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C:Accession: PT0030  
R:Etalibi, M.; Baratti, J.C.  
Agric. Biol. Chem. 54, 61-68, 1990  
A:Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.  
A:Reference number: PT0030; MUID:90344234; PMID:1368526  
A:Accession: PT0030  
A:Molecule type: protein  
A:Residues: 1-8 <ETT>  
A:Cross-references: UNIPROT:Q7M4U4; UNIPARC:UPI00001783B3  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 29.8%; Score 14; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FDY 8  
|:|  
Db 1 FNY 3

## RESULT 4

T13818  
cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)  
C:Species: mitochondrion Myxine glutinosa (Atlantic hagfish)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13818  
R:Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A:Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI  
A:Reference number: Z17775; MUID:97398704; PMID:9254918  
A:Accession: T13818  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-8 <DEL>  
A:Cross-references: UNIPROT:O21079; UNIPARC:UPI000016D463; EMBL:Y09527; NID:g2340019; PI  
C:Genetics:  
A:Genome: mitochondrion  
A:Note: COI  
C:Keywords: mitochondrion

Query Match 29.8%; Score 14; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVFF 6  
|:|  
Db 5 RWFF 8

## RESULT 5

PQ0012  
cholecystokinin - southeastern quoll  
N:Alternate names: CCK  
C:Species: Dasyurus viverrinus (southeastern quoll)  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: PQ0012  
R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.  
Peptides 9, 429-431, 1988  
A:Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.  
A:Reference number: PQ0012; MUID:88234141; PMID:3375140  
A:Accession: PQ0012  
A:Molecule type: protein  
A:Residues: 1-8 <FAN>  
A:Cross-references: UNIPROT:P30369; UNIPARC:UPI000002CDD4  
C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein  
P:2/Binding site: sulfate (Tyr) (covalent) #status predicted

F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 27.7%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8  
|:|  
Db 1 DY 2

## RESULT 6

A43001  
cholecystokinin - tammar wallaby  
N:Alternate names: CCK  
C:Species: Macropus eugenii (tammar wallaby)  
C>Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 09-Jul-2004  
C:Accession: A43001; PQ0012  
R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.  
Peptides 9, 429-431, 1988  
A:Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.  
A:Reference number: PQ0012; MUID:88234141; PMID:3375140  
A:Accession: A43001  
A:Molecule type: protein  
A:Residues: 1-8 <FAN>  
A:Cross-references: UNIPROT:P30369; UNIPARC:UPI000002CDD4  
C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein  
P:2/Binding site: sulfate (Tyr) (covalent) #status predicted  
F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 27.7%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8  
|:|  
Db 1 DY 2

## RESULT 7

PH1618  
Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1618  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315387  
A:Accession: PH1618  
A:Molecule type: DNA  
A:Residues: 1-8 <LEV>  
A:Cross-references: UNIPARC:UPI000017C6A7  
A:Experimental source: Bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 27.7%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG 2  
|:|  
Db 6 YG 7

## RESULT 8

PQ0701  
unidentified 6.5/31K protein [imported] - rice (fragment)  
C:Species: Oryza sativa (rice)  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: PQ0701  
R:Komatsu, S.; Kajiwara, H.; Hirano, H.



Theor. Appl. Genet. 86, 935-942, 1993  
 A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension  
 A;Reference number: PQ0696

C;Accession: PQ0701

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <KOW>

A;Cross-references: UNIPROT:Q7M1U0; UNIPARC:UPI0000017B129

Query Match 27.7%; Score 13; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG 2

DB 1 YG 2

#### RESULT 9

JS0318

leucokinin VIII - Madeira cockroach

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C;Accession: JS0318

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 31-34, 1987

A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the first

A;Reference number: JS0317

A;Accession: JS0318

A;Molecule type: protein

A;Residues: 1-8 <HOL>

A;Cross-references: UNIPROT:P19990; UNIPARC:UPI000012E29F

C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act

C;Keywords: amidated carboxyl end; cephalomyotropic peptide

F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 27.7%; Score 13; DB 2; Length 8;

Best Local Similarity 28.6%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 GRVFFDY 8

DB 1 GADFYSW 7

#### RESULT 10

S68325

blood cell protein A8 - Ascidia ceratodes (fragment)

N;Alternate names: Abcp-A

C;Species: Ascidia ceratodes

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004

C;Accession: S68325

R;Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th

A;Reference number: S68325; MUID:96132650; PMID:8554314

A;Accession: S68325

A;Molecule type: protein

A;Residues: 1-8 <TAY>

A;Cross-references: UNIPROT:Q7M3L7; UNIPARC:UPI000017CA56

F;2,3,4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

Query Match 27.7%; Score 13; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8

DB 1 DY 2

#### RESULT 11

B33099

158K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: B33099

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: B33099

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <NIC>

A;Cross-references: UNIPARC:UPI000017B5DF

Query Match 25.5%; Score 12; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FD 7

DB 2 FD 3

#### RESULT 12

E47393

neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)

C;Species: Calliphora vomitoria

C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: E47393

R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.

Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993

A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen

A;Reference number: A47393; MUID:93211980; PMID:8460157

A;Accession: E47393

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <DUV>

A;Cross-references: UNIPROT:P41841; UNIPARC:UPI000002EAB5

A;Experimental source: whole flies

A;Note: sequence extracted from NCBI backbone (NCBI:P:128482)

Query Match 25.5%; Score 12; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 FDY 8

DB 4 YDF 6

#### RESULT 13

PT0279

Ig heavy chain CRD3 region (clone 4-91A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0279

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0279

A;Molecule type: DNA

A;Residues: 1-8 <YAM>

A;Cross-references: UNIPARC:UPI0000017C203

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 23.4%; Score 11; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GR 3

DB 5 GR 6

## RESULT 14

B27867  
homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment)  
C:Species: Drosophila melanogaster  
C>Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 09-Jul-2004  
C:Accession: B27867  
R:Saari, G.; Bienz, M.  
EMBO J. 6, 1775-1779, 1987  
A:Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.  
A:Reference number: A91072  
A:Accession: B27867  
A:Molecule type: mRNA  
A:Residues: 1-8 <SAA>  
A:Cross-references: UNIPROT:P83949; UNIPARC:UPI000016BDEE  
C:Genetics:  
A:Gene: FlyBase:Ubx  
A:Cross-references: FlyBase:FBgn0003944  
C:Keywords: DNA binding; nucleus; transcription regulation

Query Match 23.4%; Score 11; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 FFD 7  
:|:  
Db 4 YFE 6

## RESULT 15

A61467  
penalbumin - Adelie penguin (fragment)  
C:Species: Pygoscelis adeliae (Adelie penguin)  
C>Date: 07-Oct-1994 #sequence\_revision 04-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A61467  
R:Osuga, D.T.; Amlinari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, R.E.  
J. Protein Chem. 2, 43-62, 1983  
A:Title: Sulfhydryl proteins of penguin egg white: ovalbumin and penalbumin. Comparisons  
A:Reference number: A61467  
A:Accession: A61467  
A:Molecule type: protein  
A:Residues: 1-8 <OSU>  
A:Cross-references: UNIPROT:Q7L2I8; UNIPARC:UPI000017C04A  
C:Comment: Penalbumin is a major protein component of egg whites from penguins but not f  
C:Keywords: egg white; glycoprotein

Query Match 23.4%; Score 11; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVF 5  
:|:  
Db 1 GSIY 4

Search completed: December 30, 2005, 15:56:00  
Job time : 37 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 15:36:05 ; Search time 224 Seconds  
(without alignments)  
25.197 Million cell updates/sec

Title: US-10-735-916A-12  
Perfect score: 47  
Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 707

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	38.3	8	2	Q6EX60_9LAMI
2	17	36.2	8	2	Q4X617_PLACH
3	16	34.0	8	2	O13591_YEAST
4	15	31.9	8	2	Q56759_XANTHOBACTE
5	15	31.9	8	2	Q7M032_RAT
6	15	31.9	8	2	Q80H91_9PARA
7	14	29.8	8	2	Q7M4U4_ASPFII
8	14	29.8	8	2	Q40530_TOBAC
9	14	29.8	8	2	Q99NX9_HYDHY
10	14	29.8	8	2	Q9TD02_9SMEG
11	13	27.7	8	1	ALL16_CARMA
12	13	27.7	8	1	CKKN_DASVI
13	13	27.7	8	1	CKKN_MACEU
14	13	27.7	8	1	LCK8_LEUMA
15	13	27.7	8	2	Q35792_YEAST
16	13	27.7	8	2	Q6BC29_HUMAN
17	13	27.7	8	2	Q9UDZ4_HUMAN
18	13	27.7	8	2	Q9UMH9_HUMAN
19	13	27.7	8	2	Q7M317_9ASCI
20	13	27.7	8	2	Q5RLS1_PIG
21	13	27.7	8	2	Q7M1U0_ORYSA
22	13	27.7	8	2	Q6DQZ1_CLOBE
23	13	27.7	8	2	Q09258_SYNECHOCOCC
24	13	27.7	8	2	O85406_COXBU
25	13	27.7	8	2	Q5Y8D4_ONCMY
26	13	27.7	8	2	Q5YDW3_9PERC
27	13	27.7	8	2	Q68LFI1_MYRMO
28	13	27.7	8	2	Q68LGI3_9PASS
29	12	25.5	8	1	ALL5_CALVO
30	12	25.5	8	1	ALL5_CVDPO
31	12	25.5	8	1	ANGT2_BORJA

32	12	25.5	8	1	ORMY_ORCLI
33	12	25.5	8	2	O15899_BABOV
34	12	25.5	8	2	Q8MC18_QUIIN
35	12	25.5	8	2	Q8MC20_COMBRETUM
36	12	25.5	8	2	Q7X139_9STAP
37	12	25.5	8	2	Q7X145_STASA
38	12	25.5	8	2	Q9RQ49_9ENTR
39	12	25.5	8	2	Q9RQ57_9ENTR
40	12	25.5	8	2	O8JFN8_CHICK
41	11	23.4	8	2	Q6SE42_DROSI
42	11	23.4	8	2	Q9TWH6_9ANNE
43	11	23.4	8	2	Q28866_MEGNO
44	11	23.4	8	2	Q6R4Q8_BUBBU
45	11	23.4	8	2	Q9GWH3_LAGOB

ALIGNMENTS

RESULT 1  
Q6EX60\_9LAMI  
ID Q6EX60\_9LAMI PRELIMINARY; PRT; 8 AA.  
AC Q6EX60;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DB Ribosomal protein (fragment).  
GN Name: rps16;  
OS Isodon pharicus.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Isodon.  
OX NCBI\_TaxID=204134;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Willis F.,  
RA Powell M.P., Savolainen V.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ505344; CAD45467.1; -; Genomic\_DNA.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR Chloroplast; Ribosomal protein.  
FT NON TER 1 1  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 881 MW; 175059C732C87877 CRC64;

Query Match 38.3%; Score 18; DB 2; Length 8;  
Best Local Similarity 57.1%; Pred. No. 2.2e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	2	GRVFFDY	8
Db	2	GGVLFY	8

RESULT 2  
Q4X617\_PLACH  
ID Q4X617\_PLACH PRELIMINARY; PRT; 8 AA.  
AC Q4X617;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=PC405959.00.0;  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5825;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

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RA Quail M.A.; Ormond D.; Doggett J.; Trueman H.E.; Mendoza J.;
RA Bidwell S.L.; Rajandream M.A.; Carucci D.J.; Yates J.R.; Kafatos F.C.;
RA Janse C.J.; Barrell B.; Turner C.M.R.; Waters A.P.; Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RL transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: CAJ01009638; CAH87659.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 8 AA; 1098 MW; E24B4B5449D2D2C6 CRC64;

Query Match 36.2%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFFDY 8
Db | | |
2 VFFNY 6

RESULT 3
ID O13591_YEAST PRELIMINARY; PRT; 8 AA.
AC O13591;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF YNL337w (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Obermaier B.; Piravandi E.; Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA MIPS;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71612; CAA96271.2; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1005 MW; 5CA441B449C9C720 CRC64;

Query Match 34.0%; Score 16; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFFDY 8
Db | | |
2 LFFNH 6

RESULT 4
Q56759_XANAU PRELIMINARY; PRT; 8 AA.
ID Q56759;
AC Q56759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Halocid dehalogenase (Fragment).
GN Names-dhlB;
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC SFRATN=G310;
RX MEDLINE=95173113; PubMed=7868610;
RA Van der Ploeg J.; Willemse M.; van Hall G.; Janssen D.B.;

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RT "Adaptation of Xanthobacter autotrophicus G310 to bromoacetate due to
RT activation and mobilization of the haloacetate dehalogenase gene by
RT insertion element IS1247.";
RL J. Bacteriol. 177:1348-1356(1995).
DR EMBL; X84038; CAA58857.1; -; Genomic_DNA.
FT NON_TER 8
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;

Query Match 31.9%; Score 15; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFFD 7
Db | | |
5 VVFD 8

RESULT 5
Q7M032_RAT PRELIMINARY; PRT; 8 AA.
ID Q7M032;
AC Q7M032;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Telomeric and tetraplex DNA binding protein qTBP42 III
DE (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=97445086; PubMed=9299414; DOI=10.1006/bbrc.1997.7198;
RA Sarig G.; Weisman-Shomer P.; Fry M.;
RT "Telomeric and tetraplex DNA binding properties of qTBP42: A homologue
of the CARG box binding protein CBF-A.";
RL Biochem. Biophys. Res. Commun. 237:617-623(1997).
DR PIR; PC4373; PC4373.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 928 MW; 7839C72059C879C8 CRC64;

Query Match 31.9%; Score 15; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.2e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFF 6
Db | | |
2 FGFIIF 7

RESULT 6
Q80H91_9PARA PRELIMINARY; PRT; 8 AA.
ID Q80H91;
AC Q80H91;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HN/HNO (Fragment).
GN Name=HN/HNO;
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Avulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94175786; PubMed=8129624;
RA Collins M.S.; Strong I.; Alexander D.J.;
RT "Evaluation of the molecular basis of pathogenicity of the variant
Newcastle disease viruses termed 'pigeon PMV-1 viruses'.";
RL Arch. Virol. 134:403-411(1994).
DR EMBL; S69419; AAP19628.1; -; Genomic_DNA.

```

```
FT NON TER 1 1
SQ SEQUENCE 8 AA; 929 MW; 33D4087AA337205B CRC64;

Query Match
Best Local Similarity 31.9%; Score 15; DB 2; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GRV 4
Db |||
6 GRV 8

RESULT 7
Q7M4U4 ASPFI
ID Q7M4U4 ASPFI PRELIMINARY; PRT; 8 AA.
AC Q7M4U4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inulinase (EC 3.2.1.7) (Fragment).
OS Aspergillus ficum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurytiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5058;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90344234; PubMed=1368526;
RA Etalibi M., Baratti J.C.;
RT "Molecular and kinetic properties of Aspergillus ficum inulinases.";
RL Agric. Biol. Chem. 54:61-68(1990).
DR PIR: PT0030; PT0030.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 1102 MW; 9A1B4776DAB5449 CRC64;

Query Match
Best Local Similarity 29.8%; Score 14; DB 2; Length 8;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FDY 8
Db |||
1 FNY 3

RESULT 8
Q40530 TOBAC
ID Q40530 TOBAC PRELIMINARY; PRT; 8 AA.
AC Q40530;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE N.tabacum P20 with a leader peptide.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87089808; PubMed=3540612;
RA Herman L.M.F., Montagu M.C.V., Depicker A.G.;
RT "Isolation of tobacco DNA segments with plant promoter activity.";
RL Mol. Cell. Biol. 6:4486-4492(1986).
DR EMBL; M14685; AAA34090.1; -; Genomic DNA.
SQ SEQUENCE 8 AA; 1109 MW; E257205B19C9C6 CRC64;

Query Match
Best Local Similarity 29.8%; Score 14; DB 2; Length 8;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FPD 7
Db |||
3 FFE 5
```

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RESULT 9
Q99NX9 HYDHY
ID Q99NX9 HYDHY PRELIMINARY; PRT; 8 AA.
AC Q99NX9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Amyloid beta protein (Fragment).
GN Name=APP;
OS Hydrochoerus hydrochaeris (Capybara) (Carpincho).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Hydrochaeridae; Hydrochaeris.
OX NCBI_TaxID=10149;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011342; AAG47377.1; -; Genomic_DNA.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 1071 MW; 1356D686DB19C9C3 CRC64;

Query Match
Best Local Similarity 29.8%; Score 14; DB 2; Length 8;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FPD 7
Db |||
2 FFE 4

RESULT 10
Q9TD02 9SMEG
ID Q9TD02 9SMEG PRELIMINARY; PRT; 8 AA.
AC Q9TD02;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
OS Terranatos dolichopterus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Terranatos.
OX NCBI_TaxID=61836;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
RT (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective.";
RL Evolution 53:1200-1216(1999).
DR EMBL; AF092421; AAF03041.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
FT NON TER 8 8
FT NON TER 8 8
SQ SEQUENCE 8 AA; 1084 MW; F0C9D3640DD4056 CRC64;

Query Match
Best Local Similarity 29.8%; Score 14; DB 2; Length 8;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RVFF 6
Db |||
5 RWFF 8
```

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RESULT 11
ALL16_CARMA
ID ALL16_CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinus maenas-16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the allatostatin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC Anidation; Direct protein sequencing; Multigene family; Neuropeptide.
KW Leucine amide.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG 2
Db 6 YG 7

RESULT 12
CCKN_DASVI
ID CCKN_DASVI STANDARD; PRT; 8 AA.
AC P68125; P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cholecystokinin (CCK).
GN Name=CCK;
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus.
OX NCBI_TaxID=9279;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140; DOI=10.1016/0196-9781(88)90280-X;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -!- FUNCTION: This peptide hormone induces gall bladder contraction
CC and the release of pancreatic enzymes in the gut. Its function in
CC the brain is not clear.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A43001; A43001.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Anidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 2 2
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8
Db 1 DY 2

RESULT 13
CCKN_MACEU
ID CCKN_MACEU STANDARD; PRT; 8 AA.
AC P68126; P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cholecystokinin (CCK).
GN Name=CCK;
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140; DOI=10.1016/0196-9781(88)90280-X;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -!- FUNCTION: This peptide hormone induces gall bladder contraction
CC and the release of pancreatic enzymes in the gut. Its function in
CC the brain is not clear.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A43001; A43001.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Anidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 2 2
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8
Db 1 DY 2

RESULT 14
LCK8_LEUMA
ID LCK8_LEUMA STANDARD; PRT; 8 AA.

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CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

DR PIR; PQ0012; PQ0012.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KW Anidation; Direct protein sequencing; Hormone; Sulfation.  
 FT MOD\_RES 2 2  
 FT MOD\_RES 8 8  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8  
 Db 1 DY 2

#### RESULT 13

CCKN\_MACEU  
 ID CCKN\_MACEU STANDARD; PRT; 8 AA.

AC P68126; P30369;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Cholecystokinin (CCK).

GN Name=CCK;

OS Macropus eugenii (Tamar wallaby).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.

OX NCBI\_TaxID=9315;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=88234141; PubMed=3375140; DOI=10.1016/0196-9781(88)90280-X;

RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;

RT "Cholecystokinin octapeptide purified from brains of Australian

RT marsupials.";

RL Peptides 9:429-431(1988).

CC -!- FUNCTION: This peptide hormone induces gall bladder contraction

CC and the release of pancreatic enzymes in the gut. Its function in

CC the brain is not clear.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

CC

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC

CC PIR; A43001; A43001.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; 1.

KW Anidation; Direct protein sequencing; Hormone; Sulfation.

FT MOD\_RES 2 2

FT MOD\_RES 8 8

FT MOD\_RES 8 8

SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8  
 Db 1 DY 2

#### RESULT 14

LCK8\_LEUMA

ID LCK8\_LEUMA STANDARD; PRT; 8 AA.

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DY 8  
Db 3 DY 4Search completed: December 30, 2005, 15:55:19  
Job time : 226 secs

AC P19990;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Leucokinin-8 (Leucokinin VIII) (L-VIII).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RN PROTEIN SEQUENCE.  
RC TISSUE=Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure and synthesis of leucokinin VII and  
RT VIII: the final members of this new family of cephalomyotropic  
RT peptides isolated from head extracts of Leucophaea maderae.";  
RL Comp. Biochem. Physiol. 89C:31-34(1987).  
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile  
CC activity of cockroach prothorax (hindgut).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC PIR; JS0318; JS0318.  
DR Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD RES 8 Glycine amide.  
FT SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;  
Query Match 27.7%; Score 13; DB 1; Length 8;  
Best Local Similarity 28.6%; Pred. No. 2.2e+06;  
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 GRVFFDY 8  
Db 1 GADFYW 7

RESULT 15  
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ID Q35792 YEAST PRELIMINARY; PRT; 8 AA.  
AC Q35792;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Inside intron 3 (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=D273-10B;  
RX MEDLINE=81069885; PubMed=6254986;  
RA Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;  
RT "Assembly of the mitochondrial membrane system. Structure and  
RT nucleotide sequence of the gene coding for subunit 1 of yeast  
RT cytochrome oxidase.";  
RL J. Biol. Chem. 255:11927-11941(1980).  
RL EMBL; V00694; CAA24063.1; -; Genomic DNA.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 1025 MW; 084693345B5AA337 CRC64;  
Query Match 27.7%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:48:10 ; Search time 45 Seconds  
(without alignments)  
14.698 Million cell updates/sec

Title: US-10-735-916A-12  
Perfect score: 47  
Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 18170

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgm2\_6/ptodata/1/iaa/6 COMB.pap.\*  
3: /cgm2\_6/ptodata/1/iaa/H COMB.pap.\*  
4: /cgm2\_6/ptodata/1/iaa/PCTUS COMB.pap.\*  
5: /cgm2\_6/ptodata/1/iaa/RE COMB.pap.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				ALIGNMENTS	
Result No.	Score	Query Match	Length DB ID	Description	
1	28	59.6	8	1 US-08-704-655-13	Sequence 13, Application US/08704655
2	28	59.6	8	2 US-09-920-174-19	Patent No. 5869453
3	28	59.6	8	2 US-09-920-195A-19	GENERAL INFORMATION:
4	25	53.2	8	1 US-08-350-260A-423	APPLICANT: Moss, Denis J.
5	25	53.2	8	1 US-08-350-260A-486	APPLICANT: Burrows, Scott R.
6	25	53.2	8	2 US-09-104-337A-423	APPLICANT: Khanna, Rajiv
7	25	53.2	8	2 US-09-104-337A-486	APPLICANT: Kerr, Veberly M.
8	23	48.9	8	2 US-09-211-715-206	APPLICANT: Burrows, Jacqueline M.
9	22	46.8	8	1 US-08-350-260A-380	APPLICANT: Suhrbier, Andreas
10	22	46.8	8	1 US-08-350-260A-391	TITLE OF INVENTION: Cytotoxic T Cell Epitopes
11	22	46.8	8	1 US-08-350-260A-487	NUMBER OF SEQUENCES: 36
12	22	46.8	8	2 US-08-649-100-23	CORRESPONDENCE ADDRESSES:
13	22	46.8	8	2 US-08-649-100-39	ADDRESSEE: ARNOLD, WHITE & DURKEE
14	22	46.8	8	2 US-09-104-337A-391	STREET: P.O. Box 4433
15	22	46.8	8	2 US-09-104-337A-487	CITY: Houston
16	22	46.8	8	2 US-08-802-083-9	STATE: Texas
17	22	46.8	8	2 US-08-350-260A-471	COUNTRY: USA
18	21.5	45.7	8	1 US-08-350-260A-471	ZIP: 77210-4433
19	21.5	45.7	8	1 US-09-104-337A-471	COMPUTER READABLE FORM:
20	21	44.7	8	2 US-08-350-260A-463	MEDIUM TYPE: Floppy disk
21	21	44.7	8	2 US-09-104-337A-463	COMPUTER: IBM PC compatible
22	20	42.6	8	1 US-08-279-906A-6	OPERATING SYSTEM: PC-DOS/MS-DOS
23	20	42.6	8	1 US-08-279-906A-7	SOFTWARE: PatentIn Release #1.0, Version #1.30
24	20	42.6	8	1 US-08-279-906A-8	CURRENT APPLICATION DATA:
25	20	42.6	8	1 US-08-279-906A-9	APPLICATION NUMBER: US/08/704,655
26	20	42.6	8	1 US-08-713-254-4	FILING DATE: 13-SEP-1996
27	20	42.6	8	1 US-08-487-860-61	CLASSIFICATION: 514
					PRIOR APPLICATION DATA:
					APPLICATION NUMBER: PCT/AU95/00140
					FILING DATE: 16-MAR-1994
					ATTORNEY/AGENT INFORMATION:
					NAME: Highlander, Steven L.
					REGISTRATION NUMBER: 37,642
					REFERENCE/DOCKET NUMBER: FBRC002
					TELECOMMUNICATION INFORMATION:
					TELEPHONE: (512) 418-3000
					TELEFAX: (712) 789-2679
					INFORMATION FOR SEQ ID NO: 13:
					SEQUENCE CHARACTERISTICS:
					LENGTH: 8 amino acids
					TYPE: amino acid
					STRANDEDNESS:
					TOPOLOGY: linear
					US-08-704-655-13
					Query Match 59.6%; Score 28; DB 1; Length 8;
					Best Local Similarity 80.0%; Pred. No. 4.6e+05;
					Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      4 VFPDY 8
Db      4 IFPDY 8

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-920-174-19
; Sequence 19, Application US/09920174
; Patent No. 6699477
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, THOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FERC:008USC2
; CURRENT APPLICATION NUMBER: US/09/920,174
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/920,175
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-174-19
Query Match      59.6%; Score 28; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      4 IFPDY 8

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-920-195A-19
; Sequence 19, Application US/09920195A
; Patent No. 6703024
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, THOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FERC:008USC1
; CURRENT APPLICATION NUMBER: US/09/920,195A
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-195A-19
Query Match      59.6%; Score 28; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      4 IFPDY 8

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-08-350-260A-423
; Sequence 423, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-423
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Query Match 53.2%; Score 25; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVPFYD 8  
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 Db 3 RKYFDY 8

RESULT 5  
 US-08-350-260A-486  
 ; Sequence 486, Application US/08350260A  
 ; Patent No. 5962255  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Winter, Gregory Paul  
 ; APPLICANT: Griffiths, Andrew David  
 ; APPLICANT: Williams, Samuel Cameron  
 ; APPLICANT: Waterhouse, Peter  
 ; APPLICANT: Nissim, Ahuva  
 ; APPLICANT: Johnson, Kevin Stuart  
 ; APPLICANT: Smith, Andrew John Hammond  
 ; TITLE OF INVENTION: Methods for producing members of specific  
 ; TITLE OF INVENTION: binding pairs  
 ; NUMBER OF SEQUENCES: 602  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David W. Clough  
 ; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/350,260A  
 ; FILING DATE: 05-DEC-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9110549.4  
 ; FILING DATE: 15-MAY-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9206318.9  
 ; FILING DATE: 24-MAR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB91/01134  
 ; FILING DATE: 10-JUL-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB92/00883  
 ; FILING DATE: 15-MAY-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB93/00605  
 ; FILING DATE: 24-MAR-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/150,002  
 ; FILING DATE: 31-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/307,619  
 ; FILING DATE: 16-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Clough, David W  
 ; REGISTRATION NUMBER: 36,107  
 ; REFERENCE/DOCKET NUMBER: 28111/32372  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-474-6300  
 ; INFORMATION FOR SEQ ID NO: 486:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid

STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-350-260A-486

Query Match 53.2%; Score 25; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FFDY 8  
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 Db 5 FFDY 8

RESULT 6  
 US-09-104-337A-423  
 ; Sequence 423, Application US/09104337A  
 ; Patent No. 6492160  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Winter, Gregory Paul  
 ; APPLICANT: Griffiths, Andrew David  
 ; APPLICANT: Williams, Samuel Cameron  
 ; APPLICANT: Waterhouse, Peter  
 ; APPLICANT: Nissim, Ahuva  
 ; APPLICANT: Johnson, Kevin Stuart  
 ; APPLICANT: Smith, Andrew John Hammond  
 ; TITLE OF INVENTION: Methods for producing members of specific  
 ; TITLE OF INVENTION: binding pairs  
 ; NUMBER OF SEQUENCES: 600  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Audrey L. Bartnicki  
 ; STREET: Marshall, Gerstein & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/104,337A  
 ; FILING DATE: 25-Jun-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/350,260  
 ; FILING DATE: 05-DEC-1994  
 ; APPLICATION NUMBER: GB 9110549.4  
 ; FILING DATE: 15-MAY-1991  
 ; APPLICATION NUMBER: GB 9206318.9  
 ; FILING DATE: 24-MAR-1992  
 ; APPLICATION NUMBER: PCT/GB92/00883  
 ; FILING DATE: 15-MAY-1992  
 ; APPLICATION NUMBER: PCT/GB93/00605  
 ; FILING DATE: 24-MAR-1993  
 ; APPLICATION NUMBER: US 08/150,002  
 ; FILING DATE: 31-MAR-1994  
 ; APPLICATION NUMBER: US 08/307,619  
 ; FILING DATE: 16-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bartnicki, Audrey L.  
 ; REGISTRATION NUMBER: 40,499  
 ; REFERENCE/DOCKET NUMBER: 28111/32372A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-474-6300  
 ; INFORMATION FOR SEQ ID NO: 423:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 423:  
 US-09-104-337A-423

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Query Match      53.2%; Score 25; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RVFFDY 8
Db      3 RKYFDY 8

RESULT 7
US-09-104-337A-486
; Sequence 486, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 486:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 486:

US-09-104-337A-486

Query Match      53.2%; Score 25; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 FFYD 8
Db      5 FFYD 8

RESULT 8
US-09-211-715-206
; Sequence 206, Application US/09211715
; Patent No. 6759384
; GENERAL INFORMATION:
; APPLICANT: Al-Obeidi, Fahad
; Lebl, Michal
; APPLICANT: Ostrem, James A.
; APPLICANT: Safar, Pavel
; APPLICANT: Stierandova, Alena
; APPLICANT: Strop, Peter
; APPLICANT: Walser, Armin
; TITLE OF INVENTION: Factor Xa Inhibitors
; FILE REFERENCE: P-SE3243
; CURRENT APPLICATION NUMBER: US/09/211,715
; CURRENT FILING DATE: 1998-12-14
; EARLIER APPLICATION NUMBER: 08/233,054
; EARLIER FILING DATE: 1994-04-26
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 206
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (8)-
; OTHER INFORMATION: AMIDATION

US-09-211-715-206

Query Match      48.9%; Score 23; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
Db      1 YIRFFSDY 8

RESULT 9
US-08-350-260A-380
; Sequence 380, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 380:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-380

Query Match 46.8%; Score 22; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RVFFDY 8
Db 3 RTSFDY 8

RESULT 10
US-08-350-260A-391
; Sequence 391, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSES: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 391:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-391

Query Match 46.8%; Score 22; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 1 YKSLSFY 8

RESULT 11
US-08-350-260A-487
; Sequence 487, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSES: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
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COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/350,260A  
FILING DATE: 05-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9110549.4  
FILING DATE: 15-MAY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01134  
FILING DATE: 10-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00605  
FILING DATE: 24-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/150,002  
FILING DATE: 31-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/307,619  
FILING DATE: 16-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/32372  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 487:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-350-260A-487

Query Match 46.8%; Score 22; DB 1; Length 8;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FPDY 8  
Db 5 YFDY 8

RESULT 12  
US-08-649-100-23  
Sequence 23, Application US/08649100  
Patent No. 6114507  
GENERAL INFORMATION:  
APPLICANT: SHIRAKAWA, KAMON  
APPLICANT: MATSUE, TOMOKAZU  
APPLICANT: NAGATA, SHIGEKAZU  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA

COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/649,100  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1110-160  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLSCULE TYPE: peptide  
US-08-649-100-23

Query Match 46.8%; Score 22; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FPDY 8  
Db 5 YFDY 8

RESULT 13  
US-08-649-100-39  
Sequence 39, Application US/08649100  
Patent No. 6114507  
GENERAL INFORMATION:  
APPLICANT: SHIRAKAWA, KAMON  
APPLICANT: MATSUE, TOMOKAZU  
APPLICANT: NAGATA, SHIGEKAZU  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/649,100  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1110-160  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 39:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-100-39
Query Match 46.8%; Score 22; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFDY 8
Db 5 YFDY 8

RESULT 14
US-09-104-337A-380
; Sequence 380, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 380:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 391:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-104-337A-380
Query Match 46.8%; Score 22; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RVFFDY 8
Db 3 RTSFDY 8

RESULT 15
US-09-104-337A-391
; Sequence 391, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 391:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 391:
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US-09-104-337A-391

Query Match 46.8%; Score 22; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRVFPDY 8  
| : ||  
Db 1 YKSLSPDY 8

Search completed: December 30, 2005, 15:56:51  
Job time : 45 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:56:06 ; Search time 160 Seconds  
(without alignments)  
20.891 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47  
Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 31696

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	28	59.6	8	3	US-09-920-174-19
3	28	59.6	8	3	US-09-920-195A-19
4	28	59.6	8	4	US-10-777-053-80
5	28	59.6	8	4	US-10-777-053-588
6	28	59.6	8	4	US-10-837-217-80
7	28	59.6	8	4	US-10-837-217-588
8	28	59.6	8	5	US-10-752-380-19
9	26	55.3	8	3	US-09-880-748-3179
10	26	55.3	8	4	US-10-293-418-3179
11	25	53.2	8	4	US-10-094-699-55
12	25	53.2	8	4	US-10-160-232-17
13	25	53.2	8	4	US-10-044-896-12
14	25	53.2	8	4	US-10-117-937-401
15	25	53.2	8	5	US-10-855-013-31
16	25	53.2	8	6	US-11-067-064-401
17	25	53.2	8	6	US-11-067-159-401
18	24	51.1	8	4	US-10-447-257-8
19	24	51.1	8	5	US-10-496-628-8
20	24	51.1	8	5	US-10-996-316-195
21	22	46.8	8	3	US-09-972-656-62
22	22	46.8	8	3	US-09-802-083-9
23	22	46.8	8	4	US-10-209-372-37
24	22	46.8	8	4	US-10-165-732A-9
25	22	46.8	8	4	US-10-172-785-9
26	22	46.8	8	4	US-10-449-566-62
27	22	46.8	8	4	US-10-275-046-33

Sequence 472, App  
Sequence 601, App  
Sequence 473, App  
Sequence 9, Appli  
Sequence 9, Appli  
Sequence 41, Appli  
Sequence 523, App  
Sequence 131, App  
Sequence 581, App  
Sequence 582, App  
Sequence 582, App  
Sequence 582, App  
Sequence 60, Appl  
Sequence 581, App  
Sequence 16, Appli  
Sequence 3, Appli  
Sequence 308, App

#### ALIGNMENTS

##### RESULT 1

US-10-735-916A-12  
; Sequence 12, Application US/10735916A  
; Publication No. US20050084906A1  
; GENERAL INFORMATION:  
; APPLICANT: GOETSCH, Liliane  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: LEGER, Olivier  
; APPLICANT: DUFLOS, Alain  
; APPLICANT: BECK, Alain  
; APPLICANT: HAEUW, Jean-Francois  
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 017753-183  
; CURRENT APPLICATION NUMBER: US/10735,916A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: FR 03/08 538  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178  
; PRIOR FILING DATE: 2003-01-20  
; PRIOR APPLICATION NUMBER: FR 02/00 653  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/00 654  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: FR 02/05 753  
; PRIOR FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-735-916A-12

Query Match 100.0%; Score 47; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8  
| | | | | | | |  
DB 1 YGRVFFDY 8

##### RESULT 2

US-09-920-174-19  
; Sequence 19, Application US/09920174  
; Patent No. US20020150590A1  
; GENERAL INFORMATION:  
; APPLICANT: KHANNA, RAJIV  
; APPLICANT: KERR, BEVERLEY M.  
; APPLICANT: MISKO, IHOR S.

```
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FERC:008USC2
; CURRENT APPLICATION NUMBER: US/09/920,174
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/920,175
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-920-174-19

Query Match          59.6%; Score 28; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      :||||
        4 IPFDY 8

RESULT 3
US-09-920-195A-19
; Sequence 19, Application US/09920195A
; Publication No. US20030175300A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FERC:008USC1
; CURRENT APPLICATION NUMBER: US/09/920,195A
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-920-195A-19

Query Match          59.6%; Score 28; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      :||||
        4 IPFDY 8

RESULT 4
US-10-777-053-80
; Sequence 80, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
```

```
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-10-777-053-80

Query Match          59.6%; Score 28; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      :||||
        4 IPFDY 8

RESULT 5
US-10-777-053-588
; Sequence 588, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus (EBNA)
US-10-777-053-588

Query Match          59.6%; Score 28; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      :||||
        4 IPFDY 8

RESULT 6
US-10-837-217-80
; Sequence 80, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
```

## ; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN

; FILE REFERENCE: MANK 022C2  
; CURRENT APPLICATION NUMBER: US/10/837,217  
; CURRENT FILING DATE: 2004-04-30  
; PRIOR APPLICATION NUMBER: 10/292,413  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: 60/336,968  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 979  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 80  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Epstein-Barr Virus  
US-10-837-217-580

Query Match 59.6%; Score 28; DB 4; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFFDY 8  
:||||  
Db 4 IFFDY 8

## RESULT 7

US-10-837-217-588  
; Sequence 588, Application US/10837217  
; Publication No. US20040203051A1  
; GENERAL INFORMATION:  
; APPLICANT: Simard, John J. L.  
; APPLICANT: Diamond, David C.  
; APPLICANT: Qiu, Zhiyong  
; APPLICANT: Lei, Xiang-Dong  
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF  
; FILE REFERENCE: MANK 022C2  
; CURRENT APPLICATION NUMBER: US/10/837,217  
; CURRENT FILING DATE: 2004-04-30  
; PRIOR APPLICATION NUMBER: 10/292,413  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: 60/336,968  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 979  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 588  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Epstein-Barr Virus (EBNA)  
US-10-837-217-588

Query Match 59.6%; Score 28; DB 4; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFFDY 8  
:||||  
Db 4 IFFDY 8

## RESULT 8

US-10-752-380-19  
; Sequence 19, Application US/10752380  
; Publication No. US20050084498A1  
; GENERAL INFORMATION:  
; APPLICANT: KHANNA, RAJIV  
; APPLICANT: KERR, BEVERLEY M.  
; APPLICANT: MISKO, IHOR S.  
; APPLICANT: MOSS, DENIS J.  
; APPLICANT: BURROWS, SCOTT R.  
; TITLE OF INVENTION: EBV CTL EPITOPES  
; FILE REFERENCE: FBRC:008  
; CURRENT APPLICATION NUMBER: US/10/752,380

; CURRENT FILING DATE: 2004-01-06  
; PRIOR APPLICATION NUMBER: US/09/194,450  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-752-380-19

Query Match 59.6%; Score 28; DB 5; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFFDY 8  
:||||  
Db 4 IFFDY 8

## RESULT 9

US-09-880-748-3179  
; Sequence 3179, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3179  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-3179

Query Match 55.3%; Score 26; DB 3; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RVFFDY 8  
:||||  
Db 3 RYFFDY 8

## RESULT 10

US-10-293-418-3179  
; Sequence 3179, Application US/10293418  
; Publication No. US2003022396A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 3179  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-3179

Query Match 55.3%; Score 26; DB 4; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVFFDY 8  
| : |||  
Db 3 RYFFDY 8

RESULT 11  
US-10-094-699-56  
; Sequence 56, Application US/10094699  
; Publication No. US20030046714A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMARD, John, J.L.  
; APPLICANT: DIAMOND, David, C.  
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR  
; FILE REFERENCE: CTLIMM.015A  
; CURRENT APPLICATION NUMBER: US/10/094,699  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 60/274,063  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-094-699-56

Query Match 53.2%; Score 25; DB 4; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVF 5  
| : |||  
Db 4 YGKVP 8

RESULT 12  
US-10-160-232-17  
; Sequence 17, Application US/10160232  
; Publication No. US20030088075A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: ITO, MIKITO  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KAWADA, YOKO  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: SHIBUYA, MASABUMI  
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY  
; FILE REFERENCE: 249-107

; CURRENT APPLICATION NUMBER: US/10/160,232  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US/09/453,718  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: 09/315,051  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/119,014  
; PRIOR FILING DATE: 1998-07-20  
; PRIOR APPLICATION NUMBER: PCT/JP97/04259  
; PRIOR FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-160-232-17

Query Match 53.2%; Score 25; DB 4; Length 8;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GRVFFDY 8  
| : |||  
Db 2 GDYFFDY 8

RESULT 13  
US-10-044-896-12  
; Sequence 12, Application US/10044896  
; Publication No. US20030166228A1  
; GENERAL INFORMATION:  
; APPLICANT: Chuntharapai, Anan  
; APPLICANT: Kim, Jin K.  
; APPLICANT: Stewart, Timothy G.  
; TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES  
; FILE REFERENCE: GENENT.074A  
; CURRENT APPLICATION NUMBER: US/10/044,896  
; CURRENT FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: 60/270775  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-044-896-12

Query Match 53.2%; Score 25; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FFDY 8  
| : |||  
Db 5 FFDY 8

RESULT 14  
US-10-117-937-401  
; Sequence 401, Application US/10117937  
; Publication No. US20030220239A1  
; GENERAL INFORMATION:  
; APPLICANT: CTL IMMUNO THERAPIES CORP.  
; APPLICANT: SIMARD, John, J.L.  
; APPLICANT: DIAMOND, David, C.  
; APPLICANT: LIU, Liping  
; APPLICANT: XIE, Zhidong  
; TITLE OF INVENTION: EPITOPE SEQUENCES  
; FILE REFERENCE: CTLIMM.027A

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; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 401
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-401
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```
Query Match 53.2%; Score 25; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 YGRVP 5
Db 4 YGRVP 8
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RESULT 15
US-10-855-013-31
; Sequence 31, Application US/10855013
; Publication No. US20050025768A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc. et al.
; TITLE OF INVENTION: ANTIBODIES AGAINST MONOCYTE CHEMOTACTIC PROTEINS
; FILE REFERENCE: BGN-006PC
; CURRENT APPLICATION NUMBER: US/10/855.013
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/343391
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/383277
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/400469
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-855-013-31
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Query Match 53.2%; Score 25; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 5 FFDY 8
Db 5 FFDY 8
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Job time : 161 secs
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:55:26 ; Search time 12 Seconds  
(without alignments)

4.993 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 4100

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US03\_NEW\_PUB\_PEP.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	7	US-11-012-353-12
2	26	55.3	8	7	US-11-054-515-3179
3	25	53.2	8	7	US-11-073-347-56
4	25	53.2	8	7	US-11-096-046-23
5	22	46.8	8	7	US-11-152-747-37
6	22	46.8	8	7	US-11-127-677-112
7	19	40.4	8	7	US-11-016-706-76
8	19	40.4	8	7	US-11-016-706-77
9	19	40.4	8	7	US-11-054-515-3092
10	19	40.4	8	7	US-11-054-515-3111
11	19	40.4	8	7	US-11-054-515-3141
12	19	40.4	8	7	US-11-093-274-7
13	19	40.4	8	7	US-11-112-277-3
14	19	40.4	8	7	US-11-045-024-420
15	19	40.4	8	7	US-11-045-024-3592
16	19	40.4	8	7	US-11-045-024-3593
17	19	40.4	8	7	US-11-045-024-5075
18	19	40.4	8	7	US-11-045-024-5076
19	19	40.4	8	7	US-11-045-024-6906
20	19	40.4	8	7	US-11-045-024-8281
21	19	40.4	8	7	US-11-045-024-10742
22	19	40.4	8	7	US-11-045-024-10749
23	19	40.4	8	7	US-11-045-024-10751
24	19	40.4	8	7	US-11-045-024-12507
25	19	40.4	8	7	US-11-045-024-12512

#### ALIGNMENTS

##### RESULT 1

US-11-012-353-12

; Sequence 12, Application US/11012353

; Publication No. US20050249730A1

; GENERAL INFORMATION:

; APPLICANT: GOETSCH, LILIANE

; APPLICANT: CORVAIA, NATHALIE

; APPLICANT: DUFLOS, ALAIN

; APPLICANT: HAEUW, JEAN-FRANCOIS

; APPLICANT: LEGER, OLIVIER

; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-1 HYBRID

; FILE REFERENCE: 017753-198

; CURRENT APPLICATION NUMBER: US/11/012,353

; CURRENT FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 10/735,916

; PRIOR FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 0308538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR03/00178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 0205753

; PRIOR FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: FR 0200653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 0200654

; PRIOR FILING DATE: 2002-01-18

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 12

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-012-353-12

Query Match 100.0%; Score 47; DB 7; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8

Db 1 YGRVFFDY 8

##### RESULT 2

US-11-054-515-3179

; Sequence 3179, Application US/11054515

Sequence 12513, A  
Sequence 12862, A  
Sequence 83, Appl  
Sequence 89, Appl  
Sequence 96, Appl  
Sequence 116, App  
Sequence 125, App  
Sequence 128, App  
Sequence 33, Appl  
Sequence 11, Appl  
Sequence 2842, Ap  
Sequence 3481, Ap  
Sequence 3482, Ap  
Sequence 3483, Ap  
Sequence 10439, A  
Sequence 10447, A  
Sequence 10448, A  
Sequence 10449, A  
Sequence 12273, A  
Sequence 12281, A

26 19 40.4 8 7 US-11-045-024-12513  
27 19 40.4 8 7 US-11-045-024-12862  
28 19 40.4 8 7 US-11-127-677-83  
29 19 40.4 8 7 US-11-127-677-89  
30 19 40.4 8 7 US-11-127-677-96  
31 19 40.4 8 7 US-11-127-677-116  
32 19 40.4 8 7 US-11-127-677-125  
33 19 40.4 8 7 US-11-127-677-128  
34 18 38.3 8 6 US-10-997-066-33  
35 18 38.3 8 7 US-11-176-868-11  
36 18 38.3 8 7 US-11-054-515-2842  
37 18 38.3 8 7 US-11-045-024-3481  
38 18 38.3 8 7 US-11-045-024-3482  
39 18 38.3 8 7 US-11-045-024-3483  
40 18 38.3 8 7 US-11-045-024-10439  
41 18 38.3 8 7 US-11-045-024-10447  
42 18 38.3 8 7 US-11-045-024-10448  
43 18 38.3 8 7 US-11-045-024-10449  
44 18 38.3 8 7 US-11-045-024-12273  
45 18 38.3 8 7 US-11-045-024-12281

```
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3179
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3179

Query Match      55.3%; Score 26; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.4e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RVPFYD 8
        | :|||
Db      3 RYFYD 8

RESULT 3
US-11-073-347-56
; Sequence 56, Application US/11073347
; Publication No. US20050260234A1
; GENERAL INFORMATION:
; APPLICANT: SINARD, John J. L.
; TITLE OF INVENTION: DIAMOND, David C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: MANK 015C1
; CURRENT APPLICATION NUMBER: US/11/073,347
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/094,699
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-073-347-56

Query Match      53.2%; Score 25; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.4e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFD 5

; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3179
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3179

Query Match      53.3%; Score 26; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.4e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RVPFYD 8
        | :|||
Db      3 RYFYD 8

RESULT 4
US-11-096-046-23
; Sequence 23, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: NAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 23
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-23

Query Match      53.2%; Score 25; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.4e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GRVFYD 8
        | :|||
Db      2 GGFYFD 8

RESULT 5
US-11-152-747-37
; Sequence 37, Application US/11152747
; Publication No. US20050251881A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours, Inc.
; APPLICANT: Cheng, Qiong
; APPLICANT: Tao, Luan
; TITLE OF INVENTION: CAROTENOID KETOLASE GENE
; FILE REFERENCE: CL-1849 US NA
; CURRENT APPLICATION NUMBER: US/11/152,747
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Deinococcus radiodurans
US-11-152-747-37

Query Match      46.8%; Score 22; DB 7; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 YGRVFYD 8
        | :|||
Db      1 YGRFLDDW 8

RESULT 6
US-11-127-677-112
; Sequence 112, Application US/11127677
```



```
Publication No. US20050272107A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Rabbitts, Terence H
APPLICANT: Tanaka, Tomoyuki
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2462
CURRENT APPLICATION NUMBER: US/11/127,677
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: PCT/GB03/04942
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: GB 0226729.2
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn version 3.1
SEQ ID NO 112
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Derived protein sequence of intracellular Dab
US-11-127-677-112

Query Match      46.8%; Score 22; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.4e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RVFPDY 8
| | | |
Db 3 RLPFDY 8

RESULT 7
US-11-016-706-76
Sequence 76, Application US/11016706
Publication No. US20050244334A1
GENERAL INFORMATION:
APPLICANT: CASTILLO, GERARDO
APPLICANT: LAKE, THOMAS P.
APPLICANT: NGUYEN, BETH P.
APPLICANT: SANDERS, VIRGINIA J.
APPLICANT: SNOW, ALAN D.
TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
FILE REFERENCE: PROTEO.P03C13
CURRENT APPLICATION NUMBER: US/11/016,706
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 09/962,955
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/938,275
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 08/947,057
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 77
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
FEATURE:
NAME/KEY: MOD RES
LOCATION: (8)
OTHER INFORMATION: Tyr or not present
US-11-016-706-77

Query Match      40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGRVVF 6
| | | |
Db 1 HGRLVF 6

RESULT 9
US-11-054-515-3092
Sequence 3092, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
```

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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3092
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3092

Query Match          40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FDY 8
Db      6 FDY 8

RESULT 10
US-11-054-515-3111
; Sequence 3111, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,816
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3111
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3111

Query Match          40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FDY 8
Db      6 FDY 8

RESULT 11
US-11-054-515-3141
; Sequence 3141, Application US/11054515
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; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3141
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3141

Query Match          40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FDY 8
Db      6 FDY 8

RESULT 12
US-11-093-274-7
; Sequence 7, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-7

Query Match          40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YGRVF 5
```

```
Db      :|||
        2 WGRAP 6

RESULT 13
US-11-112-277-3
; Sequence 3, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONUGATES
; FILE REFERENCE: 50082003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: K5 Analogue
; NAME/KEY: MOD_RES
; LOCATION: 8
; OTHER INFORMATION: Xaa is Lys linked to MPA
US-11-112-277-3

Query Match      40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 RVFFDY 8
        |||
Db      2 RKLYDY 7

RESULT 14
US-11-045-024-420
; Sequence 420, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3592
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3592

Query Match      40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 VFFDY 8
        |||
Db      3 VFIEY 7

RESULT 15
US-11-045-024-3592
; Sequence 3592, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3592
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3592

Query Match      40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 VFFDY 8
        |||
Db      3 VFIEY 7
```

Search completed: December 30, 2005, 16:06:47  
Job time : 12 secs

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